Antimicrobial Resistance in thermotolerant *Campylobacter* from a Global Perspective: Insights from Phenotypic and Genomic Analyses

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2 Declaration of Authorship

I hereby declare that I alone am responsible for the content of my doctoral dissertation and that I have only used the sources or references cited in the dissertation.

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3 Summary

Campylobacter jejuni and *Campylobacter coli* are considered the primary causative agents of campylobacteriosis in humans, which has significant public health implications worldwide. In Europe, they account for by far the most cases of bacterial gastroenteritis. Particularly feared, though underestimated by the general population, are the long-term consequences of an infection that can occur in rare cases, such as Guillain-Barré syndrome, reactive arthritis, and irritable bowel syndrome. The excessive use of antibiotics in human and veterinary medicine has led to increasing resistance of these bacteria to antimicrobial agents, limiting treatment options. Consequently, the Centers for Disease Control and Prevention (CDC) classifies *Campylobacter*, especially due to its fluoroquinolone resistance, as a high-priority resistant bacterium and a serious public health threat.

This study aimed to compare the antibiotic resistances of *Campylobacter* isolates from different regions of the world to identify resistance determinants relevant to human medicine and imminent in Europe, which develop under high selection pressure and pose a challenge to global public health. Based on the results of this comparative study, a novel warning tool should be developed that can be used at the molecular level in routine monitoring programs.

The results of our comparative study showed differences in the extent of various resistances depending on the origin of the *Campylobacter* isolates. For example, the isolates from Georgia and Germany showed particularly high resistance to fluoroquinolones and tetracyclines. In contrast, resistance to aminoglycosides and macrolides was less common. The *Campylobacter* isolates from Vietnam, however, showed nearly complete resistance to fluoroquinolones and tetracyclines, and particularly the Vietnamese *C. coli* isolates exhibited very high resistance to aminoglycosides and macrolides. These high resistance rates in Vietnam are possibly

due to the extensive use of antibiotics in livestock farming.

Through the application of whole genome sequencing, phenotypic resistances could be linked to the presence of resistance determinants in the individual isolates. This showed that distinct *Campylobacter* populations carry different resistance markers and that Vietnamese *Campylobacter* isolates carried more resistance determinants.

We further investigated to what extent a data analysis based on whole genome data can be used to predict the expression of phenotypic resistance. We found that for the most part, the prediction matched the phenotypic resistance. However, discrepancies between the whole genome sequencing data and the phenotypic resistance profiles were also discovered. Problems included missing or inaccurately annotated AMR genes, detection issues due to multiple gene copies or variants, and novel mutations affecting gene functionality. Additionally, unknown resistance mechanisms were identified, such as resistance to ciprofloxacin without concurrent nalidixic acid resistance.

Another resistance mechanism leading to aminoglycoside resistance was deciphered and characterized in the course of this study. By applying natural transformation and analyzing genome data, a point mutation in the 16S rRNA of *Campylobacter* was identified, which was causally related to aminoglycoside resistance. We were able to show that the stability of the resistance depended on how many of the three copies of the 16S rRNA present in *Campylobacter* had undergone this mutation.

Using Nanopore long-read sequencing technology, combined with short-read data, hybrid assemblies were created for individual isolates. This allowed several isolates to be represented with their fully circular chromosome and, where applicable, additional epichromosomal units (e.g. plasmids). This provided insights into the localization and

mode of spread of the identified resistance determinants.

Ultimately, based on the whole genome data, it was possible to design new primers and probes and subsequently develop a pentaplex real-time PCR system. This was adequately tested and validated during this study and will be available in the future as a cost-effective alternative to whole genome sequencing to routinely monitor the most important resistance markers such as fluoroquinolone, macrolide, and tetracycline resistances.

In conclusion, the great genetic diversity and observed resistances in *Campylobacter*, especially in regions with intensive antibiotic use, stresses the necessity for continuous monitoring of circulating resistances in a global context to control and contain the spread of resistant strains. Furthermore, this work serves as an incentive to improve public health in the future and raise awareness about reducing antibiotic consumption.

4 Zusammenfassung

Campylobacter jejuni und *Campylobacter coli* gelten als die wichtigsten Erreger der Campylobacteriose beim Menschen, die weltweit große Auswirkungen auf die öffentliche Gesundheit hat. In Europa stellen sie mit Abstand die meisten Fälle von bakteriell verursachter Gastroenteritis dar. Besonders gefürchtet, aber dennoch von der allgemeinen Bevölkerung unterschätzt, sind die Langzeitfolgen einer Erkrankung, die in seltenen Fällen auftreten können, wie das Guillain-Barré-Syndrom, reaktive Arthritis und das Reizdarmsyndrom. Der übermäßige Einsatz von Antibiotika in der Human- und Veterinärmedizin hat zu einer zunehmenden Resistenz dieser Bakterien gegen antimikrobielle Mittel geführt, was die Behandlungsmöglichkeiten einschränkt. Entsprechend wird *Campylobacter* von der Centers for Disease Control and Prevention (CDC) insbesondere wegen seiner Fluorchinolon-Resistenz als resistentes Bakterium mit hoher Priorität und als ernsthafte Bedrohung der öffentlichen Gesundheit eingestuft.

Diese Studie hatte zum Ziel, die Antibiotikaresistenzen von *Campylobacter*-Isolaten aus unterschiedlichen Regionen der Welt zu vergleichen, um für die Humanmedizin relevante und für Europa bevorstehende Resistenzdeterminanten zu identifizieren, die sich unter hohem Selektionsdruck entwickeln und eine Herausforderung für die öffentliche Gesundheit darstellen. Aufgrund der Ergebnisse dieser vergleichenden Studie sollte ein neuartiges Warninstrument entwickelt werden, welches auf molekularer Ebene für den Einsatz in Routineüberwachungsprogrammen verwendet werden kann.

Die Ergebnisse unserer vergleichenden Studie zeigten Unterschiede in der Ausprägung verschiedener Resistenzen je nach Herkunftsort der *Campylobacter*-Isolate. So wiesen die Isolate in Georgien und Deutschland im besonderen hohe Resistenzen gegenüber Fluorchinolonen und Tetrazyklinen auf. Hingegen waren

Resistenzen gegenüber Aminoglykosiden und Makroliden eher seltener zu beobachten. Die *Campylobacter*-Isolate aus Vietnam zeigten indes eine nahezu vollständige Resistenz gegen Fluorochinolone und Tetrazykline und besonders die vietnamesischen *C. coli* Isolate wiesen sehr hohe Resistenz gegenüber Aminoglykosiden und Makroliden auf. Diese hohen Resistenzraten in Vietnam sind womöglich auf den umfangreichen Einsatz von Antibiotika in der Tierhaltung zurückzuführen.

Durch die Anwendung der Ganzgenomsequenzierung konnten die phänotypischen Resistenzen mit dem Vorhandensein von Resistenzdeterminanten in den einzelnen Isolaten verknüpft werden. Dies zeigte, das distinkte *Campylobacter* Populationen unterschiedliche Resistenzmarker tragen und das vietnamesische *Campylobacter* Isolate mehr Resistenzdeterminanten trugen.

Wir fragten uns ferner inwieweit eine Datenanalyse basierend auf Ganzgenomdaten zur Vorhersage einer Ausprägung einer phänotypischen Resistenz herangezogen werden kann. Wir stellten fest, dass zwar für einen Großteil die Vorhersage mit der phänotypischen Resistenz übereinstimmte. Jedoch konnten auch Diskrepanzen zwischen den Daten der Ganzgenomsequenzierung und den phänotypischen Resistenzprofilen aufgedeckt werden. Zu den Problemen gehörten fehlende oder ungenau annotierte AMR-Gene, Nachweisprobleme aufgrund von Mehrfachgenkopien oder -varianten sowie neuartige Mutationen, die die Genfunktionalität beeinflussten. Außerdem wurden auch unbekannte Resistenzmechanismen identifiziert, wie die Resistenz gegen Ciprofloxacin ohne gleichzeitige Nalidixinsäure-Resistenz.

Ein weiterer Resistenzmechanismus, der zu einer Aminoglykosidresistenz führt, konnte im Rahmen der Studie entschlüsselt und charakterisiert werden. Durch Anwendung der natürlichen Transformation und Analyse von Genomdaten, konnte eine Punktmutation in der 16S rRNA von *Campylobacter* ausfindig gemacht werden,

die im kausalen Zusammenhang mit der Aminoglykosidresistenz stand. Wir konnten zeigen, dass die Stabilität der Resistenz davon abhängt, wie viele der drei Kopien der in *Campylobacter* vorkommenden 16S rRNA dieser Mutation unterlaufen waren.

Durch Anwendung der Nanopore Long-Read Sequenzieruntechnik, konnten zusammen mit den Short-Read Daten für vereinzelte Isolate sogenannte Hybrid Assemblies erstellt werden. Somit konnten mehrere Isolate mit ihrem vollständig zirkulärem Chromosom und ggf. weiteren epichromosomalen Einheiten (Plasmide) dargestellt werden. Dies gab Aufschluss über die Lokalisierung und Art der Verbreitung der identifizierten Resistenzdeterminanten.

Anhand der Ganzgenomdaten war es letztendlich möglich neue Primer- und Sonden zu designen und daraufhin ein Pentaplex-Real-Time PCR System zu entwickeln. Dieses wurde während der Zeit der Studie hinreichend getestet und validiert und steht in Zukunft als kostengünstige Alternative zur Ganzgenomsequenzierung bereit um routinemäßig die wichtigsten Resistenzmarker wie Fluorochinolon-, Makrolid- und Tetrazyklin Resistenzen zu beobachten.

Schlussendlich lässt sich sagen, dass die große genetische Vielfalt und die beobachteten Resistenzen bei *Campylobacter*, insbesondere in Regionen mit starkem Antibiotikaeinsatz, die Notwendigkeit einer kontinuierlichen Überwachung zirkulierender Resistenzen im globalen Kontext unterstreichen, um die Ausbreitung resistenter Stämme zu kontrollieren und einzudämmen. Ferner stellt diese Arbeit einen Anreiz dar, zukünftig die öffentliche Gesundheit zu verbessern und das Bewusstsein im Sinne der Antibiotikaverbrauchsmengenreduzierung zu schärfen.

5 Introduction

5.1 The Genus *Campylobacter* spp.

The bacteria of the genus *Campylobacter* were probably first identified in 1886. At this time the German-Austrian pediatrician Theodor Escherich observed spiral-shaped bacteria under the microscope, but was unable to cultivate them (1). In 1913 a *Vibrio*-like organism was isolated from aborted fetuses and subsequently named "*Vibrio fetus*" (2). Fifty years later, in 1963, Sebald and Véron introduced the name "*Campylobacter*" to the genus, attributing it to the bacteria's distinctive shape and specific growth preferences, while also highlighting biological differences from *Vibrio* species (3). The name *Campylobacter* originates from the Greek words "campylo," meaning "curved," and "bacter," which translates to "rod." Yet, it wasn't until the 1970s that they were successfully isolated from stool samples of humans with acute enteritis, a significant achievement given the challenges associated with cultivating these bacteria under known conditions due to their specific growth requirements (4-6). *Campylobacter* species commonly exhibit a helical morphology, are classified as Gram-negative, and have a microaerobic metabolism (7). To date, the Genus *Campylobacter* comprises 48 species and 13 subspecies (8), of which *Campylobacter jejuni* and *Campylobacter coli* play the most important role for public health as they are the two primary agents in *Campylobacter* associated gastroenteritis (9). Nonetheless, several other species, such as *C. upsaliensis*, *C. hyointestinalis*, and *C. lari*, can also cause infections in humans (10, 11). They are highly motile due to their flagella, which are situated at the polar ends of the bacterium (12). Unlike other pathogenic bacteria they are very susceptible to various environmental conditions such as desiccation (13), osmotic stress (14), oxidative stress (15), and low pH (16).

5.2 Campylobacteriosis as zoonotic disease

5.2.1 Prevalence

Thermotolerant *Campylobacter* have been recognized as the leading cause of gastroenteritis worldwide and rank among the most prevalent human enteric pathogens in both developed and developing countries (9, 17-20). In 2022, Campylobacteriosis surpassed 137,000 reported cases EU-wide, which is more than twice the reported number of *Salmonella* infections (65,208) (21). Thus, *Campylobacter* spp. remains the leading cause of bacterial gastroenteritis in the European Union. However, the true incidence is likely even higher. For instance, Havelaar and colleagues suggest it could be as much as 47 times greater than what is reported by EU member states (22). However, they also note that asymptomatic cases may not always be consistently classified, and there are differences between countries in reporting practices, which can affect the comparability of the data.

5.2.2 Clinical presentation, health burden, and economic impact

Campylobacteriosis is characterized by symptoms such as watery and/or bloody diarrhea, abdominal pain, fever, and nausea but can also only show mild symptoms (23, 24). While the illness is typically self-limiting, it can have severe outcomes. A study suggested, that individuals infected with ciprofloxacin-resistant *Campylobacter* experienced prolonged diarrhea compared to those with ciprofloxacin-susceptible *Campylobacter* infection, while the reason for this is still unclear (25). Particularly concerning are the potential long-term autoimmune sequelae, such as Guillain-Barré syndrome, reactive arthritis, and irritable bowel syndrome (26, 27). These autoimmune diseases contribute to a considerable public health burden, often underestimated by the general population. Hence, the Foodborne Disease Burden Epidemiology

Reference Group (FERG) of the WHO published an estimation of the global *Campylobacter* disease burden. In 2010, a total of 600 million cases of foodborne illnesses were attributed to thirty-one distinct hazards, with *Campylobacter* estimated to account for 96 million of these cases. Among these *Campylobacter* cases, approximately 21,000 deaths and over 2.1 million Disability Adjusted Life Years (DALYs) were recorded, primarily associated with Guillain-Barré Syndrome, as data on other long-term sequelae was limited. DALYs are a measure of overall disease burden, expressed as the total number of years lost due to illness, disability, or premature death. Thus, globally, *Campylobacter* ranked sixth among the thirty-one hazards associated with foodborne illnesses with respect to the amount of DALYs per 100,000 population (28).

In the United States, the estimated annual cost of illness is approximately 1.9 billion US dollars, with over half of this (56%; 1.1 billion US dollars) attributed to Guillain-Barré syndrome (29), although only 0.07% of acute cases develop this long-term sequelae (26). Based on data from 2017, Schorling et al. estimated the total cost of *Campylobacter* enteritis in Germany to be 95.2 million Euros. Sequelae also contributed notably to these costs, comprising approximately 30%. Here, chronic inflammatory bowel disease substantially contributed to the calculated costs (30). In addition to healthcare expenses, illness and mortality result in additional non-healthcare costs, such as productivity losses (31, 32).

5.2.3 Transmission routes and risk factors

In high-income countries, the majority of *Campylobacter* spp. infections are caused by consuming undercooked contaminated animal derived food or by cross-contamination of ready-to-eat food by contaminated meat. Fresh meat from poultry, notably chicken, is considered the primary source of human infections associated with

the pathogen (33, 34). Animals colonized asymptomatically serve as carriers, shedding bacteria into the environment and becoming a potential source of infection for both uncolonized animals and susceptible humans (35-37). Transmission from living animals can occur through direct contact or indirectly via environments contaminated with feces (38). Apart from these transmission routes, *Campylobacter* infections are also commonly associated with the consumption of raw milk (21, 34, 39). According to a meta-analysis, the primary risk factor for campylobacteriosis is international travel, followed by eating undercooked chicken, environmental exposure, and direct contact with farm animals (40).

5.2.4 Diagnosis and treatment

The diagnosis of *Campylobacter* in stool samples can be conducted through conventional culture methods (27, 41-43) or assessed culture-independently, e.g. using enzymatic immunoassays (EIA) (44) or polymerase chain reaction (PCR) (45). Recently, culture-independent methods are replacing traditional culture techniques (46). Nevertheless, cultural evidence is important in order to enable antimicrobial resistance testing and whole-genome sequencing if necessary.

The World Health Organization (WHO) recommends oral rehydration as the first-line treatment to replace water, electrolytes, and nutrient deficiencies caused by diarrhea (47). To further support the reduction of dehydration, ancillary drugs such as antiemetics (48) or the antimotility drug loperamide (49) may be utilized as adjuncts in diarrhea treatment. Since 2017, healthcare professionals in the US have been advised to use azithromycin, a macrolide, as the preferred antimicrobial for treating campylobacteriosis, and ciprofloxacin, a fluoroquinolone, as an alternative option (27). In the US, the prevalence of oral antibiotic prescriptions shows that macrolide and fluoroquinolone treatments range from 35% to 37% in patients with and without

post infection irritable bowel syndrome, respectively, with combinations of both prescribed 12% and 13% of the time (50). In a case-control study performed from 2011 to 2014 in Germany, 31% of the patients reported that they were treated with antibiotics, mostly with ciprofloxacin and erythromycin (51). Meanwhile, Schorling et al., based on data gathered in Germany over one year from a large health insurance, found that 8.7% of patients diagnosed with severe campylobacteriosis and 13.1% of those with moderate cases received antibiotics (30). A study from 2011 conducted in Georgia (Caucasus) found that 45% of Georgian health care practitioners' use antimicrobials in the case of diarrheal disease, of which 65% used antibiotics only in case of presence of blood in stool (52). In China, children that suffer from severe or prolonged campylobacteriosis receive antibiotic treatment with azithromycin or erythromycin as preferred antimicrobials (53).

5.3 Antimicrobial resistance in *Campylobacter* spp.

The discovery of antibiotics in the early 20th century revolutionized the treatment of bacterial infections, allowing for the effective control and cure of various diseases that were once life-threatening, thus extending the average human lifespan by approximately 23 years since their introduction (54). Initially, antibiotic resistance was rare, but over time, the prevalence of resistant strains increased rapidly. Organisms, particularly those that developed resistance to multiple, unrelated antibiotics, had a considerable impact on human health, as antibiotic treatment was no longer effective for the first time (55). Today, antibiotic resistant bacteria are a major threat to human health globally (56). Notably, *Campylobacter* has been identified as a serious threat by the Centers for Disease Control and Prevention (CDC) (57) and is classified as a high-priority antibiotic-resistant pathogen by the WHO (58).

5.3.1 Antimicrobial resistance mechanisms in *Campylobacter* spp.

Phenotypic antimicrobial resistance in *Campylobacter* is driven by various molecular mechanisms such as target site modification by point mutations or modifying enzymes, enzymatic inactivation of the antimicrobial, and efflux pumps. Antimicrobial resistance may complicate the treatment of infections, particularly with commonly used antibiotics like quinolones. Understanding these resistance mechanisms is crucial for developing effective strategies to combat *Campylobacter* infections and resistance spread.

5.3.1.1 Macrolide resistance

Macrolide antibiotics are a class of antibiotics that include erythromycin, azithromycin, and clarithromycin. These antibiotics bind to the large subunit of the ribosome, specifically the 50S subunit, at the peptidyl transferase center (59).

Campylobacter spp. can develop resistance to macrolide antibiotics by point mutations in their 23S rRNA genes. Mutations at positions 2074 or 2075, such as A2075G, A2074G, A2074C, and A2074T, are described, which can lead to high-level resistance to erythromycin when present in all three copies of the gene (60-62). There have also been isolates identified with fewer than three copies of the altered 23S rRNA gene, yet they exhibit similar minimum inhibitory concentration (MIC) values to those harboring mutations in all three copies (63). One *C. jejuni* isolate with even two different mutations on all three 23S rRNA gene copies was detected by Real-time PCR using a melting curve analysis (64). The A2075G mutation is the predominant alteration found in isolates from food animals (65-67). 23S rRNA mutations associated with macrolide resistance have been shown to be transferable via natural transformation and were, apart from one exception of seven strains, stable upon subculturing in absence of selection pressure (63). The point mutation A2075G resulted in bacterial fitness loss for colonization of *C. jejuni* in the chicken host, as evidenced by pairwise *in vivo*

competition tests with mutated resistant and isogenic susceptible strains (68). Meanwhile, Zeitouni et al. found that when mono-inoculated or co-inoculated into chickens, macrolide susceptible *C. jejuni* outcompeted the macrolide resistant population. However, a spontaneous mutant that evolved in vivo showed a colonization capacity similar to the susceptible strain. In contrast, macrolide susceptible and resistant *C. coli* displayed similar levels of colonization in chickens, both in separated inoculations and during competitive assays (69).

Another target site modification mechanism is the methylation of binding sites of the macrolide antibiotic by rRNA methyltransferases. The genes encoding these enzymes were described in 1995 in *Campylobacter rectus* from patients with periodontitis (70). These adenine-specific N-methyltransferases are encoded by the *erm* gene class (erythromycin ribosome methylation). They utilize S-adenosylmethionine (SAM) to methylate a single adenine residue in the 23S rRNA gene, specifically targeting A2058 in *E. coli* numbering. This methylation results in the formation of either N6-mono- or dimethyladenine (71). *Campylobacter* spp. mainly harbors the *erm*(B) gene, which has already been identified in isolates from different continents such as Africa (72), Australia (73), Asia (67, 74, 75), Europe (76, 77) and North America (78). It was described first in a *C. coli* strain isolated from swine in China (79) and probably derived from gram-positive bacteria (80).

5.3.1.2 Quinolone resistance

Quinolones have been utilized since the 1960s, starting with the clinical application of nalidixic acid as the initial agent. The incorporation of a fluorine molecule at position 6 marked a major advancement in inhibiting bacterial growth, exhibiting minimum inhibitory concentrations 100 times greater compared to those observed with nalidixic acid (81). Today fluoroquinolones are frequently used in human (82, 83) and veterinary medicine (84). Fluoroquinolones (e.g. ciprofloxacin, enrofloxacin) target bacterial DNA

synthesis through inhibition of two enzymes crucial for DNA replication: DNA gyrase, formed by GyrA and GyrB, which introduces negative supercoils into DNA, and topoisomerase IV, consisting of ParC and ParE, responsible for decatenating DNA molecules and resolving DNA entanglements (85). In *Campylobacter*, however, the ParC/E appear to be absent, leaving DNA gyrase as the sole target for fluoroquinolones (86). Thus, resistance to fluoroquinolones mainly arises from amino acid substitutions within the quinolone resistance-determining region (QRDR), specifically due to mutations in the *gyrA* gene (87). The most frequent mutation associated with fluoroquinolone resistance is the T86I mutation (66, 67, 88-90). Additionally, other mutations have been identified, such as T86V (67), T86K (91), D90N (91), D90Y (92), and T86A (92), although the latter only confers low-level resistance to ciprofloxacin (2 mg/L). *In vivo* studies on the fitness cost of the T86I mutation highlighted an even increased bacterial fitness for some *C. jejuni* strains, as they were able to outcompete their susceptible counterparts (93). Similarly, observations of the growth kinetics of susceptible and resistant isogenic *C. jejuni* in competitive *in vitro* experiments indicated that fluoroquinolone-resistant strains might exhibited a small but significant growth advantage over the fluoroquinolone-susceptible strains (94). Zeitouni and Kempf found that fluoroquinolone resistance in *Campylobacter* strains incurs fitness costs *in vitro*, *in vivo*, and on food matrices (95). *In vitro* experiments revealed general fitness costs associated with fluoroquinolone resistance, while in vivo studies using chicken models showed that fluoroquinolone-resistant strains were outcompeted by susceptible strains during competitive colonization. Additionally, on food matrices such as chicken skin, the acquisition of fluoroquinolone resistance led to the rapid disappearance of resistant strains, indicating reduced survival in competitive scenarios.

5.3.1.3 Aminoglycoside resistance

Aminoglycosides are derived from the bacteria *Actinomycetes* and function by inhibiting protein synthesis (96). An ATP-dependent transport mechanism is used by aerobic bacteria to import aminoglycosides into the cell. Once inside, these agents specifically attach to the A-site decoding area of the 16S rRNA (97). Streptomycin, introduced in 1944, was the first aminoglycoside utilized as an antibiotic. Throughout the years, several additional antibiotics belonging to this class have either been isolated from bacteria (such as gentamicin, kanamycin, and tobramycin) or created through semi-synthetic methods (like amikacin) (96).

The mechanism of action of aminoglycosides relies on their chemical structure. While gentamicin, kanamycin, and tobramycin have a 2-deoxystreptamine (2-DOS) core structure in common, streptomycin exhibits a streptidine moiety, leading to different binding patterns. The 2-DOS aminoglycosides directly interact with the ribosomal RNA, specifically targeting the aminoacyl-(A) tRNA decoding site situated in the helix 44, resulting in translational misreading. In contrast, streptomycin additionally binds to helices from all four different domains and also interacts with the ribosomal protein S12, resulting in a different mode of action (98).

In *Campylobacter* spp., resistance to aminoglycosides is primarily correlated with the presence of genes encoding enzymes that alter the chemical structure of the aminoglycosides (99). These enzymes are thought to convey either acetylation of an amino group (*N*-Acetyltransferases, AAC), adenylation of a hydroxyl group (*O*-Adenyltransferases, ANT), or phosphorylation of a hydroxyl group (*O*-Phosphotransferases, APH) of the target aminoglycoside (100). Gentamicin, kanamycin, and tobramycin resistance is correlated with the presence of aminoglycoside 2''-phosphotransferase genes (*aph(2'')*) (100), of which several distinct variants have been identified in *Campylobacter* to date (101-104). Furthermore,

bifunctional enzyme encoding genes like *aac(6')-Ie/aph(2")-Ia* and *aac(6')-Ie/aph(2")-If* may also play a pivotal role in resistance to these substances (67, 104). Kanamycin resistance was suggested to additionally be conferred by 3'-phosphotransferase genes (*aph(3')*) such as *aph(3')-IIIa* (105) and *aph(3')-VIIa* (106). Meanwhile, streptomycin resistance in *Campylobacter* is associated with the occurrence of 6-Adenyltransferase genes (*ant(6)*), of which *ant(6')-Ia* (also named *aadE*) is the most frequently encountered gene (88, 90, 107). Additionally, the streptomycin resistance genes *ant(6')-Ib* (88) and a *C. coli* specific version of *aadE*, designated *aadE-Cc* (65, 90), have also been identified in *Campylobacter*. Besides the inactivation of streptomycin by enzymes, mutations in the ribosomal protein S12 (encoded by the *rpsL* gene) can confer resistance, with the point mutations K43R and K88R being identified in *Campylobacter* (67, 107, 108).

5.3.1.4 Tetracycline resistance

Discovered in the 1940s, tetracyclines, including tetracycline, doxycycline, and minocycline, hinder protein synthesis by binding to the 16S rRNA of the 30S ribosomal subunit, thereby obstructing the binding of aminoacyl-tRNA to the ribosomal acceptor site (109). Unlike what is observed with macrolides and aminoglycosides, resistance to tetracyclines is rarely mediated by mutations in ribosomal RNA or proteins, nor by methylation of specific RNA residues. Instead, it is conferred by other proteins. These proteins either i) export tetracycline across the cell membrane using an energy-dependent efflux mechanism (110, 111), ii) chemically alter the drug to deactivate it (112), or iii) mimic elongation factors to displace the bound antibiotic from the ribosome, thereby protecting the ribosome, and thus are designated ribosomal protection proteins (RPPs) (113, 114). Tetracycline resistance in *Campylobacter* is mainly conferred by the RPPs of which the later designated Tet(O) was probably the first to be described (113, 115). The RPP encoding gene *tet*(O) is the predominantly

found resistance gene conferring tetracycline resistance in *Campylobacter* spp. (66, 104, 116). Other types of RPP encoding genes have also been identified in *Campylobacter*, such as *tet*(32) (117) and *tet*(W) (67). In addition, mosaic like RPP encoding genes have been observed in *Campylobacter* spp. like *tet*(O/M/O) (118) and *tet*(O/32/O) (119). Additionally, the presence of the efflux pump coding gene *tet*(L) has recently been discovered in China (120).

5.3.2 Prevalence of antimicrobial resistance in *Campylobacter* spp.

The EU summary report on antimicrobial resistance in 2021/22 showed a prevalence of 69.1% and 70.6% ciprofloxacin-resistant *C. jejuni* and *C. coli* human isolates from 22 member states, respectively. Meanwhile, resistance to erythromycin was less pronounced with 0.9% of *C. jejuni* and 7.8% of *C. coli* resistant human isolates. Similar to the higher proportion of macrolide-resistant *C. coli*, they were also more resistant to tetracyclines (71.2%) compared to their *C. jejuni* counterparts (46.6%). Gentamicin resistance was also low, with 0.5% in *C. jejuni* and 3.0% in *C. coli*. Similar prevalences in the occurrence of resistance were observed in cecal samples from broilers from 27 EU member states and the United Kingdom. The highest resistances were observed in *C. coli* from cattle under the age of 1 year, with 90.5% resistance to tetracycline, 35.7% to erythromycin, 79.7% to ciprofloxacin, and 12.4% to gentamicin (121).

Antibiotic resistances among *Campylobacter* isolates in Southeast Asia vary considerably by country. For instance, Vietnam exhibited very high resistance rates to ciprofloxacin (63 - 100%), nalidixic acid (88 - 100%), and tetracyclines (75 - 100%), along with moderate to high resistance rates to gentamicin (25 - 56%), streptomycin (63 - 100%), and erythromycin (25 %) in *C.* spp from chicken and pork (122-124). In a study conducted by Lim et al. (2017), poultry meat products from Manila (Philippines) displayed very high resistance rates to erythromycin (98.6%) and clindamycin (98.6%)

(125). Additionally, frequent resistance to ciprofloxacin and tetracyclines was observed in Thailand (81.2% and 40.6%, respectively), while here the isolates were moderately resistant to erythromycin (9.4%) (126).

During a study spanning from 2017 to 2018 in Beijing, China, elevated rates of resistance to ciprofloxacin (94.5% and 94.4%) and tetracycline (93.5% and 94.4%) were observed in human isolates of *C. jejuni* and *C. coli*, respectively. Erythromycin resistance was more prevalent among *C. coli* isolates (44.4%) compared to *C. jejuni* (9.0%), showing more than four times higher prevalence. Likewise, gentamicin resistance was present in 50.0% of *C. coli* isolates and in 13.0% of *C. jejuni* isolates. Difference in streptomycin resistance was even more pronounced in *C. coli* (72.2%) than in *C. jejuni* (9.5%) (127). Notably, *Campylobacter coli* often exhibits higher resistance levels than *C. jejuni*, as evidenced by the different studies mentioned. Additionally, *Campylobacter* spp. isolates from Asia tend to be more resistant than their European counterparts.

5.3.3 Surveillance of antimicrobial resistance

Since the primary driver of the rise in antimicrobial resistance is the use of antimicrobial agents (57), several countries and regions have introduced antimicrobial resistance surveillance systems along with mitigation strategies to minimize antimicrobial use and resistance in bacteria.

5.3.3.1 AMR Surveillance in the United States

In 1996, the National Antimicrobial Resistance Monitoring System (NARMS) was established to prospectively monitor changes in antimicrobial susceptibilities of selected zoonotic enteric pathogens like *Salmonella* spp. and *Campylobacter* spp. (128, 129). As NARMS initiated monitoring of antimicrobial resistance in bacterial

isolates from humans, it wasn't long until data from this program (130) and another source (131) revealed an increase in fluoroquinolone resistance among *Campylobacter* from humans subsequent to the approvals of the fluoroquinolones sarafloxacin and enrofloxacin in poultry (129). This prompted the withdrawal of fluoroquinolones, particularly enrofloxacin, from poultry use in the United States (132). This withdrawal was the first case of an animal drug being taken off the market due to the associated emergence of resistance in humans. This led the FDA to develop an evidence-based approach for approving animal antimicrobial drugs of clinical importance to humans for use in primary production (133). Nowadays NARMS is being crucial in monitoring antimicrobial resistance in enteric bacteria in the US, aiding in identifying emerging threats across humans, animals, and food. Its data inform policies, regulatory actions, and educational efforts to reduce resistance and protect public health, continuously evolving to address changing bacterial environments and technologies (129).

5.3.3.2 AMR Surveillance in the European Union

Over the past decades, several EU Member States had established own surveillance programs to monitor antimicrobial resistance in bacterial isolates from animals raised for food production (134-137). However, with the introduction of Directive 2003/99/EC, a harmonized approach was established, mandating all European Member States to monitor antimicrobial resistance in zoonotic and public health-threatening agents (138). This led to the adoption of Implementing Decision 2013/652/EU (139) in 2013, which was later updated to Implementing Decision (EU) 2020/1729 (140). Within the EU-Decision, it is stated that Member States shall monitor thermotolerant *Campylobacter* spp. from different food-producing animals and the fresh meat thereof. For *Campylobacter*, this involves collecting samples, such as cecal content, from specified food-producing animals at the time of slaughter. This sampling is conducted

on a rotational basis, with the focus on poultry one year, and on bovine animals and pigs the following year. The antimicrobial susceptibility testing is performed by using the broth micro dilution method specified by the Clinical and Laboratory Standards Institute (CLSI) (141, 142). The interpretation of antimicrobial susceptibility data relies on epidemiological cut-off values (ECOFFs) regularly updated and published by the European Committee on Antimicrobial Susceptibility Testing (EUCAST), which was first formed in 1997 to also harmonize prior existing national committees (143). The findings are subsequently submitted on an annual basis to the European Commission, which in turn tasks the European Food Safety Authority (EFSA) with writing and publishing a summary report on antimicrobial resistance for the European Union.

In 2008, Germany started its own strategy to fight antimicrobial resistance named DART (Deutsche Antibiotika-Resistenzstrategie) (144). Following this, the 16th amendment of the Medicinal Products Act (16th AMG Amendment), which came into force in 2014, established regulations for implementing an antibiotic reduction strategy for livestock (145). The Working Group on Antibiotic Resistance of the Federal Office of Consumer Protection and Food Safety (BVL) and the Federal Institute for Risk Assessment (BfR) evaluated the antibiotic reduction strategy and found that the amount of veterinary antimicrobials dispensed has seen a notable decrease between 2011 and 2020, with a reduction of 58.9% (from 1,705.7 to 700.7 t) (146). Since the reduction strategy was considered successful (147), follow up programs were established such as DART 2020 (148) and the still ongoing DART 2030 (149).

5.3.3.3 AMR Surveillance in Asia

Southeast Asia is considered a region that contributes to emergence of drug resistance (150). Additionally, the WHO stated in a report that Southeast Asian countries lack systematic data collection regarding antimicrobial resistance (151). Hence, in 2015, the WHO adopted a global action plan, encouraging member states to create their own

tailored national action plans (NAPs) to combat antimicrobial resistance based on the One Health approach (152). Although governments showed their willingness for accelerated development of NAPs in Southeast Asia, progress on implementation should be strengthened, with e.g. regard to accountability, equity, sustainability and transparency (153). Antimicrobial usage in food animals in Myanmar, Indonesia, and Vietnam, is projected to increase by 205%, 202%, and 157%, respectively, between 2010 and 2030 (154), due to higher demand for animal products and an increase in larger production types with greater use of antimicrobial drugs.

In 2005, China established its first two nationwide surveillance systems to monitor antimicrobial usage in clinical settings, followed by another surveillance system in 2009 that aimed to track antimicrobial usage in agriculture. China then became one of the first countries to implement its own NAP, leading to further measures to reduce antimicrobial use in both clinical and agricultural settings (155). Thus, in 2016, several fluoroquinolones, such as lomefloxacin, ofloxacin, and norfloxacin, were banned in food animals but are suspected to still be used illegally (156). In 2017, colistin was also banned as a growth promoter (157). These mitigation strategies showed effectiveness, as antibiotic prescriptions decreased from 19.4% in 2010 to 7.7% in 2017 for outpatients, and from 67.3% to 36.8% for inpatients (155). Still, China is the world's largest producer and consumer of antibiotics, with per capita antibiotic use approximately ten times higher than in the United States (158). Additionally, it accounts for the largest share of antimicrobial consumption in food animal production, representing 23% of the overall global consumption in 2010 (66).

5.4 Aim of the study

Our study aimed to investigate the antibiotic resistance profiles of *Campylobacter* isolates collected from poultry samples from Germany and Vietnam and from human

and chicken samples from Georgia. Our primary objective was to gain insights into the underlying genetic mechanisms driving antimicrobial resistance in *Campylobacter* populations. This was done by correlating phenotypic resistance with the presence of genomic determinants. We aimed to identify the limitations in current predictive tools for antimicrobial resistance. For this purpose, knowledge gaps were addressed through in-depth analysis of whole-genome sequencing data combined with comprehensive phenotypic assessment. Additionally, our goal was to enhance routine resistance monitoring through the development of novel Real-time PCR assays, in order to facilitate more effective surveillance of emerging resistances within *Campylobacter* populations.

6 Publications

6.1 List of publications and own contribution

Publication 1: Comparison of Antimicrobial Susceptibility Profiles of Thermotolerant *Campylobacter* spp. Isolated from Human and Poultry Samples in Georgia (Caucasus)

M. Metreveli, S. Bulia, L. Tevzadze, S. Tsanava, M. Zarske, J. C. Goenaga, S. Preuß, G. Lomidze, S. Koulouris, P. Imnadze, K. Stingl

Antibiotics (Basel). 2022;11(10) https://doi.org/10.3390/antibiotics11101419

I contributed to NGS methodology and data analysis. I additionally reviewed and edited the manuscript.

Publication 2: Multiplex Real-Time PCR for the Detection of Tetracycline, Ciprofloxacin, and Erythromycin Resistance Determinants from Human and Foodborne *Campylobacter jejuni* and *Campylobacter coli*

V. Zeller-Péronnet, N. Bretschneider, J. Lausch, N. Hanifi, M. Pavlovic, M. Zarske, H. Q. Luu, U. Busch, K. Stingl, I. Huber

Microorganisms. 2023;11(12). https://doi.org/10.3390/microorganisms11122927

I took part in the gene target definition based on NGS analysis of Publication 3. Additionally, I contributed to the manuscript review and editing.

Publication 3: Identification of knowledge gaps in whole-genome sequence analysis of multi-resistant thermotolerant *Campylobacter* spp.

M. Zarske, H. Q. Luu, C. Deneke, M.-T. Knüver, M. Thieck, H. T. T. Hoang, N. Bretschneider, N. T. Pham, I. Huber, K. Stingl

BMC Genomics. 2024;25(1):156. https://doi.org/10.1186/s12864-024-10014-w

I performed standardized microdilution analysis and designed the custom plate formats for microdilution, sequenced Vietnamese isolates and some of the German isolates by Illumina short-read sequencing technology and contributed all Oxford Nanopore sequences. I processed the data through the Aquamis, Bakcharak and MiLongA pipelines and, if appropriate, did further analysis via webtools or Geneious Prime software. Furthermore, I contributed most of the result interpretation. I wrote the initial draft.

Publication 4: The point mutation A1387G in the 16S rRNA gene confers aminoglycoside resistance in *C. jejuni* and *C. coli*

M. Zarske, C. Werckenthin, J.C. Golz, K. Stingl

Antimicrob Agents Chemother 68:e00833-24. https://doi.org/10.1128/aac.00833-24

I took part in the conceptualization of the study. Except for isolation of the original strain, I performed all the experiments and contributed the most to data analysis and result interpretation. Additionally, I wrote the initial draft.

6.2 Publication 1: Comparison of Antimicrobial Susceptibility Profiles of Thermotolerant *Campylobacter* spp. Isolated from Human and Poultry Samples in Georgia (Caucasus)

antibiotics

MDPI

Article

Comparison of Antimicrobial Susceptibility Profiles of Thermotolerant *Campylobacter* spp. Isolated from Human and Poultry Samples in Georgia (Caucasus)

Maia Metreveli [1,*], Salome Bulia [2], Liana Tevzadze [3], Shota Tsanava [3], Michael Zarske [4], Juan Cruz Goenaga [4], Sandra Preuß [4], Giorgi Lomidze [5], Stylianos Koulouris [6], Paata Imnadze [1,3] and Kerstin Stingl [4,*]

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Abstract: Antimicrobial resistance remains a public health concern globally. This study presents antimicrobial resistance by microdilution and genetic diversity by the whole-genome sequencing of *Campylobacter* spp. from human and poultry samples isolated in Georgia in 2020/2021. The major species in poultry samples was *C. coli*, while *C. jejuni* was preferentially isolated from human samples. Resistance against tetracycline was highest (100%) in *C. coli* from industrial chicken and lowest in *C. jejuni* from clinical isolates (36%), while resistance against ciprofloxacin varied from 80% in *C. jejuni* from backyard chicken to 100% in *C. jejuni* and *C. coli* from industrial chicken. The point mutations in *gyrA* (T86I) and *tet* (O) genes were detected as resistance determinants for (fluoro-)quinolone or tetracycline resistance, respectively. Ertapenem resistance is still enigmatic. All isolates displayed sensitivity towards erythromycin, gentamicin and chloramphenicol. Multi-resistance was more frequently observed in *C. coli* than in *C. jejuni*, irrespective of the isolation matrix, and in chicken isolates compared to human isolates, independent of the *Campylobacter* species. The Georgian strains showed high variability of multi-locus sequence types (ST), including novel STs. This study provides the first antibiotic resistance data from *Campylobacter* spp. in Georgia and addresses the need for follow-up monitoring programs.

Keywords: EUCAMP3; microdilution; cgMLST; backyard chicken; whole-genome sequencing; resistance determinant; campylobacteriosis; gastroenteritis; WGS

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1. Introduction

The emergence and spread of multi-resistant bacteria continues to be a global public health concern. In the European Economic Area (EEA), it was estimated that more than 670,000 diseases were caused by antimicrobial-resistant (AMR) bacteria yearly, with about 33,000 associated deaths [1].

Campylobacteriosis is a disease caused by thermotolerant *Campylobacter* spp. It is one of the four major causes of diarrhea worldwide, and is considered to be the most common cause of bacterial food-borne human gastroenteritis [2]. *Campylobacter* species are motile, curved, microaerobic, Gram-negative rods that commonly reside in the intestinal tract of many wild and domestic warm-blooded animals.

Although campylobacteriosis is mostly self-limiting, recent reports showed that a substantial proportion (31%) of reported *Campylobacter* infections have been treated with

antibiotics [3], probably those infections with severe outcome. Concordantly, a considerable number of 21% of the reported campylobacteriosis cases resulted in hospitalization in the EU in 2020, while for comparison, salmonellosis led to 29.9% and infections by shiga-toxin-producing *E. coli* to 40.9% of hospitalization [4].

Based on the joint report of European Food Safety Authority (EFSA), European Centre for Disease Prevention and Control (ECDC), European Medicines Agency (EMA) and Organization for Economic Co-operation and Development (OECD) the overall consumption of antibiotics in humans decreased by 23% and in food-producing animals by 43% between 2011 and 2020 in the EEA [5]. Harmonized AMR key indicator bacteria, such as fully susceptible *Escherichia coli* for food-producing animals and Methicillin-resistant *Staphylococcus aureus* (MRSA) for humans varied depending on the country and the years. In the majority of the countries, the proportion of fully susceptible *E. coli* increased and MRSA decreased between 2014 and 2018, being in-line with reduced use of antibiotics [6]. However, the percentage of *E. coli* from human samples resistant against third-generation cephalosporins increased in half of the countries and decreased in the other half. Of particular concern is the increase in carbapenem resistance with, e.g., almost a quarter of EU/EEA countries reporting at least 10% carbapenem-resistant *K. pneumoniae* [1]. Carbapenems are not authorized for use in veterinary medicine in the EU [7] and in Georgia [8]. Combined resistance to both ciprofloxacin and erythromycin, which is considered critically important for treatment of campylobacteriosis, was marginal with 0.5% in *C. jejuni* and still low with 8.9% in *C. coli* in 2020. However, relatively high levels of combined resistance were reported by Finland and Portugal for *C. coli* (36.8–40.6%) [6]. In a global world, emerging resistant strains identified at one location can be spread around the world, thus, the issue requires a global systematic approach and international action [9].

AMR surveillance data from Georgia are scarce in the public health system and absent at the food production and veterinary sectors. The Central Asian and European Surveillance of Antimicrobial Resistance (CAESAR) 2019 report [10] described resistance data gathered in twelve countries of the WHO European Region including Georgia. Data from Georgia were assessed reliable with limitations of small number of samples, focus on samples from the capital and lack of harmonized AST guidelines [10]. Data on *Campylobacter* spp. were lacking.

Antimicrobial resistance monitoring in *Campylobacter* from poultry samples in Europe is performed based on the regulation 2003/99/EC, laying down the monitoring of zoonoses and zoonotic agents isolated from distinct food and animal matrices and their characterization using harmonized panels of antimicrobial substances [11]. In several countries, an increase in resistance in *C. jejuni* from broilers against tetracycline and ciprofloxacin was detected. In addition, *C. jejuni* isolates from human samples also showed increasing resistance to these antimicrobials [6].

On the way of EU integration, the regulation for monitoring of zoonoses and zoonotic agents based on the 2003/99/EC went into force in Georgia in 2020. According to this regulation monitoring of antimicrobial resistance has to be carried out at primary production level and/or at other stages of the food chain. The regulation covers zoonoses including *Campylobacter* spp.; however, implementation of the regulation is not in action yet.

Our study presents first data on genetic diversity of *Campylobacter* spp. strains from human stool and poultry samples isolated in Georgia based on whole genome sequencing analysis and identifies antimicrobial resistance patterns of *C. jejuni* and *C. coli* including their genetic determinants. The study encourages future monitoring programs for in-depth analysis of thermotolerant *Campylobacter* spp. in Georgia in order to improve food safety.

2. Materials and Methods

2.1. Sampling and Transport

In total, 160 *Campylobacter* isolates were obtained from chicken cecal samples from February 2020 until September 2021 in Georgia. The 110 so-called "backyard" chicken samples were gathered at the Digomi live animal market in Tbilisi, where poultry is sold

reared at small farms and households from all over the country and directly processed on the market slaughterhouse. Another 50 *Campylobacter* strains were isolated from samples collected at a medium-sized 'intensive-rear' poultry farm slaughterhouse, located at the eastern part of Georgia. In addition, 382 human stool samples had been previously collected from July 2020 to July 2021 at the Tbilisi Children Infectious Diseases Clinical Hospital from hospitalized children with diarrhea, from which 60 were positive for *Campylobacter* spp. [12]. Human stool samples were transported on Cary-Blair medium (Biolife Italiana srl, Milan, Italy) at cooling temperatures without microaerobic conditions and analyzed within 24 h. Chicken cecal samples were transported in plastic bags on ice and analyzed within 3–6 h after sampling.

2.2. Detection and Phenotypic Identification of Campylobacter spp.

Campylobacter detection was performed according to ISO 10272-1:2017 part C on modified charcoal cefoperazone deoxycholate agar (mCCDA) (Thermo Fisher Specialty Diagnostics Ltd., Hampshire, UK). For the clinical samples, *Campylobacter* Chromogenic agar *Campylobacter* (CHROMagar, France) was applied as an additional second selective medium to increase sensitivity [12]. Less than 20% of the clinical samples were also enriched with Preston broth (Biolife Italiana S.r.l., Milan, Italy) [13], but the results showed no enhanced detection [12].

Ceca were aseptically cut and the content mixed. One 1 µL loop of the cecal material was directly streaked on the mCCDA agar plate and distributed over the surface by using a fresh loop. The human stool samples were treated similarly but in addition to mCCDA a second selective plate was used in parallel. Incubation was performed at 42 °C in a microaerobic gas mixture consisting of 85% nitrogen, 10% carbon dioxide and 5% oxygen (LTD Argoni, Tbilisi, Georgia).

Suspicious colonies were sub-cultured on Columbia Blood Agar (ColbA; AES Laboratories, Bruz Cedex, France). Confirmation of colonies was initially performed applying the Biomerieux system ApiCampy (Biomerieux Inc, Marcy-l'Etoile, Lyon, France), consisting of 20 microtubes containing dehydrated substances. One half contained enzymatic tests and the other half substrates for assimilation or inhibition. In the latter, growth of bacteria is monitored. The specific pattern of growth and presence of enzymatic activity is used as read-outs for identification of bacteria. In addition, colonies were observed by microscopy after Gram-straining. All isolates were stored at −80 °C for further characterization.

2.3. Confirmation of Campylobacter Species and Differentiation by Real-Time PCR Analysis

At the National Reference Laboratory for *Campylobacter* at BfR the 220 strains, from which 160 were derived from chicken and 60 from human sources, were re-cultured on ColbA for 48 h under microaerobic atmosphere. In case no growth or some contamination was obtained, a parallel enrichment in Bolton broth (Oxoid, Thermo Fisher Scientific Inc., Waltham, MA, USA) with 5% lysed defibrillated horse blood (Oxoid, Thermo Fisher Scientific Inc., Waltham, MA, USA) was streaked on mCCDA and incubated for another 48 h. Single suspected colonies were sub-cultured on ColbA and incubated 24 h under similar conditions.

Isolates of *Campylobacter* spp. were species-differentiated by real-time PCR [14]. For this purpose, cell material of isolates was resuspended in 5% Chelex 100 resin (Bio-Rad Laboratories GmbH, Feldkirchen, Germany) and heated for 15 min at 95 °C for thermal lysis. Cell debris was centrifuged for 5 min at 14,000× *g*, and the supernatant containing bacterial DNA was used for PCR analysis at a volume of 2.5 µL after 1:100 dilution. Oligos and dark-quenched (DQ) probes in HPLC-grade were as follows: for *C. jejuni*, *mapA*-F, 5′-CTG GTG GTT TTG AAG CAA AGA TT-3′, *mapA*-R, 5′-CAA TAC CAG TGT CTA AAG TGC GTT TAT-3′ and *mapA*-probe, 5′FAM-TTG AAT TCC AAC ATC GCT AAT GTA TAA AAG CCC TTT-3′DQ; for *C. coli*, *ceuE*-F, 5′-AAG CTC TTA TTG TTC TAA CCA ATT CTA ACA-3′, *ceuE*-R, 5′-TCA TCC ACA GCA TTG ATT CCT AA-3′ and *ceuE*-probe, 5′JOE-TTG GAC CTC AAT CTC GCT TTG GAA TCA TT-DQ; for *C. lari*, *gyrA*1-F1, 5′-GAT AAA GAT

ACG GTT GAT TTT GTA CC-3′, *gyrA*1-R1, 5′-CAG CTA TAC CAC TTG ATC CAT TAA G-3′, *gyrA*1-F2, 5′-GAT AAA GAT ACA GTT GAT TTT ATA CC-3′, *gyrA*1-R2, 5′-TGC AAT ACC ACT TGA ACC ATT A-3′ and *gyrA*1-probe, 5′Cy5-TTA TGA TGA TTC TAT GAG TGA GCC TGA TG-DQ; for the internal amplification control, IPC-ntb2-F, 5′-ACC ACA ATG CCA GAG TGA CAA C-3′, IPC-ntb2-R, 5′-TAC CTG GTC TCC AGC TTT CAG TT-3′ and IPC-ntb2-probe, 5′TAMRA-CAC GCG CAT GAA GTT AGG GGA CCA-DQ. Note that *gyrA*1-F2 bears one base exchange T3A relative to the original publication due to oligo optimization for the validation study [15]. Oligos at final concentrations of 300 nM (Sigma Aldrich, Steinheim, Germany), 100 nM dark-quenched probes (TIB MOLBIOL, Berlin, Germany) and 1 U of Platinum Taq DNA polymerase (Thermo Fisher Scientific Inc., Waltham, MA, USA) were used. As amplification control, 25 copies of the IPC-ntb2 plasmid [16] was added per PCR reaction.

2.4. Antimicrobial Susceptibility Testing

Isolates were tested for AMR according to the prescriptions given in Commission Implementing Decision (CID) (EU) 2020/1729 (European Commission, 2020) [17]. Broth microdilution susceptibility testing was performed according to M45-A (Clinical and Laboratory Standards Institute [CLSI], 2015) [18] and VET06 (CLSI, 2017) [19] with the in-house validated modification of the use of fetal calf serum (PAN-Biotech GmbH, Aidenbach, Germany) instead of lysed horse blood in the culture medium for improved readability of *Campylobacter* growth. For this purpose, strains were subcultured on Columbia blood agar for 24 ± 2 h at 42 °C under microaerobic atmosphere (5% O_2, 10% CO_2, 85% N_2). Cation-supplemented Mueller–Hinton broth (TREK Diagnostic Systems, United Kingdom) supplemented with 5% fetal calf serum was inoculated with 2–8 × 10^5 colony forming units/mL. Minimum inhibitory concentrations (MICs) were determined using the European standardized microtiter plate format EUCAMP3 (TREK Diagnostic Systems). Antimicrobials tested included chloramphenicol (CHL; 2–64 mg/L), erythromycin (ERY; 1–512 mg/L), gentamicin (GEN; 0.25–16 mg/L), ciprofloxacin (CIP; 0.12–32 mg/L), tetracycline (TET; 0.5–64 mg/L) and ertapenem (ETP; 0.12–4 mg/L). Epidemiological cut-off values (ECOFFs) were taken from the European Committee for Antimicrobial Susceptibility Testing (EUCAST; https://mic.eucast.org/Eucast2 (accessed on 7 September 2022)) laid down in the CID 2020/1729. For *C.* spp. ECOFFs were as follows: 16 mg/L (CHL), 0.5 mg/L (CIP), 0.5 mg/L (ETP) and 2 mg/L (GEN). For ERY and TET, species-specific cut-off values were used (4 or 8 mg/L (ERY) and 1 or 2 mg/L (TET) for *C. jejuni* or *C. coli*, respectively). Incubation was performed for 44 ± 4 h at 37 °C under microaerobic atmosphere. MICs (mg/L) were semi-automatically analyzed using the Sensititre Vizion system (TREK Diagnostic Systems), which has an integrated camera and a mirror, recording a translucent picture from the microtiter plates. The MIC data were stored and exported using Sensi Vizion Software 2.0 (MCS Diagnostics BV, Swalmen, The Netherlands).

2.5. NGS Methodology

Genomic DNA was extracted from *Campylobacter* strains sub-cultured overnight using the PureLink Genomic DNA Mini Kit (Thermo Fisher Scientific, Waltham MA, USA) according to the manufacturer's instructions. DNA was fluorimetrically quantified by Qubit 3.0 Fluorometer (dsDNA HS Assay Kit 0.2–100 ng; Thermo Fisher Scientific, Waltham, MA, USA). The quality of the DNA was evaluated by spectral analysis (NanoDrop Spectrophotometer, Thermo Fisher Scientific, Waltham, MA, USA). DNA libraries were prepared using the Illumina DNA Prep, (M) Tagmentation Kit according to manufacturer's instructions (Illumina Inc., San Diego, CA, USA) but with using half of the volume of all reagents. Paired-end sequencing was performed on the Illumina MiSeq System (2 × 151 cycles) using the MiSeq Reagent Kit v3 (600 cycles, Illumina Inc., San Diego, CA, USA). Trimming and de novo assembly of raw reads were carried out using the AQUAMIS pipeline v1.3.8 (https://gitlab.com/bfr_bioinformatics/AQUAMIS (accessed on 7 September 2022)). The quality of the assembled genome contigs was au-

tomatically evaluated using the teQuilR in-house pipeline. Sequences were published within the BioProject No. PRJNA844526 at the NCBI sequence read archive (SRA). Ridom Seqsphere+ v8.2.0 (Ridom, Muenster, Germany) was used to perform phylogenetic analysis on assembled genome contigs using the cgMLST scheme of 1343 gene targets previously defined [20] with 98% required identity and 98% required percentage of coverage to one of the alleles of the reference sequence NC_002163.1.gb (*C. jejuni* NCTC 11168). At least 95% "good targets" were found for cgMLST-based analysis using the previously proposed cgMLST scheme. New MLST alleles and MLST-ST types were uploaded to PubMLST (www.pubmlst.org). Prediction of antimicrobial resistance determinants and plasmid markers within assembled genome contigs was performed by using the BakCharak pipeline v2.0 (https://gitlab.com/bfr_bioinformatics/bakcharak (accessed on 7 September 2022)). Tools in the pipeline include ABRicate v1.0.1 (https://github.com/tseemann/abricate (accessed on 7 September 2022)) and AMRFinderPlus v3.6.15 [21] and its associated database for antimicrobial resistance determinant, as well as Platon v1.1.0 for plasmid prediction (https://github.com/oschwengers/platon (accessed on 7 September 2022), [22] and plasmid blaster, a tool that performs a BLAST analysis against the NCBI RefSeq plasmid database. BLAST results were filtered with at least 20% coverage of the contig length.

2.6. Statistical Analyses

Isolates were categorized into susceptible and resistant, using the epidemiological cut-off values as mentioned in Section 2.4. The dependent variable was resistant vs. susceptible (reference category) to the antimicrobial in question. In addition to the individual antimicrobial, an outcome variable "2-3-fold resistance" was defined for an isolate resistant against two or three tested antimicrobials. This means that first, isolates were categorized according to their MIC and the epidemiological cut-off value (ECOFF) as sensitive or resistant towards every individual antimicrobial. Second, the number of resistances per isolate was counted and those with 2 or more resistances were defined as displaying "2-3-fold resistance".

Multiple logistic regression with forward selection was used to establish independent predictors for tetracycline resistance (variables of matrix source (human vs. chicken (reference category)) and bacterial species (*C. coli* vs. *C. jejuni* (reference category)) were included). A Nagelkerke R Square and a non-standardized beta coefficient (B) were calculated. An odds ratio with 95% confidence interval (CI) was calculated as an exponential of the B coefficient (Exp [B]).

For all analyses, *p*-values of less than 0.05 were considered statistically significant. Statistical analyses were performed using SPSS (IBM SPSS Statistics for Windows, Version 21.0. Armonk, NY, USA: IBM Corp).

3. Results

3.1. Collection of Campylobacter spp. Strains and Identification of Species

Campylobacter spp. isolates from chicken cecal content were obtained from February 2020 until September 2021. "Backyard" chicken samples aged between several days to one year were collected from chicken reared on small farms and in households all over the country and sold at a live market in Tbilisi. In addition, *Campylobacter* strains were isolated from samples collected at a medium-sized industrial poultry slaughterhouse, located at the eastern part of Georgia and supplying Tbilisi with fresh chicken meat. Those chickens were "standardized" with an age between 38 and 42 days. In addition, human stool isolates had been previously collected from hospitalized children with diarrhea from July 2020 to July 2021 [12]. Hence, the samples correlated in time and space. From a total of 220 isolates—160 derived from chicken and 60 from human sources (Supplementary Materials Table S1)—sixteen were non-culturable after transport to BfR. However, from these sixteen non-culturable samples, *Campylobacter* spp. were still detectable by real-time PCR in twelve of the enrichment inoculums, showing either *C. coli*

(4/12) or *C. jejuni* (3/12) in seven cases and mixed cultures of *C. coli* and *C. jejuni* in five cases (41%, *n* = 5/12).

Out of 204 strains re-cultured, 37.7% (*n* = 77) were identified as *C. jejuni* and 62.3% (*n* = 127) as *C. coli* applying real-time PCR [14]. The distribution of isolated species differed between human stool samples and cecal chicken samples (Figure 1).

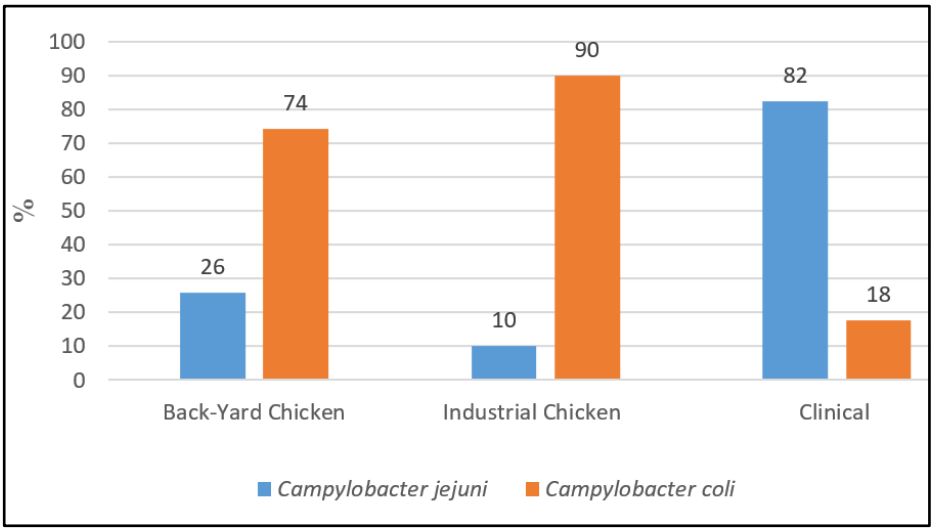

Figure 1. *Campylobacter* species distribution (%) in poultry and human samples.

From the isolates of backyard chicken, 25.8% were identified as *C. jejuni* (*n* = 25/97) and 74.2% (*n* = 72/97) as *C. coli*; in cecal samples from industrial chicken, *C. coli* was even more dominant with 90% (*n* = 45/50). In contrast, out of 57 clinical strains of children stool samples, 82.5% (*n* = 47/57) were identified as *C. jejuni* and 17.5% (*n* = 10/57) as *C. coli* (Figure 1) [12].

3.2. Prevalence of Antimicrobial Resistance in Campylobacter Isolates

All isolates were tested for their resistance to the six antimicrobials chloramphenicol, ciprofloxacin, ertapenem, erythromycin, gentamicin and tetracycline according to the European standardized EUCAMP3 plate format. Results from resistance testing are shown in Table 1. All tested strains were sensitive towards gentamicin, erythromycin and chloramphenicol. Resistance in both human and poultry isolates and in both bacterial species was highest against ciprofloxacin and tetracycline.

Table 1. Antimicrobial susceptibility of *Campylobacter jejuni* and *Campylobacter coli* strains isolated from three different sources.

Antimicrobial	ECOFF (µg/mL) (R>)		No. (%) of Resistant Isolates							
			Backyard Chicken (*n* = 97)		Industrial Chicken (*n* = 50)		Human (*n* = 57)		Total (*n* = 204)	
	C. jejuni	*C. coli*	*C. jejuni* (*n* = 25)	*C. coli* (*n* = 72)	*C. jejuni* (*n* = 5)	*C. coli* (*n* = 45)	*C. jejuni* (*n* = 47)	*C. coli* (*n* = 10)	*C. jejuni* (*n* = 77)	*C. coli* (*n* = 127)
Chloramphenicol	16	16	0	0	0	0	0	0	0	0
Ciprofloxacin	0.5	0.5	20 (80%)	69 (96%)	5 (100%)	45 (100%)	41 (87%)	9 (90%)	66 (86%)	123 (97%)
Erythromycin	4	8	0	0	0	0	0	0	0	0
Ertapenem	0.5	0.5	0	27 (37%)	0	37 (82%)	0	6 (60%)	0	70
Gentamicin	1	1	0	0	0	0	0	0	0	0
Tetracycline	1	2	18 (72%)	52 (72%)	4 (80%)	45 (100%)	17 (36%)	8 (80%)	39 (51%)	105 (83%)

ECOFF, epidemiological cut-off for definition of resistance against antimicrobial substances (EUCAST.org); R>, maximal MIC that represents sensitivity; any MIC exceeding this concentration is defined as resistant. Note that ECOFF for erythromycin and tetracycline differs for *Campylobacter* species. n, number of tested isolates; numbers in table represent numbers of resistant isolates; in brackets, percentage of resistant isolates.

Both human and poultry *C. coli* strains showed resistance against ertapenem—37% of the strains from backyard chicken, 60% of human isolates and 82% of industrial chicken strains, while *C. jejuni* isolates were fully susceptible to this antimicrobial. Among the ertapenem-resistant *C. coli*, 89% (n = 62) had a MIC value of 1 µg/mL, just above the current cut-off value, 10% (n = 7) displayed a MIC of 2 µg/mL and a single strain had a MIC of 4 µg/mL. From the strains with MIC values ≥2 µg/mL ETP, three were derived from human samples, four from backyard chicken and one from industrial chicken.

Overall, isolates of *C. coli* were less frequently fully susceptible (3/127, 2.4%) than isolates of *C. jejuni* (9/77, 11.6%), with each six strains isolated from backyard poultry and human samples and lack of susceptible strains among the industrial isolates (Figure 2).

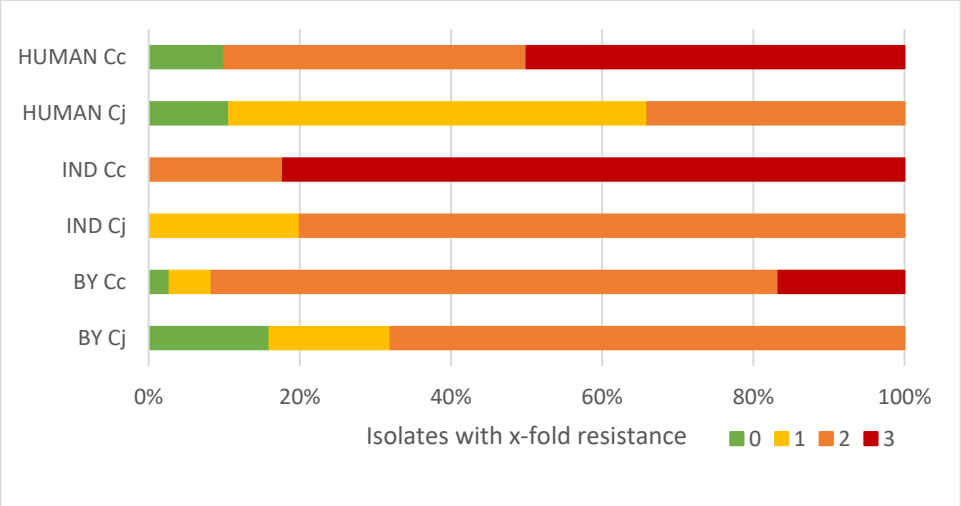

Figure 2. Resistance against antimicrobial classes in *Campylobacter* spp. isolates from different sources. Green, sensitive; yellow, 1-fold-resistant; orange, 2-fold-resistant; red, 3-fold-resistant. *Cj*, *C. jejuni*; *Cc*, *C. coli*; BY, backyard chicken; IND, industrial chicken; HUMAN, human isolates. Resistances against individual antimicrobials detailed in Table 1 were counted per isolate and percentage of isolates with resistances against x-fold antimicrobial classes are depicted here.

C. coli were more likely resistant—compared to *C. jejuni*-against ciprofloxacin (OR 5.1, 95% CI 1.6–16.7) and tetracycline (OR 4.6, 95% CI 2.5–8.8). In addition, isolates from clinical samples were less likely resistant to tetracycline compared to chicken isolates (OR 0.18, 95% CI 0.1–0.4). No statistically significant difference was observed for resistance to ciprofloxacin between human and poultry isolates.

Overall, *C. coli* was 18.5 times more likely resistant against two or more antibiotics compared to *C. jejuni* (OR 18.5, 95% CI 7.7–44.8). The same was observed in clinical isolates, where *C. coli* was 17.4 times more likely resistant to two or more antimicrobials than *C. jejuni* (OR 17.4, 95% CI 2.03–150.1); for poultry samples *C. coli* OR showed 7.9 times more probability to have resistance against two or more antibacterial agents compared to *C. jejuni* (OR 7.9,95% CI 2.6–24.6).

There was a significant association of multi-resistance probability with isolation source in *C. jejuni* strains. In particular, the probability of resistance against two or more antimicrobials for chicken isolates of *C. jejuni* was 4.5 times higher compared to human isolates (OR 4.5, 95% CI 1.7–12.1); however, we did not find a significant association between clinical and chicken isolates for *C. coli* species, probably due to low number of *C. coli* isolates from human stool samples. Additionally, no statistically significant difference was found for the presence of two or more resistances in *C. jejuni* or in *C. coli* isolates from industrial compared to backyard chicken.

Variables of bacterial species and isolates were subjected to logistic regression analysis to test association with resistance to two or more antimicrobials as dependent variables. Both variables were retained in the final model as independent variables. The Nagelkerke

pseudo R squared was 0.435 indicating that more than 43% of the variability of dependent variables is due to the independent variables model.

Multi-variate logistic regression was performed with two variables which showed significant association with tetracycline resistance. Both variables, bacterial species and sample sources were retained into final model as independent predictors. The regression model can explain more than 20% of the variation in the dependent variable (tetracycline resistance), according to the Nagelkerke pseudo R squared of 0.204. (Table 2). In other words, the predictive model, consisting of the variables "bacterial species" and "sample sources", can explain 20% of the variability of the dependent variable "tetracycline resistance". Alternatively, this means, that the remaining 80% of the variability of the dependent variable could be explained with variables, that were not measured within the study and/or are not identified as a possible predictor for the outcome variable. Nagelkerkes R squared 43% for the dependent variable "2-3-fold resistance" can be interpreted in the same way.

Table 2. Association of full susceptibility and resistance to tetracycline and resistance against ≥2 antimicrobials of *Campylobacter* spp. with bacterial species and sample sources.

Anti-Microbial	Covariate	Coefficient of Regression	Standard Error	Wald	Degrees of Freedom	*p*-Value	Odds Ratio	95% Confidence Interval of Odds Ratio		Nagelkerke Pseudo R Squared
								Lower	Upper	
TET	Chicken vs. human	1.153	0.403	8.203	1	0.004	3.167	1.439	6.971	
	C. coli vs. *C. jejuni*	0.947	0.391	5.858	1	0.016	2.577	1.197	5.547	0.204
2-3-fold resistance	Chicken vs. human	1.361	0.442	9.487	1	0.002	3.901	1.641	9.276	
	C. coli vs. *C. jejuni*	2.271	0.496	21.000	1	<0.001	9.693	3.669	25.607	0.435

TET, tetracycline; Coding of variables: *C. coli* (1) vs. *C. jejuni* (0); poultry isolates (1) vs. human isolates (0).

3.3. Campylobacter spp. Isolates Are Phylogenetically Diverse

We additionally analyzed forty *Campylobacter* strains by whole-genome sequencing, twenty derived from poultry and another twenty from human samples, approximately each ten *C. jejuni* and *C. coli* per matrix. The poultry isolates were both from backyard samples (n = 14) and from industrial chicken (n = 6). After de novo assembly of the raw reads, multi-locus sequence type analysis (MLST, based on 7 housekeeping genes) and, for more precise resolution, the core-genome MLST (cgMLST) scheme based on the comparison of 1343 gene alleles was used for phylogenetic analysis. Missing cgMLST loci were pairwise ignored.

As expected, we obtained a high variability of multi-locus sequence types (ST, n = 24), including three strains with either unknown *uncA* allele and/or unknown ST-type. The *C. jejuni* (n = 22) belonged to 15 different ST-types, while the *C. coli* (n = 18) displayed 9 different ST-types (Figure 3). The most frequent ST-types were ST-855 (n = 6), ST-356 (n = 4), and ST-902 (n = 3). The *C. coli* ST-types most frequently grouped within the common clonal complex ST-828 (17/18). Supplementary Materials Table S2 highlights new ST-types and their respective allelic combinations not previously reported in the PubMLST database as well as the metadata of the dataset.

Within the limited number of sequenced strains, we even found three sequence clusters. One of this clusters (ST-855) included four highly similar *C. coli* strains from industrial chicken, collected in June/July 2021 during three independent samplings, with maximal two cgMLST allele differences. Two further *C. jejuni* clusters with each two strains identified among the human isolates belonged both to ST-type 356 and were separated from each other by 226 allele difference. One of these clusters included two *C. jejuni* strains isolated from children in September and October 2021, harboring identical pairwise cgMLST. The other cluster included two *C. jejuni* strains isolated from children in July and September 2021.

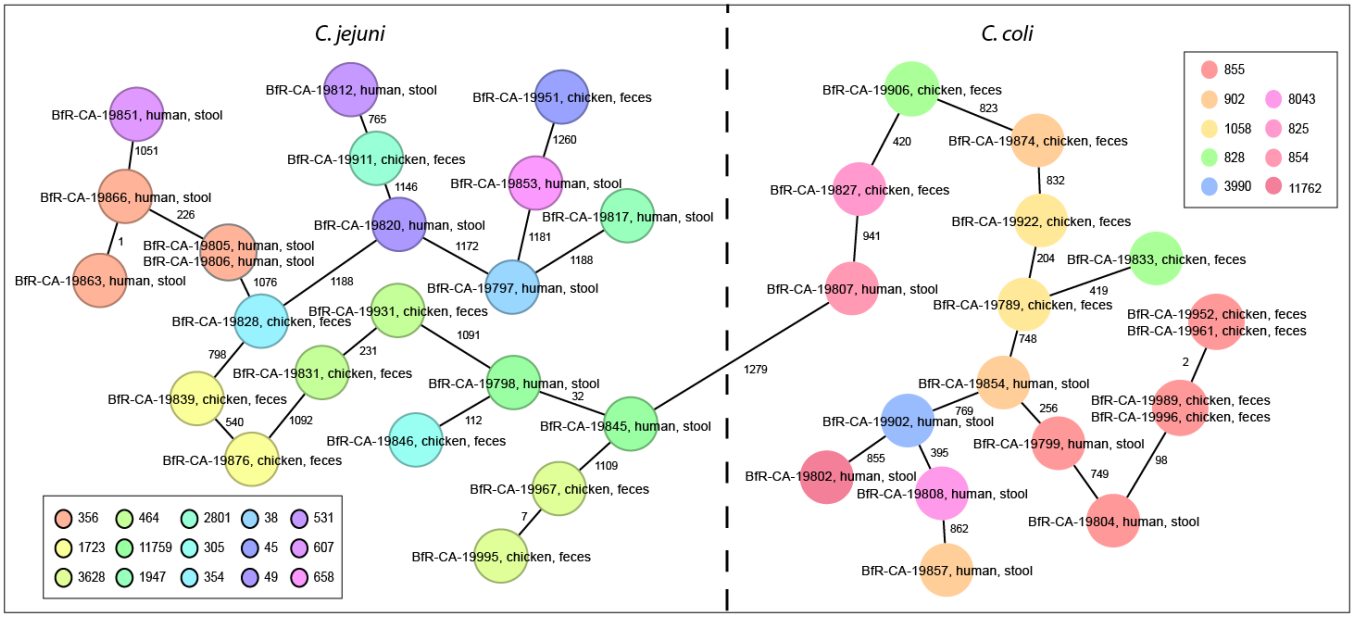

Figure 3. Whole-genome sequences of the isolates from chicken and human samples in Georgia displayed high variability. Minimum spanning tree of cgMLST analysis was based on 1343 core genes defined previously [20]. Missing alleles were pairwise ignored. Each colored circle with (*C. jejuni*) our without frame (*C. coli*) represents an ST-type of the 7 housekeeping genes MLST scheme as depicted in the inlay boxes per species. Numbers next to the connecting lines illustrate the number of allele differences analyzed by cgMLST between nearest neighbors. One new *uncA* allele and two new ST-types were found. More details, including all ST-types are shown in Supplementary Materials Table S2.

Eighteen *Campylobacter* isolates (45%) putatively carried plasmids (Supplementary Materials Table S2), since contigs of the whole genome assembly were predicted as epichromosomal elements by Platon and BLAST analysis using the NCBI RefSeq plasmid database. All plasmids had at least 20% coverage of homology to known *Campylobacter* spp. plasmids (Supplementary Materials Table S3), except for BfR-CA-19911, which harbored a small plasmid without any match in the RefSeq database.

3.4. Detection of Antimicrobial Resistance Genes

Whole-genome sequencing analysis also revealed several resistance genes, responsible for the observed phenotypes. The presence of the *tet*(O) gene, which mediates resistance to tetracycline, was detected in all tetracycline-resistant strains (70%, $n = 28/40$). The most common mutation in the *gyrA* gene (T86I) was identified in all ciprofloxacin-resistant isolates (90% ($n = 36/40$)). The presence of $bla_{\text{OXA-61}}$ family genes (OXA-193, OXA-452, OXA-460, OXA-461, OXA-489, OXA-594), which confer resistance to beta-lactams, was observed in 75% ($n = 30/37$) of strains. In addition, we found the *aadE-Cc* gene in three *C. coli*, putatively conferring streptomycin resistance. Streptomycin and ampicillin are not part of EUCAMP3 plate format, so the phenotype was not confirmed. The AMRFinderPlus database also annotated the mutation 50S_L22_A103V of the L22 ribosomal protein as a putative resistance marker for macrolide resistance in 30% ($n = 12/37$) of the strains; however, all isolates were sensitive towards erythromycin. The resistance mechanism against ertapenem is still unknown. According to Platon prediction, all resistance determinants were chromosomally located.

4. Discussion

EU countries have made significant strides in developing and implementing national monitoring plans on antimicrobial resistance [6]; however, in Georgia, monitoring programs are still lacking.

Our study results on antibiotic resistance in Georgian *Campylobacter* spp. isolates from chicken show similarities to the AMR data profiles of *Campylobacter* spp. in EU member states. In particular, both *C. jejuni* and *C. coli* from poultry sources in the EU exhibited high resistance against (fluoro-)quinolones and tetracycline, which is in line with our data [6,23,24]. However, notably, the resistance rate to ciprofloxacin and tetracycline was 100% in isolates from industrial poultry samples in Georgia, while in backyard chicken and in human isolates *Campylobacter* strains displayed slightly lower resistance against both antimicrobials. Comparing multi-resistance in *C. jejuni* or *C. coli* in industrial versus backyard chicken, no significant difference could be found. Interestingly, all isolates were sensitive towards gentamicin, chloramphenicol and erythromycin.

Use of (fluoro-)quinolones was shown to be the major risk factor for ciprofloxacin resistance in *Campylobacter* spp. on broiler farms [25]. However, it was shown that the *gyrA* mutation, conferring resistance against (fluoro-)quinolones, can also contribute to a fitness increase in *C. jejuni* in poultry depending on the strain background [26]. The clonal spreading of (fluoro-)quinolone-resistant clones was suggested to occur in Europe [27], although the contribution of whether the resistance was selected through (fluoro-)quinolone use in individual countries and/or transmission between countries is still unclear [28]. Moreover, the differences in resistance rates between the bacterial species from the same source and, therefore, the same antimicrobial exposure indicated that antimicrobial use alone cannot explain differences in resistance profiles of *C. jejuni* and *C. coli* [29]. *C. coli* from the same matrix exhibited higher resistance than *C. jejuni* towards multiple antimicrobials tested [29]. The reason for this phenomenon is still unclear. (Fluoro-)quinolones are among WHOs "Highest Priority Critically Important Antimicrobials" (HPCIA) [30]. Increases in resistance to (fluoro-)quinolones in *Campylobacter* spp. are of concern, as resistance in *Campylobacter* from animals has been shown to be associated with resistance of *Campylobacter* from human infections [6]. When Georgian isolates were compared according to their origin, the chicken *C. coli* or *C. jejuni* isolates were each significantly more resistant towards two and three classes of antimicrobials than the human strains. This might hint to additional infection routes other than cross-contamination from preparing fresh chicken meat and/or direct contact to animals on chicken farms in Georgian children suffering from campylobacteriosis. In addition to the preparation of poultry meat and contact with poultry animals, contact with sand in a sandbox with putative contact to animal feces such as that from dogs and wild animals was also identified in a German study as risk factor positively associated with a *Campylobacter* infection for children under 5 years of age [3].

Furthermore, our study showed a high prevalence of *C.coli* in comparison to *C.jejuni* from poultry samples, which was untypical in a number of countries even in the Caucasus region [6,31–33]. However, there are other studies that identified a higher prevalence of *C. coli* than *C. jejuni* in swab samples from farms and neck skins at slaughter in Italy [34] or some alterations of species distribution depending on the stage of broiler production [35]. A long-term study over seven years showed a gradual decrease in the prevalence of *C. jejuni* and a concomittant increase in *C. coli* in cecal samples from chicken in China [36], while in Malaysia both species were frequently isolated from different broiler parts [37].

One explanation for different species distribution might be age and race of the chicken, which is not likely in our study, since we obtained a similar species distribution from backyard chicken of different age and industrial chicken with standardized rearing period of 38–42 days. Our results may additionally hint at the fact that initially, we might have isolated mixed cultures of both *C. jejuni* and *C. coli* in some cases, since PCR results of inoculums identified the presence of both species, which in turn could not be recultivated together.

All tested isolates from Georgia were sensitive towards erythromycin and gentamicin, which was similar for isolates in the EU. Erythromycin resistance in *Campylobacter* isolates from human cases of campylobacteriosis and from broilers in sixteen EU member states was either absent or detected at very low levels in *C. jejuni*, but was observed at higher levels in *C. coli* isolates. Overall, erythromycin resistance was reported in 10% (2020)

and 12.9% (2019) of human isolates and 4.4% of broiler isolates. Combined resistance to both ciprofloxacin and erythromycin, which is considered critical for the treatment of campylobacteriosis, was reported to be 8.9% (2020) and 10.4% (2019) in isolates from humans and 4.1% in broilers. In 2020, EU countries reported low prevalence of gentamicin resistance [6]. Data from *C. jejuni* and *C. coli* of human and animal origin in 2019–2020 showed very high to extremely high levels of resistance to (fluoro-)quinolones, which are also critically important antimicrobial agents (CIAs) for the treatment of *Campylobacter* infections in humans [30]. WGS of isolates, especially those with multi-drug resistance, high-level resistance to erythromycin or ciprofloxacin, or resistance to gentamicin or ertapenem, is strongly recommended in order to decipher the antimicrobial resistance determinants involved, their genetic location, and the potential for horizontal transmission [38].

5. Conclusions

Preventive and control activities in Georgia are still limited concerning the monitoring and antimicrobial susceptibility profiling of thermotolerant *Campylobacter* spp. Our first national study showed similar AMR patterns of thermotolerant *Campylobacter* spp. strains isolated in Georgia to those reported by the European Union. In particular, resistances against (fluoro-)quinolones and tetracycline were high and should be considered in local therapeutic protocols for severe human cases. Antimicrobial resistance and the prevalence of thermotolerant *Campylobacter* spp. in animals, food and humans need further approaches in order to gain a representative picture of concurrent strains in the Caucasian region.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/antibiotics11101419/s1, Table S1: Complete sample list, including phenotype of antibiotic resistance; Table S2: WGS data overview and antibiotic resistance of tested samples; Table S3: WGS data-plasmid annotation.

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Institutional Review Board Statement: The study was conducted according to the guidelines of the Declaration of Helsinki and approved by the Ethics Committee of Tbilisi Children Infectious Diseases Clinical Hospital (protocol code 1 and 15 June 2020).

Informed Consent Statement: Informed consent was obtained from all subjects involved in the study.

Data Availability Statement: Sequence data are available at the Sequence Read Archive (SRA) at the National Centre for Biotechnology Information (NCBI), BioProject No. PRJNA844526, Bio Sample Accession No. SAMN28822301- SAMN28822340. Further data that support the findings of this study are available on request from the corresponding authors.

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6.3 Publication 2: Multiplex Real-Time PCR for the Detection of Tetracycline, Ciprofloxacin, and Erythromycin Resistance Determinants from Human and Foodborne *Campylobacter jejuni* and *Campylobacter coli*

microorganisms

MDPI

Article

Multiplex Real-Time PCR for the Detection of Tetracycline, Ciprofloxacin, and Erythromycin Resistance Determinants from Human and Foodborne *Campylobacter jejuni* and *Campylobacter coli*

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Abstract: *Campylobacter jejuni* and *Campylobacter coli* are the predominant thermophilic species responsible for foodborne gastroenteritis worldwide. Elevated resistance to certain antibiotics was observed due to antimicrobial therapy in farm animals and humans, while reduced antimicrobial usage partially reduced antibiotic resistance. Monitoring the antimicrobial resistance demonstrated a substantial fraction of multi-resistant isolates, indicating the necessity of reliable tools for their detection. In this study, resistance determinants in 129 German and 21 Vietnamese isolates were selected to establish a novel multiplex real-time PCR (qPCR), facilitating the simultaneous detection of four resistance determinants. These comprised *tet*(O) gene variants associated with tetracycline resistance, point mutations GyrA_T86I and GyrA_T86V associated with ciprofloxacin resistance, and the *erm*(B) gene together with the point mutation A2075G in the 23S rRNA gene, associated with erythromycin resistance. Moreover, the performance of the qPCR assay was evaluated by comparing the results of qPCR to phenotypic antimicrobial resistance profiles, obtained with standardized EUCAMP3 microdilution panel, which showed 100% similarity (inclusivity and exclusivity). Variation in measurement methods, including qPCR machines and master mixes showed robustness, essential for laboratories. The assay can be used for the rapid detection of resistance determinants, and is beneficial for monitoring the spread of antibiotic resistance in *C. jejuni* and *C. coli*.

Keywords: food safety; *Campylobacter* spp.; food and clinical isolates; antimicrobial resistance determinants; susceptibility testing; real-time PCR assay

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1. Introduction

Campylobacter is the most frequently reported foodborne bacterial pathogen in humans in the European Union [1]. Consumption of poultry meat contaminated with thermotolerant *Campylobacter* species can cause severe gastroenteritis. *C. jejuni*, followed by *C. coli*, are the predominant thermotolerant *Campylobacter* species in poultry samples and are mainly responsible for foodborne human infections [2,3]. The use of antibiotics in animal farming and for the treatment of human diseases promotes antimicrobial resistance. The relationship between antibiotic use and increasing occurrence of resistance has been frequently described [4]. In January 2022, a new Veterinary Medicinal Products Regulation (2019/06) was implemented throughout the European Union (EU) [5], which updated the rules on

the authorization and use of veterinary medicines in the EU to preserve the effectiveness of antibiotics for the future. However, due to enhanced and prolonged antimicrobial usage in high selection areas, such as Southeast Asian countries, the prevalence of antibiotic-resistant *Campylobacter* on poultry meat and the risk of multi-drug resistance islands (MDRI) are increasing [6]. It is becoming crucial to identify resistance determinants independently of time- and labor-consuming phenotypic characterization and to develop fast tools for the use in European monitoring surveys of circulating resistance determinants.

Several studies addressing the impact of antibiotic usage on the formation of resistance have already revealed multiple resistance mechanisms, such as duplicated genes, mosaic genes, gene mutations, plasmids carrying resistance determinants, and transposons, all of which contribute to the spread of antibiotic resistance [4,7,8]. For ciprofloxacin resistance, the point mutation T86I in the gyrase A subunit is the most frequent resistance determinant in *Campylobacter* spp. [9–11]. Erythromycin resistance in *Campylobacter* spp. was shown to be mainly conferred by the point mutation *23S rRNA* A2075G [12,13]. However, in Asian countries [14], also sporadically in Europe (Spain) [15], and in the United States [16], the *erm*(B) gene, encoding a methyltransferase presents a second, highly transferable resistance determinant in *C. coli*. Tetracycline resistance in *Campylobacter* spp. is based on the presence of a ribosomal protection protein encoded by *tet*(O) [17] and mosaic variant genes [18,19].

Zarske et al. [20] investigated resistance determinants in German and Vietnamese thermotolerant *Campylobacter* spp. populations. Moreover, they demonstrated the presence of different resistance determinants, such as resistance genes, gene variants, and point mutations in distinct genes (*gyrA, 23S rRNA, rpsL*). Based on this genomic knowledge, worldwide prevalent resistance determinants were selected to develop a multiplex real-time PCR assay capable of covering resistance to tetracycline, ciprofloxacin, and erythromycin antibiotics.

In the last decade, polymerase chain reaction (PCR)-based detection systems have increasingly been applied to explore determinants of antimicrobial resistance among thermophilic *Campylobacter* spp. isolates. With combination of singleplex PCRs, the presence of two tetracycline resistance genes *tet*(O) and *tet*(A) can further be screened [21]. Laprade et al. [22] developed four conventional multiplex PCR assays that detect tetracycline resistance gene *tet*(O) in combination with virulence and toxin genes. A real-time PCR assay based on the amplification of a fragment of the 23S rRNA gene, surrounding bases 2074 and 2075, was developed to detect macrolide-associated mutations [23]. Additionally, Zhang et al. [13] identified the presence of the mutation in the 23S rRNA gene by mismatch amplification mutation assay (MAMA) PCR and DNA sequencing; for the presence of the *erm*(B) gene, a conventional PCR was applied. Zirnstein et al. [24] published a MAMA PCR assay, and Espinoza et al. [8] published a real-time PCR for the detection of the point mutation T86I in the gyrase A that is associated with resistance to ciprofloxacin.

In a further study, Nguyen et al. [25] characterized Vietnamese *Campylobacter* isolates in antibiotic susceptibility testing EUCAMP2 and identified resistance determinants, using MAMA PCRs for point mutations at positions 2074 and 2075 of the 23S rRNA gene, as well as for the screening of the point mutation T86I in the gyrase A. A specific conventional PCR was applied to detect the presence of the *tet*(O) gene.

In the current study, we developed a multiplex real-time PCR assay to simultaneously detect the presence of four resistance determinants in *C. jejuni* and *C. coli*. In these assays, the widely distributed resistance gene *tet*(O), *encoding the Tet(O) ribosomal protection protein* [26] and the point mutations T86I and T86V within the gyrase subunit A [8,24], were retained to screen tetracycline and ciprofloxacin resistance, respectively. In order to cover erythromycin resistance, two detection systems, including the resistance gene *erm*(B), encoding the Erm(B) ribosomal methyltransferase [13,27] as well as the point mutation A2075G in the *23S* ribosomal RNA gene [13,28], were selected. The selection of these targets for multiplexing the real-time PCR assay was based on the European Union Summary Report on Antimicrobial Resistance of EFSA and ECDC (2023) [29], which indicated that combined resistance to both ciprofloxacin and erythromycin is considered critically important for the treatment of campylobacteriosis.

A test panel consisting of 129 German isolates obtained from food and human sources, as well as 21 Vietnamese isolates derived from chicken feces and exhibiting thermotolerant characteristics were phenotypically tested for resistance to six antibiotic classes and used for the validation of the novel multiplex real-time PCR.

2. Materials and Methods

2.1. Campylobacter Isolates and Growth Conditions

A total of 68 human isolates of *Campylobacter (C.)* spp. were obtained from systematical screenings performed during the 2018–2023 period in stool samples from gastroenteritis patients at LGL, department of human bacteriology, as well as private laboratories in the south of Germany. A total of 61 food isolates of *Campylobacter* spp. were isolated at LGL or provided by the German Federal Institute for Risk Assessment (BfR) during the 2019–2022 period, mostly from chicken neck skins from slaughterhouses and chicken breast from retail shops. Vietnamese isolates were previously isolated from chicken feces [20]. The classical microbiological method to detect *Campylobacter* spp. was carried out according to ISO 10272-2:2017 [30]. Briefly, 1 mL meat rinse was spread onto the surface of three selective mCCD agar (modified Charcoal-Cefoperazone-Deoxycholate Agar, Merck, Darmstadt, Germany) plates and incubated at 42 °C for 44 ± 4 h with a concentration of 10% carbon dioxide (CO_2). Subsequently, all isolates were identified at the species level by matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) using the MALDI Biotyper (MBT) platform (Bruker Daltonics, Bremen, Germany) according to Huber et al. [31] to ensure the identification of each isolate.

In total, 85 *C. jejuni* and 44 *C. coli* isolates from Germany were collected for this study. *C. jejuni* strain DSM 4688 (DSMZ-German Collection of Microorganisms and Cell Cultures GmbH, Braunschweig, Germany) and *C. coli* strain 2012-70-443-2 (Technical University of Denmark, Lyngby, Denmark) were used as a negative control strains for phenotypic resistance testing and the multiplex real-time PCR-assay. All *Campylobacter* isolates and strains were stored at −80 °C using the MAST Cryobank system (Mast Diagnostica GmbH, Reinfeld, Germany) and are listed in Supplementary Material Table S1.

These 129 *Campylobacter* isolates, together with 21 Vietnamese isolates, were characterized phenotypically and genotypically, and formed a test panel for the design, development, and validation of a real-time PCR assay. All isolates were phenotypically tested for resistance to six antibiotics in standardized microtiter plate format EUCAMP3. For genotypical characterization, an NGS-based approach was applied to identify different genetic determinants conferring antimicrobial resistance.

2.2. Antibiotic Susceptibility Testing EUCAMP3

The European standardized Sensititre™ EU Surveillance *Campylobacter* EUCAMP3 plate system (Thermo Fisher Scientific Inc., Waltham, MA, USA) was used to identify phenotypic resistance patterns of isolates from Germany and Vietnam against six antimicrobial agents: chloramphenicol, erythromycin, gentamicin, ciprofloxacin, tetracycline, and ertapenem. According to the European Union Summary Report on Antimicrobial Resistance of EFSA and ECDC [29], these antimicrobials have been reported to be mandatory for *C. jejuni* and *C. coli* as representatives of six different antibiotic classes of phenicols, macrolides, aminoglycosides, (fluoro-)quinolones, tetracyclines, and carbapenem, respectively.

Isolates stored at −80 °C were grown on Columbia agar (ColbA), supplemented with 5% sheep blood (Oxoid, Thermo Fisher Scientific Inc.) for 24 h with a concentration of 10% CO_2 at 42 °C and subcultured once for additional 20 ± 2 h before antibiotic susceptibility testing. Isolates were inoculated at a bacterial concentration between 2×10^5 and 8×10^5 CFU/mL in cation-supplemented Mueller–Hinton broth (Thermo Fisher Scientific Inc.) with 5% fetal bovine serum (PAN-Biotech, Aidenbach, Germany) (CAMHB/FBS). A volume of 100 µL inoculated CAMHB/FBS (5×10^5 CFU/mL) was added to each well

of EUCAMP3 format plates, and the plates were incubated at 37 °C for 44 ± 4 h with a concentration of 10% carbon dioxide (CO_2).

Minimal inhibitory concentrations (MICs; in mg/L) were determined using the semi-automatically Sensititre™ Vizion™ system (Thermo Fisher Scientific Inc.) and the Sensivizion V2.0 software (MCS Diagnostics BV, Swalmen, The Netherlands). Epidemiological cut-off values (ECOFFs, Table 1) for resistance determination were based on the European Committee on Antimicrobial Susceptibility Testing [32–34].

Table 1. Epidemiological cut-off values (ECOFFs) for evaluation of antibiotic susceptibility testing results of thermotolerant *Campylobacter* spp. from Germany.

Antimicrobial	MIC [mg/L] Resistant > *C. jejuni*	MIC [mg/L] Resistant > *C. coli*	Reference
ciprofloxacin	0.5	0.5	ECOFFs for *C.* spp. [32–34]
tetracycline	1	2	
ertapenem	0.5	0.5	
erythromycin	4	8	
chloramphenicol	16	16	
gentamicin	2	2	

MIC, minimum inhibitory concentration.

2.3. DNA Extraction and Quantification

Campylobacter isolates were subcultured on ColbA or Tryptone Soy Agar with Sheep Blood (Thermo Fisher Scientific Inc., Waltham, MA, USA) (TSASB) for 20 ± 2 h with a concentration of 10% CO_2 at 42 °C. Bacteria were resuspended from agar plates in 200 µL phosphate-buffered saline buffer with pH of 6.7–6.9 (Sigma Aldrich 79383-250ML, Merck, Darmstadt, Germany) (1× PBS) and harvested by centrifugation at 14,000× *g* for 5 min. The cell pellet was either directly used for DNA extraction or stored at −20 °C. For DNA extraction, the PureLink Genomic DNA Mini Kit (Thermo Fisher Scientific Inc.) was used according to the manufacturer's instructions, using the Gram-negative bacteria genomic DNA purification protocol. Elution buffer EB (Qiagen 19086-250ML, Hilden, Germany) was used for DNA elution.

DNA concentration was quantified using a Qubit Fluorometer and the Qubit dsDNA BR Assay Kit (Thermo Fisher Scientific Inc.) according to the manufacturer's instructions. DNA concentration was adjusted for real-time PCR analysis to 10 pg/µL with sonicated salmon sperm DNA (10 ng/µL) (Agilent Technologies, Santa Clara, CA, USA) used as background DNA.

2.4. Next-Generation Sequencing (NGS) and Assembly

For short-read sequencing, DNA libraries with an average insert size of about 400 bp were generated using the NEB (New England Biolabs GmbH, Frankfurt am Main, Germany) Ultra II DNA Library Prep Kit according to the manufacturer's instructions and sequenced on the Illumina MiSeq benchtop sequencer using the MiSeq reagent kit v2 (2 × 150 bp, Illumina, Inc., San Diego, CA, USA). Paired-end reads were processed using the AQUAMIS pipeline v1.3.7 [35], which comprised quality control, trimming, and de novo assembly using Shovill. All assemblies fulfilled the quality criteria of Q30 for at least 75% and minimum coverage of 30×. The 21 Vietnamese isolates were sequenced and assembled at BfR as described in [20].

2.5. Design of Primers and Probes

Hundred *Campylobacter* isolates available at LGL (HS_1 to FS_100) and a worldwide collection of *Campylobacter* isolates from NCBI were used to design the oligonucleotides. Primers and probes were designed with the help of the NCBI Primer Blast Tool. An

additional 29 German isolates from service laboratories in southern Germany and BfR (HS_101 to FS_129), as well as 21 Vietnamese isolates (VE_01 to VE_21), were applied for validation of the designed oligonucleotides.

Prevalent resistance determinants in *Campylobacter* isolates were retained to develop a pentaplex real-time PCR (multiplex real-time PCR with detection systems in 5 channels), allowing simultaneous detection of resistance genes and point mutations associated with tetracycline, ciprofloxacin, and erythromycin resistance. The IPC-ntb2 gene fragment from *Nicotiana tabacum* was used as internal amplification control (IAC, [36]) and extracted from *E. coli* DSM 116329 (DSMZ-German Collection of Microorganisms and Cell Cultures GmbH, Braunschweig, Germany). It was applied to detect PCR inhibition and to confirm negative results. Simultaneously, a triplex real-time PCR assay (3 fluorescence channels for *tet*(O), GyrA_T86I/V, and IAC) combined with a duplex real-time PCR assay (2 fluorescence channels for *erm(*B) and *23S rRNA*_A2075G) were validated in case of limited optical modules available in the real-time PCR instruments in user laboratories.

2.6. In Silico Screening for Primer Binding Sites and Gene Alignments

In silico primer screening [37] for the selection of designed primers and probes was performed to evaluate the specificity of the real-time PCR assay.

Assembly sequences were screened for primer and probe sequences using fastaRegex-Finder [38].

NCBI reference sequences of resistance determinants (*gyrA C. coli*: GeneID: 66544015 *gyrA C. jejuni*: GeneID: 905319, *tet*(O) *C.jejuni*: GeneID: M18896.2) were blasted against a custom BlastDB based on all assembly sequences to identify and extract corresponding sequences from the assemblies. These were aligned using muscle 5.1 [39] and visualized with Aliview 1.2.6. [40].

2.7. Multiplex Real Time PCR Assay for Detection of Resistance Determinants

The real-time PCR assays were validated with QuantiNova Multiplex PCR master mix (Qiagen, Hilden, Germany) for the pentaplex assay in two different probe dye combinations, either FAM-ROX-Cy5-HEX-ATTO425 on AriaMx instrument (Agilent Technologies) or FAM-ROX-Cy5-HEX-Cy5.5 on Quantstudio5 (Thermo Fisher Scientific) and on CFX96 Touch System (Bio-Rad, Hercules, CA, USA). QuantiNova Multiplex PCR Kit was also appropriate for the combination of the triplex and duplex assays.

A total of 50 copies of the IPC-ntb2 plasmid [36] were added as IAC in the pentaplex and triplex assays. The reaction mix was filled with PCR-grade water to 20 µL. A volume of 5 µL DNA with a concentration of 10 pg/µL was added to the reaction mix. The protocols for all three reaction mix variations are given in Supplementary Material Tables S3–S6. Two Vietnamese isolates *C. coli* BfR-CA-15062 (VE_01, *tet*(O/M/O), GyrA_T86I, *erm*(B)) and *C. jejuni* BfR-CA-16092 (VE_14, *tet*(O/M/O) + *tet*(O)*x*, GyrA_T86I, *23S rRNA*_A2075G) were used as positive control strains for the real-time PCR-assays.

The primer and the probe concentrations were optimized on the AriaMx instrument to achieve an optimal fluorescence signal for all primer–probe detection systems. The optimal annealing temperature of 60 °C was determined via a gradient PCR experiment on Quantstudio5 in which an annealing temperature gradient between 58 °C and 62 °C was applied. No significant differences were detected in real-time PCR results between 58 °C and 62 °C, but the fluorescence of the amplification curves was optimal for all detection systems at an annealing temperature of 60 °C. Amplification conditions with QuantiNova Multiplex PCR Kit on all three PCR instruments consisted of enzyme activation at 95 °C for 2 min followed by 40 cycles of 95 °C for 10 s, 60 °C for 20 s, and 72 °C for 20 s.

For the detection systems *tet*(O), *erm*(B), and IAC, labeled double-quenched probes were used, as they reduce background signals and crosstalk between the different channels of the real-time PCR instruments in multiplex PCR.

2.8. In-House Validation of the Pentaplex Real-Time PCR Assay

2.8.1. Selectivity

The applicability of the pentaplex real-time PCR assay for detecting the resistance determinants was checked on all 129 DNAs of German *Campylobacter* isolates (HS_101 to FS_129) as well as on all 21 DNAs of Vietnamese isolates (VE_01 to VE_21) supplied by BfR.

2.8.2. Determination of Efficiency and $LOD_{95\%}$

To access the efficiency and the limit of detection ($LOD_{95\%}$) of the detection systems for resistance determinants on AriaMx equipment (Agilent Technologies, Santa Clara, CA, USA), serial dilution of two *Campylobacter* isolates were applied to cover both erythromycin resistance determinants (*erm*(B) gene and the point mutation *23S rRNA*_A2075G), as well as both GyrA_T86I detection systems (*C. jejuni* and *C. coli*). *C. coli* isolate VE_01 with *erm*(B) gene and *C. jejuni* isolate VE_14 with *23S rRNA*_A2075G were selected.

The DNA copy number was adjusted to 5000 copies/µL DNA in ddPCR [41] based on an absolute quantification of DNA copy number. All DNAs were diluted to five dilution levels (5000, 1000, 500, 100, and 50 copies/µL DNA). Each dilution level was measured in three technical replicates to evaluate the efficiency of the pentaplex real-time PCR. The percentage of efficiency and the coefficient of determination R^2 were calculated.

To determine the lowest copy number still detectable with a 95% confidence interval ($LOD_{95\%}$) a serial dilution of the target DNAs was prepared at 8 low copy number levels (20, 10, 4, 2, 1, 0.4, 0.2, and 0.02 copies/µL) and each dilution level was measured in 12 independent technical replicates. The probability of detection (POD curve) and $LOD_{95\%}$ was computed via a web service provided by QuoData (QuoData Web Service [42]) according to BVL guidelines [43,44].

2.8.3. Robustness

The robustness of the real-time PCR assay was tested on two different real-time PCR machines from two additional manufacturers (Quantstudio5, Thermo Fisher Scientific, and CFX96 Touch System, Bio-Rad). The HiDi® Taq DNA Polymerase and 10× buffer (MyPols Biotec, Konstanz, Germany) were used to check the suitability of a single components master mix in the real-time PCR assay. A 25 µL PCR reaction mix contained 1 × HiDi® buffer, 2 IU per reaction of HiDi® Taq DNA Polymerase, 1.5 mM $MgCl_2$ (Thermo Fisher), 200 µM of each deoxynucleoside triphosphate (Takara Bio Inc., Kusatsu, Japan) and 5 mL of the sample DNA. The amplification conditions with HiDi® Taq Polymerase were enzyme activation at 95 °C for 2 min followed by 40 cycles of 95 °C for 15 s, 60 °C for 30 s, and 72 °C for 30 s.

The combination of both factors (master mix/PCR equipment) was tested to detect potential effects on the real-time PCR performance. For this purpose, the efficiency was calculated using standard curves, as described in 2.8.2, with two *Campylobacter* isolates at five dilution levels (5000, 1000, 500, 100, and 50 copies/µL DNA).

3. Results

For the development of a multiplex real-time PCR assay, a test panel consisting of 129 *Campylobacter* isolates from Germany and 21 isolates from Vietnam was genotypically and phenotypically characterized for antimicrobial resistance. The correct assignment of phenotypic results (see Section 3.1) to genotypic results was verified in silico (see Section 3.3) and validated in the real-time PCR assay (see Sections 3.4 and 3.5).

3.1. Antimicrobial Resistance Profiles

All 129 *Campylobacter* isolates from Germany were categorized into sensitive and resistant strains using the epidemiological cut-off values, which were based on the European Committee on Antimicrobial Susceptibility Testing and the European Food Safety Authority ([32–34], Table 1). The results of resistance profiles for all 129 isolates from Germany upon susceptibility testing against the six antimicrobials of the European-wide harmonized

EUCAMP3 plate format are outlined in Supplementary Material Table S1 and summarized in Table 2. The two strains *C. jejuni* strain DSM 4688 and *C. coli* strain 2012-70-443-2 served as complete sensitive controls.

Table 2. Prevalence of phenotypic resistance of human and food isolates from Germany in EUCAMP3 panel.

	Percentage of German Isolates Resistant to Antimicrobials Tested (%)					
Antibiotic	**Human Isolates (*n* = 68)**			**Food Isolates (*n* = 61)**		
	***C. jejuni* (*n* = 44)**	***C. coli* (*n* = 24)**	***C. jejuni* + *C. coli***	***C. jejuni* (*n* = 41)**	***C. coli* (*n* = 20)**	***C. jejuni* + *C. coli***
ciprofloxacin	81.8	79.2	80.9	68.3	50.0	62.3
tetracycline	65.9	62.5	64.7	43.9	55.0	47.5
ertapenem	6.8	37.5	17.6	7.3	40.0	18.0
erythromycin	0.0	8.3	2.9	0.0	5.0	1.6
chloramphenicol	0.0	0.0	0.0	0.0	0.0	0.0
gentamicin	0.0	0.0	0.0	0.0	0.0	0.0

Resistance to gentamicin and chloramphenicol was not observed in German isolates. Food and human isolates were both predominantly resistant to ciprofloxacin (62.3 to 80.9%), followed by tetracycline (47.5 to 64.7%) and finally to ertapenem (17.6 to 18.0%). Resistance to erythromycin was observed always in combination with resistance to ciprofloxacin at a low level (1.6 to 2.9%) and only in *C. coli* isolates.

The distribution of combined resistance (1-fold to 4-fold) is displayed in Figure 1. In total, 23% of the German isolates showed resistance to a single antibiotic (n = 10 for humans, n = 20 for food). Overall, 47% of the isolates were resistant to two antibiotics in different combinations (n = 39 for humans, n = 22 for food). Finally, 9% of the isolates showed resistance to three antimicrobial agents (n = 7 for humans, n = 5 for food) and one human isolate showed resistance to the four antimicrobial agents ciprofloxacin, tetracycline, ertapenem, and erythromycin. The occurrence of combined resistance to ciprofloxacin and tetracycline is very frequent. Among 129 German isolates, 11 human isolates as well as 14 food isolates displayed no resistance to any of the six antibiotics tested in the EUCAMP3 panel.

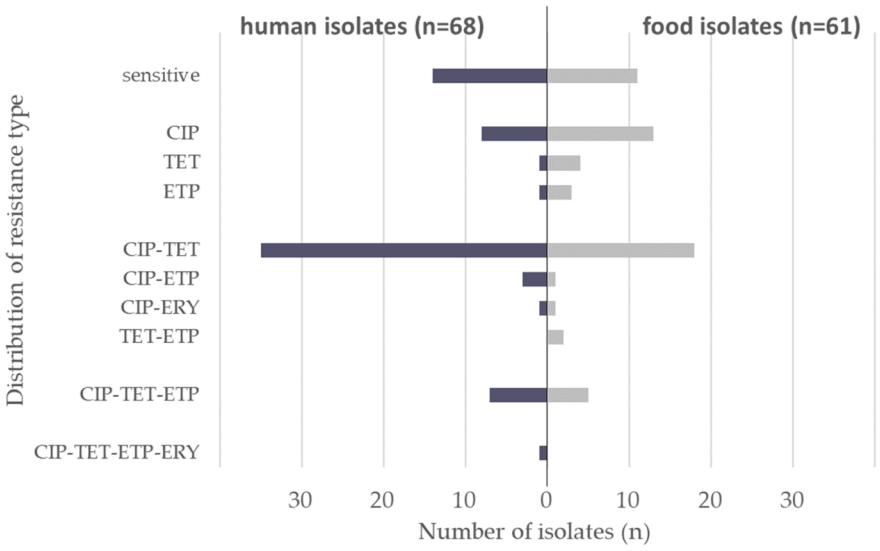

Figure 1. Distribution of resistance type (1-fold to 4-fold in EUCAMP3) for human and food isolates from Germany. HS, human isolates; FS, food isolates; CIP, ciprofloxacin; TET, tetracycline; ETP, ertapenem; ERY, erythromycin.

3.2. Design of Primer and Probes for Real-Time PCR Assays

The pentaplex real-time PCR assay included four detection systems combined with the IAC. Four resistance determinants were detected simultaneously: suitable fragments of the resistance genes *tet*(O) and *erm*(B) as well as the point mutations GyrA_T86I/V and A2075G in the 23S rRNA gene.

For the point mutation GyrA_T86I, ATT in *C. coli* and ATA in *C. jejuni* codes for isoleucine, whereas in wild-type ACT in *C. coli* and ACA in *C. jejuni* codes the threonine. In point mutant A2075G in the 23S rRNA gene, contrary to the wild type, the base A is substituted with G. In all cases, labeled single-quenched probes with 4 LNA (Locked Nucleic Acid) bases [45–47] were used to stabilize hybridization and increase thermal stability. Additionally, unlabeled LNA probes with the wild-type nucleotide sequence were added, in order to improve specificity of the detection of *gyrA* and 23S rRNA gene-resistant mutants and to suppress the unspecific binding of the labeled LNA probes to wild-type sequences. The base sequences in *gyrA* for the point mutation T86I showed considerable differences between *C. coli* and *C. jejuni*; therefore, two different primer–probe sets were needed to screen ciprofloxacin resistance in both species simultaneously. Sequences and final concentrations of primers and probes (IDT, Coralville, IA, USA and metabion, Planegg, Germany) for pentaplex real-time PCR are listed in Table 3.

Tetracycline resistance can be established by the presence of *tet*(O) and/or mosaic variants *tet*(O/M/O), and *tet*(O/32/O) [18,19]. The designed detection system for *tet*(O) delimited an area, similarly for all gene variants (Figure 2). The alignment of the sequenced tetracycline resistant *Campylobacter* isolates in Figure 2 shows the binding sites to *tet*(O) primers and probe, independently of *tet*(O) variants.

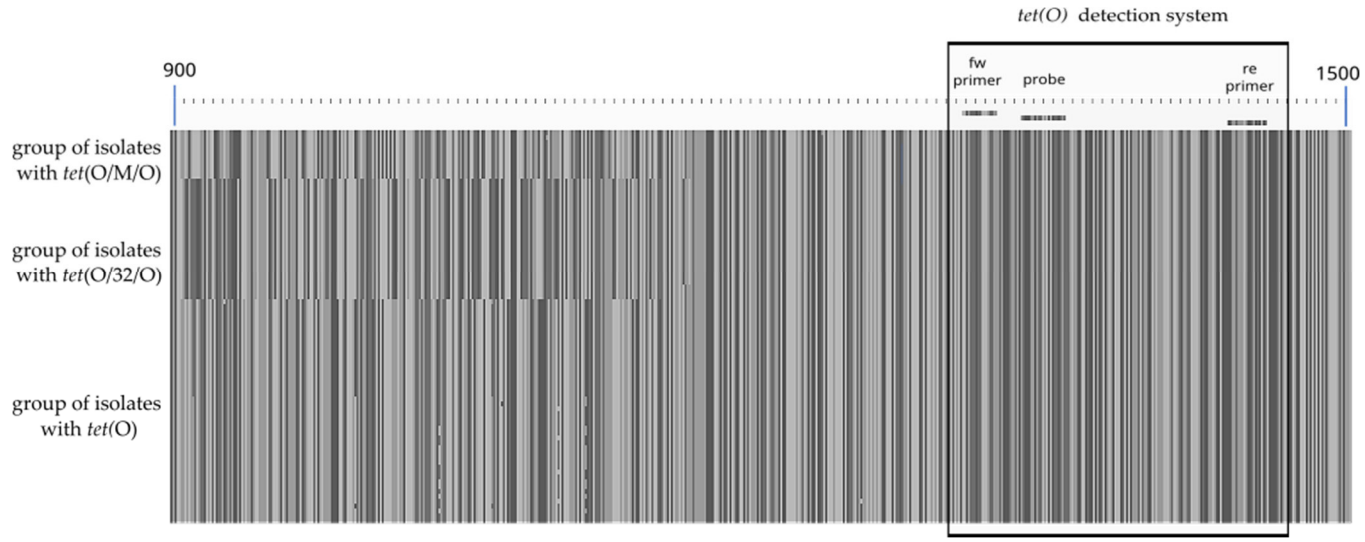

Figure 2. Detection system for *tet*(O) and *tet*(O) mosaic variants (Aliview 1.2.6.). From the top, 3 groups of isolates, with mosaic variant *tet*(O/M/O), with mosaic variant *tet*(O/32/O) and with gene *tet*(O). Figure 2 shows a segment of the alignment from nucleotides 900 to 1500. The detection system for *tet*(O) covers the nucleotides between 1304 and 1460. The complete sequence alignment extends over 1920 nucleotides.

Table 3. Oligonucleotides for pentaplex assay: *tet*(O); GyrA_T86I; *erm*(B); *23S rRNA*_A2075G, IAC.

Antimicrobial Resistance and Target	Primer/Probe Name	Oligonucleotide Sequence 5′→ 3′	Amplicon Size [bp]	Final Concentration in qPCR [nM]	Reference
Tetracycline *tet*(O) [1]	tet(O)-fw	AAGTCCCGCCAAATCCT	157 (Acc. No. NG_048257.1)	150 nM	the current study
	tet(O)-re	TGCTCGCAGCCATAAAGAA		150 nM	
	tet(O)-probe	**6-FAM** [6]—TCGGGTTGT*CCATAGAGCCG—IABkFQ [12]		100 nM	
Ciprofloxacin for *C.jejuni* GyrA_T86I [2]	gyrA_Cj_fw	GTATAGTGGGTGCTGTTAT	118 (Acc. No. wt AB104527.1, pm CP053659.1)	400 nM	the current study [8]
	gyrA_Cj_re	CCTTGTCCTGTAATACTTG		400 nM	
	gyrA_Cj_wt	CCACATGGAGAT+A+**C**+A+GCAGTTTATG **ROX** [7]—		600 nM	
	gyrA_Cj_pm	CCACATGGAGAT+A+**T**+A+GCAGTTTATG —BHQ2 [13]		200 nM	the current study
Ciprofloxacin for *C.coli* GyrA_T86I [2]	gyrA_Cc_fw	GTATAGTAGGGGATGTTATCG	118 (Acc. No. wt CP092026.1 pm CP091310.1 CP082881.1)	400 nM	the current study
	gyrA_Cc_re	CCTTGTCCATCGATACTTG		400 nM	
	gyrA_Cc_wt	CCACATGGYGAT+A+**C**+T+GCTGTTTACG [17] **ROX** [7]—		600 nM	
	gyrA_Cc_pm	CCACATGGYGAT+A+**T**+T+GCTGTTTACG —BHQ2 [13, 17]		200 nM	
Erythromycin *erm*(B) [3]	erm(B)-fw	AGGGTTGCTCTTGCACACTC	125 (Acc. No. MF134831.1)	400 nM	the current study
	erm(B)-re	GAACATCTGTGGTATGGCGG		400 nM	
	erm(B)-probe	**Cy5** [8]—AGCTGCCAG*CGGAATGCTTTCA —IAbRQSp [14]		200 nM	
Erythromycin *23S rRNA*_ A2075G [4]	23S_A2075G_fw	GTGGAGGTGAAAATTCCTC	113 (Acc. No. wt CP020776 pm GU384931.1)	400 nM	the current study
	23S_A2075G_re	CAAAGCCTCCCACCTATC		400 nM	
	23S_A2075G_wt	CAAGACGG+A+**A**+A+GACCCCGTG **HEX** [9]—		600 nM	
	23S_A2075G_pm	CAAGACGG+A+**G**+A+GACCCCGTG —BHQ1 [15]		200 nM	
Internal PCR control (target gene ntb2 [5])	IPC-ntb2-fw	ACCACAATGCCAGAGTGACAAC	125	300 nM	[36]
	IPC-ntb2-re	TACCTGGTCTCCAGCTTTCAGTT		300 nM	
	IPC-ntb2 probe	**AriaMx: ATTO425** [10]— CACGCGCAT*GAAGTTAGGGGACCA —IABkFQ [12] **QuantStudio5 and CFX96: Cy5.5** [11]— CACGCGCAT*GAAGTTAGGGGACCA —NFQ-2 [16]		150 nM	

[1] Resistance gene *tet*(O); [2] point mutation in GyrA; [3] resistance gene *erm*(B); [4] point mutation in the 23S rRNA gene; [5] methyltransferase gene of *Nicotiana tabacum*; [6] FAM, 6-carboxyfluorescein; [7] ROX, carboxy-X-rhodamine; [8] Cy5, cyanine dye; [9] HEX, hexachlorofluorescein; [10] ATTO425, tetrazine dye; [11] Cy5.5, cyanine dye; [12] IABkFQ, Iowa Black® FQ quencher; [13] BHQ2, Black Hole Quencher; [14] IAbRQSp, Iowa Black® RQ quencher; [15] BHQ1, Black Hole Quencher; [16] NFQ-2, Non-Fluorescent quencher; [17] Y (C/T), degenerated nucleotide; +A, +G, +C, +T, base notation for Locked Nucleic Acid (LNA) bases; * = ZEN™ or TAO or abNFQ-2 (internal quencher for FAM and ATTO425 or Cy5 or Cy5.5 respectively); point mutation in labeled probes (pm) and wild type in unlabeled probes (wt) are underlined.

3.3. In Silico Screening in Comparison to Phenotypic Results

Binding sites were screened in silico for the designed primers and probes for the test panel to assess their ability to detect resistance genes and point mutations. Scanning the generated assemblies revealed the presence of binding sites in 94 isolates to *tet*(O), 10 isolates to *erm*(B), 12 isolates to A2075G point mutation in the 23S rRNA gene and 114 isolates (47 *C. coli*, 67 *C. jejuni*) to the GyrA_T86I mutation. The results of the binding site screening for the designed primer sets correlated with the results of the phenotypic resistance screening in EUCAMP3 (Table 4). The presence of primer and probe binding sites are summarized in Supplementary Material Table S2. For the two sensitive control strains *C. jejuni* strain DSM 4688 and *C. coli* strain 2012-70-443-2, no primer binding to the four designed resistance detection systems was predicted. For some assemblies based on short-read sequence data, the in silico screening predicted more than one copy of the *tet*(O)

gene. This could be confirmed only with long-read sequencing, as shown in [20]. Since thermotolerant *Campylobacter* spp. harbor three copies of the ribosomal RNA operon, *23S rRNA* A2075G was occasionally detected as multiple copies in some of the assemblies [48].

Table 4. Correlation between phenotypic resistance results and primer binding sites (theoretical genotypic results).

		Tetracycline				**Ciprofloxacin**				**Erythromycin**		
		***tet*(O)**		***gyrA_T86I***		***gyrA_T86I* *Cc***		***gyrA_T86I* *Cj***		***23S rRNA*_ A2075G**		***erm*(B)**
		S	**R**	**S**	**R**	**S**	**R**	**S**	**R**	**S**	**R**	
DE (food)	pheno	32	29	23	38	10	10	13	28	60	1	
	geno	32	29	23	38	10	10	13	27 +1*	60	1	0
DE (human)	pheno	24	44	13	55	5	19	8	36	66	2	
	geno	24	44	13	55	5	19 **	8	36	66	2	0
VN (food)	pheno	0	21	0	21	0	18	0	3	2	19	
	geno	0	21	0	21	0	17 +1*	0	3	2	9	10

German (DE) and Vietnamese (VN) isolates from food and human origin; pheno, phenotypic result; geno, genotypic in silico result, S, sensitive; R, resistance; +1* no 100% concordance for two isolates with additional point mutation in *gyrA* (*C. coli* VE_21 and *C. jejuni* FS_129 with mutation GyrA_T86V for valine instead of GyrA_T86I for isoleucine); ** 18 *C. coli* isolates with binding site to probe *gyrA_T86I_Cc* pm1 (C) and one isolate with binding site to probe *gyrA_T86I_Cc* pm2 (T).

The alignment of *Campylobacter* isolates in Figure 3 shows the binding sites to GyrA_T86I primers and probe for *C. coli* (a) and *C. jejuni* (b). A degenerated base Y (mixture of C and T) was integrated at position 9 of the probes for *gyrA_T86I_Cc*, to account for approximately 6% of *C. coli* isolates available in the NCBI nucleotide database (accession on 10 August 2022, determined by using NCBI Primer Blast Tool) that contain the base T instead of base C. The in silico screening was performed with corresponding alternative bases C (pm1) and T (pm2). In our study, 18 *C. coli* isolates showed base C and one human isolate showed base T ("**" in Table 4).

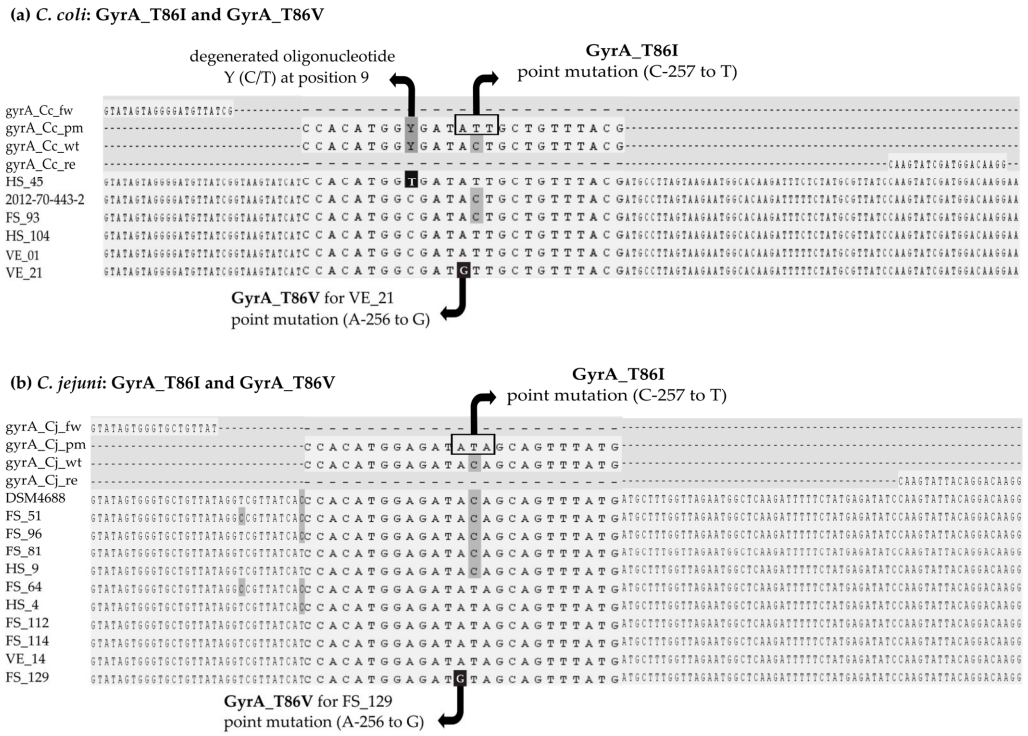

Figure 3. Primer binding sites for GyrA_T86I and GyrA_T86V of *C. coli* and *C. jejuni* (Aliview 1.2.6.); HS, human isolates; FS, food isolates; VE, Vietnamese food isolates; Cj, *C. jejuni*; Cc, *C. coli*.

Ciprofloxacin-resistant food isolates FS_129 (*C. jejuni*, Germany) and VE_21 (*C. coli*, Vietnam) harbored an alternative mutation compared to the common ciprofloxacin resistant isolates resulting in GyrA_T86V for valine instead of GyrA_T86I for isoleucine. *C. coli* VE_21 showed the base triplet GTT (valine) instead of ATT (isoleucine) in *gyrA*. Likewise, *C. jejuni* FS_129 showed the base triplet GTA (valine) instead of ATA (isoleucine). The designed LNA probes did not account for this additional mutation (A-256 to G) ("+1*" in Table 4).

3.4. Multiplex Real-Time PCR Assay

The pentaplex real-time PCR assay was developed to detect simultaneously four resistance determinants, including the suitable fragments of the resistance genes *tet*(O) and *erm*(B) as well as the point mutations GyrA_T86I and A2075G in the 23S rRNA gene. The sequences and final concentrations of primers and probes (IDT and metabion) are listed in Table 3 as well as in Supplementary Material Tables S3 and S4. The designed detection system for *tet*(O) detected all isolates with tetracycline resistance, independently of the *tet*(O) variants (see also Figure 2). For the detection of the resistance to ciprofloxacin in *C. coli* isolates, the designed probes (*gyrA_T86I_Cc*) included a degenerated base Y (mixture of C and T) at position 9. As predicted in the in silico screening, all *C. coli* isolates with ciprofloxacin resistance (18 isolates with base C and one human isolate HS_45 with base T) were detected (see also Table 4, "**").

In addition to the pentaplex real-time PCR assay, a triplex real-time PCR assay combined with a duplex real-time PCR assay consisting of the same primer and probe sequences but labeled with different fluorophores for detection were tested to allow usage of the system in case of limited optical modules in real-time PCR instruments (Supplementary Material Tables S5 and S6). The triplex real-time PCR method included two detection systems—resistance gene *tet*(O) in FAM channel (ZEN™: internal quencher, IABkFQ: Iowa Black® FQ quencher) and point mutation GyrA_T86I in ROX channel (BHQ1: Black Hole Quencher)—combined with IAC in HEX channel (ZEN™: internal quencher, IABkFQ: Iowa Black® FQ quencher). The duplex real-time PCR method covered the two resistance determinants for erythromycin resistance: resistance gene *erm*(B) in FAM channel (ZEN™: internal quencher, IABkFQ: Iowa Black® FQ quencher) and the point mutation *23S rRNA*_A2075G in HEX channel (BHQ1: Black Hole Quencher).

For evaluation of the real-time PCR assays, the threshold was set at about 10% of the maximum fluorescence of the positive control *C. coli* BfR-CA-15062 (VE_01) and *C. jejuni* BfR-CA-16092 (VE_14) for the four detection systems for resistance determinants and at 10% of the maximum fluorescence of the NTC (No Template Control) for the IAC. The triplex and duplex real-time PCR assays showed exactly the same PCR results as the pentaplex assay.

3.5. In-House Validation of the Multiplex Real-Time PCR Assay

3.5.1. Specificity and Selectivity

The performance of the pentaplex real-time PCR assay in detecting resistance determinants was tested on all 129 *Campylobacter* isolates from Germany and on 21 *Campylobacter* isolates from Vietnam. The target specificity and selectivity of the real-time PCR were assessed by studying the inclusivity and exclusivity for all four resistance determinants. Isolates, for which antimicrobial resistance was phenotypically determined in the EUCAMP3 panel and resistance determinants were predicted genotypically via sequence analysis (NGS), were also positive for these determinants in the real-time PCR assays, showing 100% inclusivity. The cycle of quantification (Cq-values) for positive signals detected via real-time PCR on AriaMx equipment is presented in Table 5. Furthermore, isolates with phenotypic susceptibility and absence of resistance-determinants, predicted via NGS, were also negative in the real-time PCR assays, showing 100% exclusivity. No false-positive or false-negative signals were detected.

Table 5. Summary of pentaplex real-time PCR results.

Antimicrobial Resistance	Resistance Determinant/Gene	Channel	Prevalence of Positive Signals in PCR	Mean Cq-Value ± Standard Deviation	Range of Cq-Values
tetracycline	*tet*(O)	FAM	*n* = 94	23.36 ± 1.23	21.06–26.45
ciprofloxacin *C. coli*	GyrA_T86I *Cc*	ROX	*n* = 47	23.87 ± 1.26	22.12–26.92
ciprofloxacin *C. jejuni*	GyrA_T86I *Cj*	ROX	*n* = 67	24.05 ± 0.97	21.94–26.14
erythromycin	*23S rRNA*_A2075G	HEX	*n* = 12	22.48 ± 0.75	21.54–23.92
erythromycin	*erm*(B)	Cy5	*n* = 10	24.10 ± 1.11	23.24–26.62
IAC	ntb2	ATTO425	*n* = 150	31.56 ± 0.46	30.67–33.10

Cq, cycle of quantification.

Amplification plots of the pentaplex real-time PCR-assay using AriaMx are presented in Figure 4. The two sensitive control strains *C. jejuni* strain DSM 4688 and *C. coli* strain 2012-70-443-2 were negative for the four detection systems for resistance determinants (Figure 4a–d). The positive control strains VE_01 and VE_14 were positive for the resistance determinants *tet*(O) and GyrA_T86I (Figure 4a,b). In addition, Figures 4c and 4d highlight the difference in the erythromycin resistance determinant, *erm*(B) gene for VE_01, and the point mutation *23S rRNA*_A2075G for VE_14 respectively.

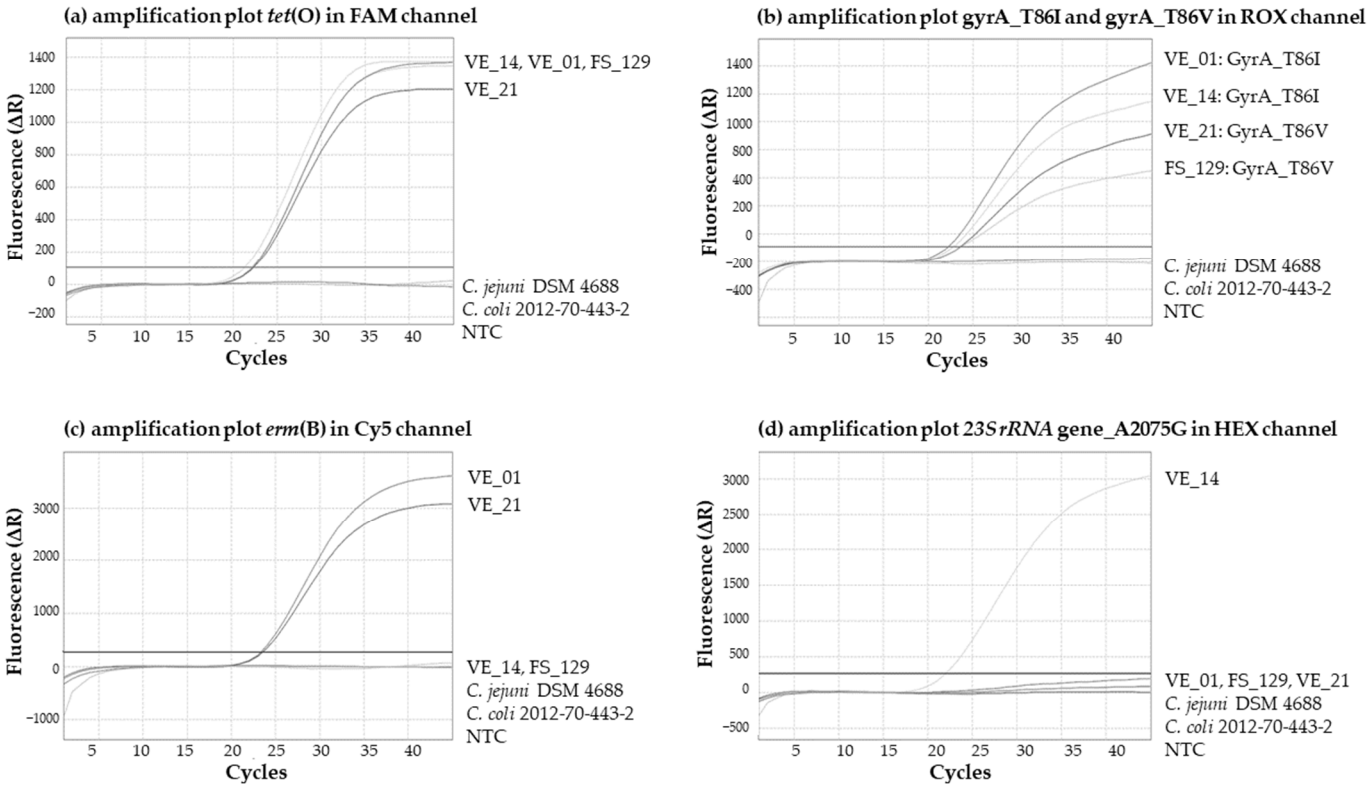

Figure 4. Amplification plots on AriaMx instrument for four resistant determinants. Real-time PCR detection of (**a**) *tet*(O); (**b**) both GyrA_T86I and GyrA_T86V mutation; (**c**) *erm*(B); (**d**) *23S rRNA*_A2075G mutation. Test strains harbored the following resistance determinants: BfR-CA-15062 (VE_01), *tet*(O)-*ermB*-GyrA_T86I; BfR-CA-16092 (VE_14), *tet*(O)-GyrA_T86I-*23S rRNA*_A2075G; FS_129, *tet*(O)-GyrA_T86V; VE_21, *tet*(O)-*ermB*-GyrA_T86V; DSM 4688 and 2012-70-443-2 served as negative controls for the four tested resistance determinants.

Two isolates FS_129 (*C. jejuni*, Germany) and VE_21 (*C. coli*, Vietnam) with the alternative mutation GyrA_T86V (see also Section 3.3 and "+1*" in Table 4) were detected in the ROX channel intended for the resistance determinant GyrA_T86I (Figure 4b). The base G (instead of A, Figure 3) did not interfere with the detection of the resistance-conferring mutation (GyrA_T86V).

3.5.2. Determination of Efficiency and $LOD_{95\%}$

The efficiency of the pentaplex real-time PCR assay was investigated on five DNA concentrations (5000, 1000, 500, 100, and 50 copies/µL DNA) for two isolates. The linear regression analysis was performed, using AriaMx software Version 2.0. With a coefficient of determination $R^2 \geq 0.98$, the efficiency was 100% with less than ± 20% deviation from theoretical value. The designed primer–probe systems met the quality criteria of the BVL guidelines [43,44], as well as the Guidelines for validation of qualitative real-time PCR methods [49]. The results of efficiency tests are presented in Supplementary Material Table S7.

The $LOD_{95\%}$ for the four detection systems for resistance determinants was investigated by measuring 12 independent DNA replicates at eight low-copy-number levels (20, 10, 4, 2, 1, 0.4, 0.2, and 0.02 copies/µL) for two isolates. The $LOD_{95\%}$, the 95% confidence interval, and the mean probability of detection (POD) curve with respect to the corresponding 95% confidence range were computed via a web service provided by QuoData (QuoData Web Service [42). It was observed that the limit of detection for *tet*(O), GyrA_T86I for *C. coli* and *23S rRNA*_A2075G is slightly lower ($LOD_{95\%} \leq 5$ copies/µL) compared to *erm*(B) and GyrA_T86I for *C. jejuni* ($LOD_{95\%} \leq 10$ copies/µL) (Table 6).

Table 6. Results of $LOD_{95\%}$.

	BfR-CA-16092 (VE_14, *C. jejuni*)		**BfR-CA-15062 (VE_01, *C. coli*)**	
	$LOD_{95\%}$	**95% Confidence Interval**	**$LOD_{95\%}$**	**95% Confidence Interval**
tet(O)	1.460 cp/µL	[0.961, 2.219]	2.533 cp/µL	[2.028, 5.229]
*gyrA*_T86I *C. jejuni*	6.115 cp/µL	[4.134, 9.093]		
*gyrA*_T86I *C. coli*			1.696 cp/µL	[1.119, 2.565]
*23S rRNA*_A2075G	1.214 cp/µL	[0.928, 2.265]		
erm(B)			5.835 cp/µL	[3.938, 8.663]

3.5.3. Robustness

The robustness of the pentaplex real-time PCR was evaluated by performing efficiency tests for the combination of two parameters, the real-time PCR equipment, and the master mix. Quantstudio5 and CFX96 Touch System as well as HiDi® Taq DNA Polymerase master mix gave the same results as the ones obtained using the AriaMx real-time PCR equipment and QuantiNova Multiplex PCR master mix. The detection systems for the four resistance determinants met the quality criteria with an efficiency between 80 and 120% and a coefficient of determination of $R^2 \geq 0.98$ for all tested combinations. The real-time PCR assay was not influenced by the changes in the tested measurement conditions. The results of efficiency tests for the robustness are presented in Supplementary Material Table S7.

4. Discussion

C. jejuni and *C. coli* are the predominant *Campylobacter* species in poultry, causing a substantial impact on public health care and leading to most foodborne zoonotic diseases in humans. The prescription of antibiotics can be necessary to treat infections. Yet, the development of antimicrobial resistance (AMR) poses a steadily increasing problem by limiting the number of effective antibiotics. The European Centre for Disease Prevention and Control (ECDC) and the World Health Organization (WHO) have underlined the

threat of antimicrobial resistance to patient safety and the need for global surveillance and concerted action throughout the European Region [50].

As van Belkum [51] presented in 2019, growth-based phenotypic analysis enables reliable antimicrobial susceptibility testing (AST) and ensures appropriate antibiotic therapy for infected patients. In our study, the EUCAMP3 microdilution panel was used for a reliable quantitative determination of the minimal inhibitory concentration (MIC) against relevant antimicrobials in food and human isolates of *C. jejuni* and *C. coli*. Among 129 German isolates, less than 20% were wholly susceptible to the six antibiotics tested. The most widespread antimicrobial resistance was against the fluoroquinolone ciprofloxacin. A high frequency of resistance to ciprofloxacin was also highlighted in the report of 2023 by the European Food Safety Authority (EFSA) and ECDC [29]. Combined resistance to ciprofloxacin and tetracycline was the most frequent resistance patterns observed in German human isolates and food isolates. In contrast, combined resistance to both ciprofloxacin and erythromycin, which is considered critically important for the treatment of campylobacteriosis [29], was not observed in *C. jejuni* and was rare in *C. coli* (8.3% for humans and 5.0% in food). The last two points were further reported in the report of EFSA and ECDC.

Comparing AMR against erythromycin, ciprofloxacin, and tetracycline in food and human isolates, no significant differences were detected in the frequency of antimicrobial resistance in our study. Moreover, due to the limited number of isolates no meaningful conclusion could be taken. This is in line with previous studies. McGill et al. [52] found similar resistance prevalence to erythromycin, ciprofloxacin, and tetracycline between food and human isolates in Ireland from 2001 to 2002. Similarly, in Estonia, Tedersoo et al. [53] found a comparable resistance to antibiotics for broiler chicken meat collected between 2018 and 2019 and human *Campylobacter* isolates. The appearance of resistant *Campylobacter* isolates in humans and animals likely reflects the wide use of antibiotics in poultry production. Yet, a few veterinary isolates (5 *C. jejuni*, 4 *C. coli*) (LGL) were investigated in EUCAMP3 and did not show a major divergence in the resistance profile compared to food and human isolates of this study. The prevalence of *Campylobacter* isolates with similar resistance profiles along the chicken food chain (high resistance rates to (fluoro-)quinolones and tetracycline and relatively low erythromycin resistance rate) was also shown in a German study from 2015 [54]. However, based on poultry data from 2014 to 2016 in Germany, Tenhagen et al. [55] demonstrated that antimicrobial resistance (AMR) and antimicrobial usage (AMU) cannot be systematically associated. Different factors, including animal species, two bacterial species (*C. jejuni* or *C. coli*), the antimicrobial agents, and the usage frequency (increase or decrease), should be further considered for a better understanding of the complex trends of the associations.

Since the early 2000s, genotypic-based methods, such as PCR assays, have been used to explore the determinants of antimicrobial resistance and are available as rapid screening methods to monitor and prevent the emergence of new bacterial antibiotic resistance. The qualitative pentaplex real-time PCR assay was developed based on the specific detection of four determinants in the current study. The elevated occurrence of resistance to ciprofloxacin and tetracycline in EUCAMP3 indicated the necessity to integrate two detection systems. First of all, the point mutation in *gyrA* led to the resistance-conferring amino acid exchange T86I in gyrase subunit A. Secondly, a detection system for the gene *tet*(O) included its *mosaic variants tet(O/M/O) and tet(O/32/O).* The frequency of these two resistance determinants was consistent with a previous study by Ghielmetti et al. [56], who illustrated an increasing prevalence of resistance to quinolones and tetracycline of *C. jejuni* isolates in Switzerland between 2003 and 2020. A combined resistance to both ciprofloxacin and erythromycin, which were considered crucial antimicrobials for the treatment of campylobacteriosis [50], was rarely detected in German isolates of this study (three isolates). Yet, it was frequently observed in isolates from Asian countries [57] and in 19 Vietnamese food isolates of the current study. To cover the resistance to erythromycin, a detection system for *erm*(B) and a detection system for the *A2075G s*ubstitution in the 23S rRNA gene were implemented in the real-time PCR assay. The gene *erm*(B) was exclusively

detected in Vietnamese food isolates, whereas the A2075G point mutation in the 23S rRNA gene was detected in isolates from Germany and Vietnam. The pentaplex real-time PCR was successfully applied to DNA from all isolates of the test panel. The results of the complete test panel in the pentaplex real-time PCR correlated with the phenotypic results assessed in the EUCAMP3 panel and with genotypic results predicted by NGS data.

Due to the simultaneous detection of four resistance determinants in *C. jejuni* and *C. coli* within a single PCR reaction, the here-developed real-time PCR has an advantage over previously described singleplex conventional PCR systems [13,21,23,24]. Compared to previously described multiplex real-time PCRs [8,22], this PCR is adapted to the current prevalence of antibiotic resistance in human and food isolates from Germany. The pentaplex real-time PCR shows a limitation regarding the point mutations A2074C/G/T in the 23S rRNA gene, which is also associated with erythromycin resistance [12,13,23]. These point mutations could not be tested via the test panel. It can only be proven with appropriate isolates if the pentaplex real-time PCR detects these point mutations. If necessary, a new detection system should be integrated. Furthermore, a real-time PCR for ertapenem might be beneficial, as many German isolates show resistance against this antimicrobial agent (see Table 2). Yet, ertapenem is firstly not included in the priority panel for *Campylobacter* monitoring of human isolates at the EU level [29], and secondly, it exceeds the capability of the real-time PCR machine in the detection of more than five channels.

The developed multiplex PCR assay in this study improved the accuracy of analysis of antibiotics resistance in *Campylobacter*. However, challenges might exist, particularly when applied to the simultaneous detection of point mutations. All four detection systems were optimized for the same annealing temperature and showed similar PCR amplification efficiencies on different PCR machines. Therefore, the accurate detection of each target was not influenced by the other detection systems. These requirements ensured reproducible Cq-values between 21 and 26 on a fixed amount of DNA. Setting the threshold at around 10% of maximum fluorescence guaranteed comparable results for tested isolates. The developed pentaplex real-time PCR in this study, showed to be robust enough to be transferred to other real-time PCR machines combined with a different master mix. In addition, the developed method was a reliable, sensitive, and easily introducible screening method for the detection of AMR related to ciprofloxacin, tetracycline, and erythromycin resistance on isolates of *Campylobacter jejuni* and *coli*.

Our development can be implemented as a warning tool in routine analysis to detect the spreading of antibiotic resistance. A decisive advantage of real-time PCR assays is that the method can further be developed to detect new incoming resistance determinants. Finally, the real-time PCR assay as rapid qualitative screening tool in combination with EUCAMP as a phenotypic tool for quantifying resistance can be considered as excellent complementary methods.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/microorganisms11122927/s1. Table S1: Sample overview, including phenotypic resistance determined with EUCAMP3 and resistance determinants relevant for real-time PCR assay. Table S2: Primer binding sites. Table S3: Protocols for pentaplex real-time PCR assay on AriaMx. Table S4: Protocols for pentaplex real-time PCR assay on CFX96 Touch System and Quantstudio5. Table S5: Protocols for triplex real-time PCR assay. Table S6: Protocols for duplex real-time PCR assay. Table S7: Results of efficiency and robustness tests for pentaplex real-time PCR assay.

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6.4 Publication 3: Identification of knowledge gaps in whole-genome sequence analysis of multi-resistant thermotolerant *Campylobacter* spp.

BMC Genomics

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Identification of knowledge gaps in whole-genome sequence analysis of multi-resistant thermotolerant *Campylobacter* spp.

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Abstract

Background *Campylobacter* spp. is the most frequent cause of bacterial food-borne gastroenteritis and a high priority antibiotic resistant bacterium according to the World Health Organization (WHO). European monitoring of thermotolerant *Campylobacter* spp. does not reflect the global burden of resistances already circulating within the bacterial population worldwide.

Methods We systematically compared whole genome sequencing with comprehensive phenotypic antimicrobial susceptibility, analyzing 494 thermotolerant *Campylobacter* poultry isolates from Vietnam and Germany. Any discrepancy was checked by repeating the wet lab and improving the dry lab part. Selected isolates were additionally analyzed via long-read Oxford Nanopore technology, leading to closed chromosomes and plasmids.

Results Overall, 22 different resistance genes and gene variants (e. g. *erm*(B), *aph(3')-IIIa*, *aph(2")-If*, *catA*, *lnu*(C), bla_{OXA}, *sat4*) and point mutations in three distinct genes (*gyrA*, 23S rRNA, *rpsL*) associated with AMR were present in the *Campylobacter* isolates. Two AMR genes were missing in the database and one falsely associated with resistance. Bioinformatic analysis based on short-read data partly failed to identify *tet*(O) and *aadE*, when the genes were present as duplicate or homologous gene variants. Intriguingly, isolates also contained different determinants, redundantly conferring resistance to chloramphenicol, gentamicin, kanamycin, lincomycin and streptomycin. We found a novel *tet*(W) in tetracycline sensitive strains, harboring point mutations. Furthermore, analysis based on assemblies from short-read data was impaired to identify full length phase variable *aad9*, due to variations of the poly-C tract within the gene. The genetic determinant responsible for gentamicin resistance of one isolate from Germany could not be identified. GyrT86I, presenting the main determinant for (fluoro-)quinolone resistance led to a rare atypical phenotype of ciprofloxacin resistance but nalidixic acid sensitivity. Long-read sequencing predicted AMR genes were mainly located on the chromosome, and rarely on plasmids. Predictions from long- and short-read sequencing, respectively, often differed. AMR genes were often organized in multidrug resistance islands (MDRI) and partially located in proximity to transposase genes, suggesting main mobilization of resistance determinants is via natural transformation and transposition in *Campylobacter*.

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Conclusions The results of this study suggest that there is frequent resistance gene duplication, mosaicism, and mutation leading to gene variation and truncation in *Campylobacter* strains that have not been reported in previous studies and are missing from databases. Furthermore, there is a need for deciphering yet unknown resistance mechanisms and resistance spread in thermotolerant *Campylobacter* spp. that may pose a challenge to global food safety.

Keywords NGS, Susceptibility testing, Antibiotic resistance, Long-read sequencing, Multidrug resistance islands, AMR, Mosaic genes, Resistance monitoring, Southeast Asia

Background

Spread of multidrug-resistant bacteria is a global public health threat, contributing to more than 670,000 diseases and 33,000 deaths annually in the European Union/European Economic Area (EU/EEA) [1]. Thermotolerant *Campylobacter* species are not yet under strict control through the implementation of a safety criterion but constitute the most common bacterial cause of gastroenteritis in the European Union (EU), with around 220,000 official cases in 2019 [2]. A study estimated the true incidence of campylobacteriosis to be 47 times (95% CI 14–117) higher than reported in the EU but varying considerably between member states [3]. In the EU in 2020, a slightly lower number of campylobacteriosis cases (21%) were hospitalized compared to *Salmonella* infections (29.9%) [4]. Epidemiological data on campylobacteriosis in Vietnam is scarce due to lack of surveillance programs. *Campylobacter* spp. accounted for the largest proportion of all isolates in Vietnamese rural children with diarrheal disease [5]. Furthermore, 20% of stool samples from infants with acute diarrhea in southern Vietnam were tested positive for *Campylobacter* spp. [6].

Acute campylobacteriosis is characterized by watery and bloody diarrhea, abdominal cramps, fever and nausea [7]. In addition, long-term autoimmune sequelae might occur such as the Guillain-Barré syndrome in 0.07%, reactive arthritis in approximately 1–5% and irritable bowel syndrome in around 4% of acute cases [8]. These long-term diseases caused by campylobacteriosis contribute to a public health burden largely underestimated by the public.

A recent study showed that 31% of the reported campylobacteriosis cases were treated with antibiotics, mainly ciprofloxacin and macrolides [9]. According to the World Health Organization (WHO), *Campylobacter* spp. are high-priority antibiotic-resistant pathogens, particularly with regard to their fluoroquinolone resistance [10].

C. jejuni and *C. coli* asymptomatically colonize the intestinal tract of various animal species, both wild and domestic, which constitutes a potential reservoir for human infections. In particular, poultry is recognized as major source of *Campylobacter* spp. infections in humans, most probably via the consumption of cross-contaminated food during handling of raw meat or direct animal contact [11]. Zoonosis monitoring in Germany revealed a high prevalence of 51.8% *Campylobacter* spp. positive fresh chicken meat in 2020 [12]. Likewise, 31% of the tested chicken meat from Hanoi was contaminated with thermotolerant *Campylobacter* spp. [13]. Previous studies showed that *Campylobacter* isolates from Vietnam were frequently resistant to (fluoro-)quinolones (62.5–95%) and tetracyclines (71.4–75%), moderately frequent to frequently resistant to streptomycin (21.4–62.5%), and rarely to less frequently resistant to erythromycin (7.4–25%) and gentamicin (7.1–25%) [14–16]. In Germany, recent results from the 2020 zoonosis monitoring program from broiler ceca [12] revealed frequent resistance of *C.* spp. to ciprofloxacin (83.4% for *C. jejuni* and 81% for *C. coli*) and tetracycline (66.4% for *C. jejuni* and 69% for *C. coli*). All broiler isolates from cecal content were sensitive to gentamicin. Resistances to macrolides were only observed in *C. coli* isolates (17.2%). Streptomycin resistance was higher in *C. jejuni* (35%) than in *C. coli* (3.4%), which was a new observation compared to the previous years [17, 18].

Increasing occurrence of antimicrobial resistance (AMR), impeding the effectiveness of antibiotics used for treatment of bacterial diseases, poses a threat to global health [19]. Use of antimicrobials in animal production is recognized as one of the drivers of AMR [20, 21]. In order to reduce the spread of antibiotic resistance in animal production, livestock farms in Germany have been obliged to report and reduce their use of antibiotics since 2011. The overall significant decrease of antibiotic use in all farm animals by 31.6% between mid-2014 compared to mid-2017 was only marginally reflected in the poultry production chain, with a maximum reduction of 3.8% observed in turkey production [22]. From 2017 until 2021, antibiotic use in poultry was significantly reduced by 11.5% in chicken and 13.1% in turkey, while during the same time period antibiotic use in all animals was reduced by 18.2% [23]. In Vietnam, antimicrobial use in livestock accounted for 71.7% (2,751 t) of the total antimicrobials used in 2015. This corresponded to nearly the same amount of antimicrobials per kg of biomass used for human and animal treatment and a 1.6-fold higher use compared to the EU [24]. Some of the antimicrobials used in both countries were among the "highest priority critically important antimicrobials" defined by WHO, i.e.

(fluoro-)quinolones, polypeptide antibiotics and macrolides [25–28].

Systematic analysis and reliable diagnostics of multiresistant bacterial pathogens are essential to prevent their global spread. A number of studies, delivering whole genome sequencing data with some phenotypic analysis of thermotolerant *Campylobacter* spp. have previously been published [29–35]. However, rigorous in-depth analyses, aiming to identify and solve discrepancies between whole genome sequencing data and phenotypic resistance profiles are scarce for *Campylobacter* spp. Here, we evaluated a common strategy, the prediction of AMR resistant determinants by AMRFinderPlus based on short-read assembly data by recording concordances and experimentally re-analyzing discrepancies between pheno- and genotype of nearly 500 thermotolerant *Campylobacter* spp. from Germany and Vietnam. A selection of isolates was also processed by long-read sequencing using the Oxford Nanopore Technology. The study aimed at identifying knowledge gaps to be addressed in order to use WGS as a tool to reliably predict AMR in *Campylobacter* spp. In particular, it should be clarified, which specific features of AMR in *Campylobacter* spp. still pose problems for current routine WGS analysis and have to be addressed in the future.

Methods

Isolates and growth conditions

C. coli and *C. jejuni* isolates from Germany were isolated within the zoonosis monitoring program from different poultry matrices from 2013 to 2021 by the federal state laboratories according to EN ISO 10272-1 valid in the respective year [36, 37]. Isolates from Vietnam were isolated from fresh chicken feces from primary production and chicken meat from retail in Hanoi and Haiphong between 11/2016 and 03/2018 by the National Institute of Veterinary Research (Hanoi, Vietnam) by direct streaking on modified charcoal cefoperazone deoxycholate agar (mCCDA, Thermo Fisher Scientific Inc., Waltham, MA, USA) according to EN ISO 10272-1:2017 [37]. At the National Reference Laboratory, isolates were subcultured on Columbia agar supplemented with 5% sheep blood (Oxoid, Thermo Fisher Scientific Inc., Waltham, MA, USA) (ColbA) or passaged in Bolton broth (Oxoid, Thermo Fisher Scientific Inc.) and subcultured on mCCDA in case isolates still exhibited non-*Campylobacter* background flora. Incubation was performed for 48 h under microaerobic conditions (5% O_2, 10% CO_2, rest N_2) at 42 °C. The isolates were stored at −80 °C using the cryobank system (Mast Diagnostica GmbH, Reinfeld, Germany). For DNA extraction and antibiotic susceptibility testing isolates from −80 °C stock cultures were grown on ColbA for 24 h under microaerobic conditions at 42 °C and subcultured once for another 20±2 h prior to use.

Species differentiation by PCR

DNA of the isolates was extracted by resuspension of a quarter 10 µL loop of cell material in 400 µL Tris-EDTA buffer (1 mM Tris, 0.1 mM sodium ethylenediaminetetraacetic acid at pH 8.0) followed by 1:100 dilution in 5% Chelex 100 resin (Bio-Rad Laboratories GmbH, Feldkirchen, Germany). Subsequently, thermal lysis was performed for 15 min at 95 °C. After centrifugation at 14,000 x g at 4 °C for 10 min, 2.5 µl of the supernatant was used for real-time PCR analysis, targeting specific fragments of the *C. jejuni mapA*, the *C. coli ceuE* and the *C. lari glyA* genes [38, 39].

Antibiotic susceptibility testing by microdilution

Broth microdilution susceptibility testing was performed according to M45-A and VET06 [40, 41]. Strains subcultured for 24±2 h at 42°C on ColbA were inoculated in cation-supplemented Mueller-Hinton broth (Thermo Fisher Scientific Inc., Waltham, MA, USA) with 5% fetal calf serum (PAN-Biotech, Aidenbach, Germany) (CAMHB/FCS) at a bacterial concentration of $2–8\times10^5$ CFU/ml. For this purpose, bacteria were suspended at an OD_{600} of 0.2 in buffered peptone water (10 g/L peptone, 5 g/L NaCl, 9 g/L $Na_2HPO_4\times12\ H_2O$, 1.5 g/L KH_2PO_4, pH 7.0±0.2 at 25°C), which corresponds to approximately 5×10^8 CFU/ml [42]. Upon a 10^{-3} dilution in CAMHB/FCS, 100 µl of the resulting 5×10^5 CFU/ml were used as inoculum per well. The inoculum was occasionally controlled by plating 100 µl of a further 10^{-3} dilution in duplicate on ColbA in order to obtain approximately 50 CFU per plate. Minimum inhibitory concentrations were determined using the European standardized EUCAMP2 plate (Thermo Fisher Scientific Inc., Waltham, MA, USA). In addition, custom plate formats were prepared with the following antimicrobial agents (Sigma Aldrich, St. Louis, MO, USA) and their concentration ranges: ampicillin (0.5–512 mg/L), chloramphenicol (2-128 mg/L), florfenicol (0.25-16 mg/L), kanamycin (2-1024 mg/L), lincomycin (0.25–128 mg/L), nourseothricin (mixture of streptothricins C, D, E and F; 1-512 mg/L) and spectinomycin (2-512 mg/L). Stock solutions of the antimicrobials were prepared in H_2O, for florfenicol in dimethyl sulfoxide, and for chloramphenicol in ethanol. The microtiter plates with U-bottom (Greiner Bio-One International GmbH, Frickenhausen, Germany) were prepared one day in advance by adding 50 µl CAMHB/FCS supplemented with the respective double-concentrated antimicrobial per well and stored sealed at 5°C before inoculation. Test strains were prepared as described above except that the inoculum was double-concentrated in a volume of 50 µL (1×10^6 CFU/ml), which was added to each well of

the custom plates, already loaded with 50 µl of double-concentrated antimicrobial per well. Samples were incubated at 37°C for 44±4 h under microaerobic conditions. Minimal inhibitory concentrations (MICs; in mg/L) were semi-automatically analyzed using the Sensititre™ Vizion™ system (Thermo Fisher Scientific Inc., Waltham, MA, USA) and the Sensivizion V2.0 software (MCS Diagnostics BV, Swalmen, The Netherlands). Epidemiological cut-off values (ECOFFs, Table 1) for resistance determination were based on the European Committee on Antimicrobial Susceptibility Testing [43], if available for *Campylobacter* spp. Otherwise, "elevated non-wildtype MICs" were considered based on EUCAST *Campylobacter* spp. MIC distributions and the data obtained in our study for kanamycin (Figure S1). For lincomycin, the "elevated non-wildtype MICs" were based on a previous publication [44]; furthermore, the "elevated non-wildtype MICs" were established based on data from this study for nourseothricin and spectinomycin (Figure S1). For quality assessment of EUCAMP2 plate format, *C. jejuni* strain DSM 4688 (DSMZ - German Collection of Microorganisms and Cell Cultures GmbH, Braunschweig, Germany) and *C. coli* strain 2012-70-443-2 (Technical University of Denmark, Lyngby, Denmark) were included, which displayed sensitive phenotypes.

The correlation of phenotypic resistance against antimicrobials on custom plates and presence of each known AMR gene was experimentally tested by analyzing at least five additional isolates without the resistance marker as negative control. For the frequently observed bla_{OXA} genes, a portion of bla_{OXA} positive isolates (139/459) underwent susceptibility testing with ampicillin (Table S1).

Whole genome sequence analysis

DNA for short-read sequencing was extracted using the PureLink Genomic DNA Mini Kit (Thermo Fisher Scientific, Waltham, MA, USA) according to the manufacturer's protocol. For this purpose *Campylobacter* isolates were subcultured on ColbA for 20±2 h under microaerobic atmosphere at 42°C and bacteria were harvested from 1 mL of resuspended bacteria at OD_{600} of 2 by centrifugation at 14,000 x g for 5 min. The cell pellet was either directly used for DNA extraction or stored at -20°C. DNA for long-read sequencing was extracted using the MagAttract HMW Genomic Extraction Kit (Qiagen N.V., Venlo, The Netherlands) following manufacturer's instructions, except starting with a cell pellet derived from 1 mL of bacteria at an OD_{600} of 2 upon centrifugation, followed by incubation for 1.5 h at 56°C and 900 rpm of agitation. The quality of the DNA was evaluated by spectral analysis (NanoDrop Spectrophotometer, Thermo Fisher Scientific, Waltham, MA, USA) and the concentration was fluorimetrically quantified by Qubit 3.0 Fluorometer (dsDNA HS Assay Kit 0.2–100 ng; Thermo Fisher Scientific, Waltham, MA, USA). DNA extracts for long-read sequencing were analyzed with the 5200 Fragment Analyzer System (Agilent Technologies Corp., Santa Clara, CA, USA) using DNF-464 HS Large Fragment Kit (Agilent Technologies Corp., Santa Clara, CA, USA) to check for DNA degradation/RNA contamination as well as sufficient length (>10,000 bp) of the DNA fragments. DNA libraries for short-read sequencing were prepared using the Illumina DNA Prep, (M) Tagmentation Kit according to the manufacturer's instructions (Illumina, Inc., San Diego, CA, USA) but using half of the volume of all reagents. Paired-end sequencing was performed on the Illumina MiSeq benchtop sequencer using the MiSeq

Table 1 Epidemiological cut-off values (ECOFFs, if available) or "elevated non-wildtype MIC values" for evaluation of antibiotic susceptibility testing results of thermotolerant *Campylobacter* spp.

Antimicrobial	MIC [mg/L], resistant >, *C. jejuni*	MIC [mg/L], resistant >, *C. coli*	Reference
Ampicillin	16	16	ECOFF for *C.* spp. [43]
Chloramphenicol	16	16	ECOFF for *C.* spp. [43]
Ciprofloxacin	0.5	0.5	ECOFF for *C.* spp. [43]
Erythromycin	4	8	ECOFF for *C.* spp. [43]
Florfenicol	4	4	ECOFF for *C.* spp. [43]
Gentamicin	2	2	ECOFF for *C.* spp. [43]
Kanamycin	16	16	elevated non-wildtype MICs ([43]; Fig. S1)
Lincomycin	8	8	elevated non-wildtype MICs [44]
Nalidixic acid	16	16	ECOFF for *C.* spp. [43]
Nourseothricin	4	4	elevated non-wildtype MICs (Fig. S1)
Spectinomycin	64	64	elevated non-wildtype MICs (Fig. S1)
Streptomycin	4	4	ECOFF for *C.* spp. [43]
Tetracycline	1	2	ECOFF for *C.* spp. [43]

reagent kit v3 (600 cycles, Illumina, Inc., San Diego, CA, USA) or on the Illumina NextSeq 500 sequencer using the NextSeq 500/550 mid output kit v2.5 (300 cycles, Illumina, Inc., San Diego, CA, USA) with read lengths ranging between 2×149 and 2×301, respectively. DNA libraries for long-lead sequencing (Oxford Nanopore Technology (ONT)) were prepared using the Rapid Barcoding Kit 96 (SQK-RBK110.96, Oxford Nanopore Technologies Limited, Oxford, United Kingdom) according to manufacturer's instructions. Sequencing was performed on the MinION Mk1C instrument using a MinION FlowCell (R9.4.1, Oxford Nanopore Technologies Limited, Oxford, United Kingdom). For verification of truncation of the housekeeping multi-locus sequence typing (MLST) gene *aspA* in BfR-CA-16251, a PCR amplification of *aspA* was performed using the following primers, *aspA*-A9 (5'-AGT ACT AAT GAT GCT TAT CC-3') and *aspA*-A10 (5'-ATT TCA TCA ATT TGT TCT TTG C-3') [45; https://pubmlst.org/, last accessed on 05/01/2024]. Subsequently, the PCR fragment was purified using QIAquick PCR Purification Kit (Qiagen, N.V., Venlo, The Netherlands) and suitable amounts of DNA supplemented with either sequencing primer *aspA*-S3 (5'-CCA ACT GCA AGA TGC TGT ACC-3') or *aspA*-S6 (5'-TTC ATT TGC GGT AAT ACC ATC-3') [45; https://pubmlst.org, last accessed on 01/05/2024] were Sanger sequenced (Eurofins Scientific SE, Luxembourg City, Luxembourg).

Bioinformatic Analysis

Illumina paired-end reads were trimmed and *de-novo* assembled with the AQUAMIS pipeline v1.3.8 [46], which implements e.g. fastp v0.23.2 for read quality control and trimming [47] and shovill v1.1.0 for assembly [48] as well as Quast v. 5.0.2 for assembly quality control. Sufficient quality was defined as base accuracy Q30 (error rate 1:1000) for more than 80% of the reads, and a minimum read coverage of 40. In addition, 10 sequences (Table S2) were also assembled using SKESA assembler using the NCBI Read Assembly and Annotation Pipeline Tool (RAPT at https://www.ncbi.nlm.nih.gov/rapt; last accessed on 01/05/2024).

Assembled contigs were analyzed for presence of resistance determinants as well as for plasmid markers using the BakCharak pipeline v3.0.3 [49]. The pipeline is composed of various modules, each serving a specific purpose. It includes the antimicrobial resistance gene finder module which identifies AMR determinants through the use of AMRFinderPlus v3.10.45 [50] and its corresponding AMRFinder database 2023-08-08.2. The Plasmidfinder employs ABRicate v1.0.1 [51] and utilizes the Center for Genomic and Epidemiology (CGE) plasmidfinder database. Default thresholds were applied for both ABRicate and AMRFinderPlus, which included a minimum identity threshold of 80% and 90%, respectively, and a minimum coverage threshold of 50% for both tools. Furthermore, Platon v1.6 [52] was used to predict putative plasmid location of contigs.

In addition to the BakCharak pipeline, assembled whole genome sequences from isolates showing pheno-genotype discrepancies were analyzed with ResFinder v4.1 [53] using low thresholds of identity (50%) and coverage (40%). This approach not only addressed missing genes in the AMRFinderPlus database but also revealed partial genes and those with reduced homology. Identified AMR gene sequences were extracted from the assembled sequences and analysed via the NCBI Basic Local Alignment Search Tool [54, 55] in order to find the closest AMR gene homolog. The latter search was conducted either using blastn or blastp, with the corresponding databases NCBI nucleotide collection (nr/nt) or non-redundant protein sequences (nr), respectively. Alignments of translated protein sequences were created using UniProt [56]. Subsequently the draft genome assemblies were screened with ABRicate v1.0.1 for their presence/absence of the respective AMR gene homolog (Table S3) using Linux command line. The reference resistance gene and protein sequences representing the most abundant closest relatives are depicted in Table S3. Alignments of nucleotide sequences and mapping of trimmed raw reads to reference resistance genes or the promoter region of bla_{OXA} genes was performed by Geneious Prime 2020.2.2 (Biomatters Ltd., New Zealand) using default settings. For verification of truncation of the housekeeping MLST gene *aspA* in BfR-CA-16251, *aspA* reference gene Cj0087 of *C. jejuni* NCTC 11168 (NC_002163.1) was used for mapping of raw reads and additional Sanger sequences were analyzed using SeqMan Pro (Lasergene 17, DNASTAR Inc., WI, USA).

Ridom SeqSphere+v8.4.2 (Ridom, Muenster, Germany) was used to perform phylogenetic analysis on assembled genome contigs from short-read sequencing using either the seven housekeeping genes based MLST or the core genome (cgMLST) scheme of 1343 gene targets previously defined [57]. A threshold of 98% identity and 98% of coverage to one of the respective alleles of the reference sequence NC_002163.1.gb (*C. jejuni* NCTC 11168) was used. At least 95% "good targets" were found based on cgMLST analysis. In addition, the 7-genes MLST scheme was used to lower the resolution for visualization of isolate diversity [45, https://pubmlst.org]. New MLST alleles and MLST sequence types were uploaded to PubMLST [58].

The Oxford Nanopore Technology sequencing data was basecalled using Guppy v. 6.0.1 in the "super-accuracy" mode (Oxford Nanopore Technologies, Oxford, UK). Subsequently, ONT reads were assembled and quality was assessed with the MiLongA Pipeline v1.0.1. [59]. This pipeline includes various tools, such as porechop v0.2.4

[60] for trimming and Unicycler v0.4.8 [61] for hybrid assembly. Assembled hybrid genome contigs from short- and long-read sequencing were annotated with Bakta [62] and AMR determinant identification was performed using AMRFinderPlus v3.10.45 [50] and its corresponding database (v. 2023-08-08.2). Raw read sequences and either complete genomes (for those isolates sequenced by ONT) or draft genomes were published within the BioProjects No. PRJNA562653, PRJNA595957, PRJNA648048 and PRJNA872862 at the NCBI sequence read archive (SRA) and Genome database.

Statistical analyses

Campylobacter isolates were categorized into susceptible and resistant using the ECOFFs or elevated non-wildtype MIC values (Table 1). A variable "3–4 resistances" was defined for isolates with three or four resistances based on EUCAMP2 plate format, with nalidixic acid and ciprofloxacin being combined as (fluoro-)quinolones. An odds ratio (OR) with 95% confidence interval (CI) was calculated (Table S4, [63, 64]). *p*-values of less than 0.05 were considered statistically significant.

Results

The 240 *C. coli*$_{DE}$ (n=115) and *C. jejuni*$_{DE}$ (n=125) isolates from Germany were taken from the strain collection of the laboratory. They were isolated from different matrices and locations in Germany by federal state laboratories as part of the zoonosis monitoring programs (Table S1, [12, 65]). The 254 *C. coli*$_{VN}$ (n=99) and *C. jejuni*$_{VN}$ (n=155) isolates from Vietnam were derived from fresh chicken fecal samples collected between November 2016 and December 2017 from primary chicken production of 26 different chicken farms and from cecum and retail samples in 2018 in the province of Hanoi and Haiphong. The principle size of the farms varied from 100 to 5,000 animals per flock, with only a few samples taken from farms with a flock size of 50,000. When farmers were asked for use of antimicrobials for treatment of chicken during rearing, they reported application of various substances, mostly tetracyclines (chlortetracycline, doxycycline and oxytetracycline), the macrolide tylosin, colistin as polymyxin, the ß-lactam amoxicillin and aminoglycosides like gentamicin and neomycin. In total, 254 Vietnamese thermotolerant *Campylobacter* spp. isolates were obtained, of which 155 were identified as *C. jejuni* and 99 as *C. coli*.

Identification of highly resistant isolates using a standardized microtiter panel

Antimicrobial susceptibility testing was performed for all 494 isolates using the European standardized microtiter plate format EUCAMP2. The panel includes six representative antibiotics from four different antibiotic classes: aminoglycosides, (fluoro-)quinolones, macrolides, and tetracyclines. The proportion of sensitive isolates among the isolates from Germany was 10.4% (n=12) for *C. coli* and 16% (n=20) for *C. jejuni*; meanwhile, no sensitive isolates were detected among the *Campylobacter* spp. isolates from Vietnam (Fig. 1). In particular, 94.9% (94/99) of *C. coli*$_{VN}$ and 29% (45/155) of *C. jejuni*$_{VN}$ isolates were resistant to three or four compound classes. In comparison, *C. coli*$_{DE}$ and *C. jejuni*$_{DE}$ isolates were less

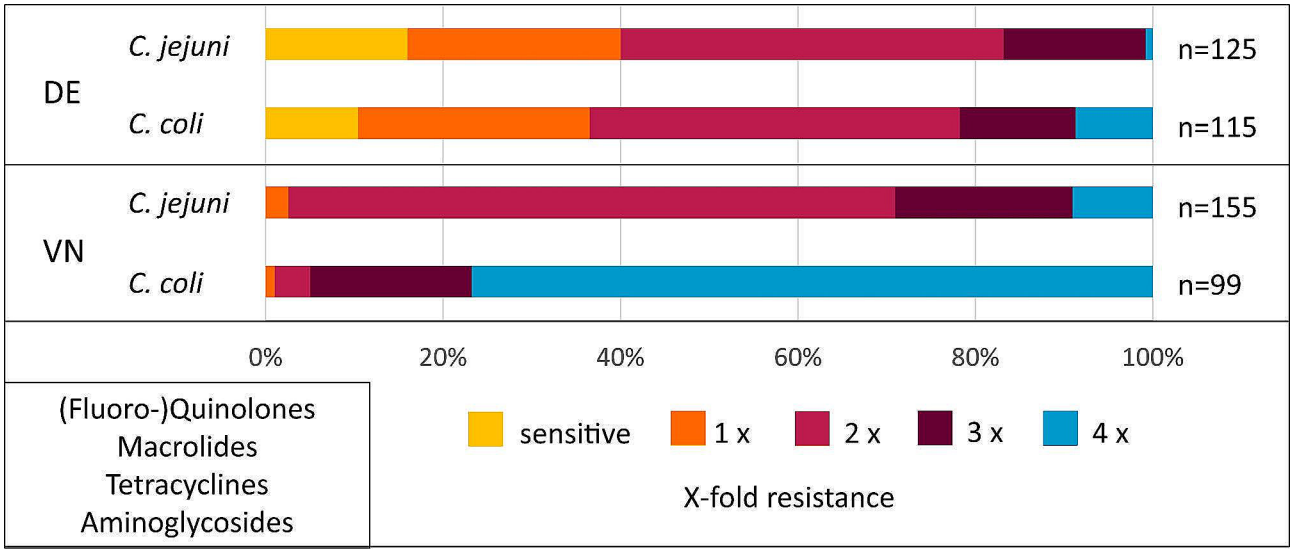

Fig. 1 Vietnamese *C. coli* isolates displayed highest prevalence of combined resistance to all tested antimicrobial classes. Susceptibility to (fluoro-)quinolones (nalidixic acid, ciprofloxacin), macrolides (erythromycin), tetracycline and aminoglycosides (gentamicin, streptomycin) was tested by microdilution. X-fold resistance, number of antimicrobial classes to which isolates showed resistance (depicted in % of total number of tested isolates per category (n)); DE, German isolates; VN, Vietnamese isolates. Odds ratios are depicted in Table S4

frequently resistant to three or four compound classes (21.7%, 25/115 and 16.8%, 21/125, respectively).

Table 2 provides an overview of the prevalence of resistance to individual antimicrobials tested within the EUCAMP2 plate format. Phenotypic resistance to ciprofloxacin was high in *C. jejuni*$_{DE}$ and *C. coli*$_{DE}$ isolates (78.4 and 80.9%, respectively) whereas 98.1% of *C. jejuni*$_{VN}$ isolates and all *C. coli*$_{VN}$ displayed resistance to ciprofloxacin, respectively. Resistance to the erythromycin was low among *C. jejuni*$_{DE}$ isolates, with only one resistant *C. jejuni*$_{DE}$ isolate identified (0.8%) and moderately frequent among *C. coli*$_{DE}$ isolates (18.3%).

In Vietnam, resistance to erythromycin was predominantly found for *C. coli*$_{VN}$ isolates (76.8%), while 11% of the *C. jejuni*$_{VN}$ isolates showed resistance to this antimicrobial substance. About two-third of *Campylobacter* isolates from Germany were tetracycline resistant (64 and 69.6% for *C. jejuni*$_{DE}$ and *C. coli*$_{DE}$, respectively). In comparison, the counterparts from Vietnam were almost completely resistant to this antibiotic (≥99%); in fact, only one *C. jejuni*$_{VN}$ and one *C. coli*$_{VN}$ isolate analyzed in this study were tetracycline sensitive. Resistance to gentamicin was only detected in two *C. coli*$_{DE}$ isolates, whereas all *C. jejuni*$_{DE}$ were sensitive. In contrast, 78.8% of the *C. coli*$_{VN}$ isolates and 21.9% of the *C. jejuni*$_{VN}$ were resistant to gentamicin. Resistance to streptomycin was highest in *C. coli*$_{VN}$ isolates (85.9%), while in *C. coli*$_{DE}$ this resistance was moderately frequent with 13%, which was similar to *C. jejuni*$_{VN}$ (12.9%). The *C. jejuni*$_{DE}$ isolates were slightly more resistant to streptomycin (18.1%) than the *C. coli*$_{DE}$ isolates and the *C. jejuni*$_{VN}$ isolates but this was not statistically significant. Overall, the isolates from Vietnam were 5.1 times more likely resistant to three or more antibiotics compared to their counterparts from Germany (OR 5.1, 95% CI 3.4–7.6; Table S4). Taking the same variable of "3–4 resistances", *C. coli* isolates from Vietnam were far more resistant against the tested antimicrobials than the *C. jejuni* isolates from the same geographic location (OR 46.0, 95% CI 17.5-120.5). The likeliness of displaying 3–4 resistances was not significantly different for *C. coli*$_{DE}$ versus *C. jejuni*$_{DE}$ (p=0.33). However, significantly different acquisition of resistance to erythromycin was observed for *C. coli* isolates compared to *C. jejuni* not only in Vietnam (OR 26.8, 95% CI 13.5–53.3) but also in Germany (OR 27.7, 95% CI 3.7-209.7).

Phylogenetic diversity of strains is a good basis for in-depth AMR analysis

All 494 isolates were subjected to whole-genome sequencing using short-read Illumina technology. To determine phylogenetic relationship of the *Campylobacter* isolates, first multi-locus sequence typing method (MLST) for comparison of the seven housekeeping genes was applied (Fig. 2). For higher resolution, the core gene MLST (cgMLST) scheme based on the comparison of 1343 core genes was used [57] with missing loci pairwise ignored (Ridom SeqSphere+) (Table S5). We identified 15 new MLST allele variants, including an *aspA* allele with a deletion of 19 bases in BfR-CA-16251 (Figure S2) and assigned 191 different sequence types (STs), of which 41 were novel (Fig. 2, Table S1). The *C. jejuni*$_{VN}$ subpopulation possessed the greatest diversity of different ST types (n=70), followed by the *C. jejuni*$_{DE}$ subpopulation (n=53). *C. coli* possessed less diversity, since isolates from Germany belonged to 45 different STs, while *C. coli* from Vietnam were attributed to 32 different STs. They were part of the common clonal complexes CC-828 (n=148) or CC-1150 (n=15) or did not belong to any CC (n=51). Although, some isolates from Germany and Vietnam shared the same MLST sequence types (n_{ST}=9, Fig. 2, circles with dashed line), they were not phylogenetically related on the basis of cgMLST (Table S5). Consistently, resistance patterns were independent of phylogenetic origin, since similar AMR patterns were distributed all over the identified MLST types (Fig. 2).

Distribution of resistant determinants in *Campylobacter* spp. from Germany and Vietnam

Short-read whole genome sequencing results were processed using the AMRFinderPlus tool [50] for identification of AMR genes. In total, 22 different resistance genes and gene variants (e. g. *erm*(B), *tet*(O), *aadE*, *aph(3')-IIIa*, *aad9*, *catA*, *lnu*(C), *bla*$_{OXA}$, *sat4*) and point mutations in three distinct genes (*gyrA*, 23S rRNA, *rpsL*) associated

Table 2 Antimicrobial resistance in *C. coli* and *C. jejuni* from Germany and Vietnam according to EUCAMP2 plates

	Campylobacter jejuni				*Campylobacter coli*			
	Germany (n=125)		Vietnam (n=155)		Germany (n=115)		Vietnam (n=99)	
	n	%	n	%	n	%	n	%
Ciprofloxacin	98	78.4	152	98.1	93	80.9	99	100.0
Erythromycin	1	0.8	17	11.0	21	18.3	76	76.8
Gentamicin	0	0.0	34	21.9	2	1.7	78	78.8
Nalidixic acid	92	73.6	149	96.1	92	80.0	99	100.0
Streptomycin	23	18.4	20	12.9	15	13.0	85	85.9
Tetracycline	80	64.0	154	99.4	80	69.6	98	99.0

ECOFFs (if available) or elevated non-wildtype MICs for resistance evaluation are depicted in Table 1; n, number of tested isolates; odds ratios are depicted in Table S4

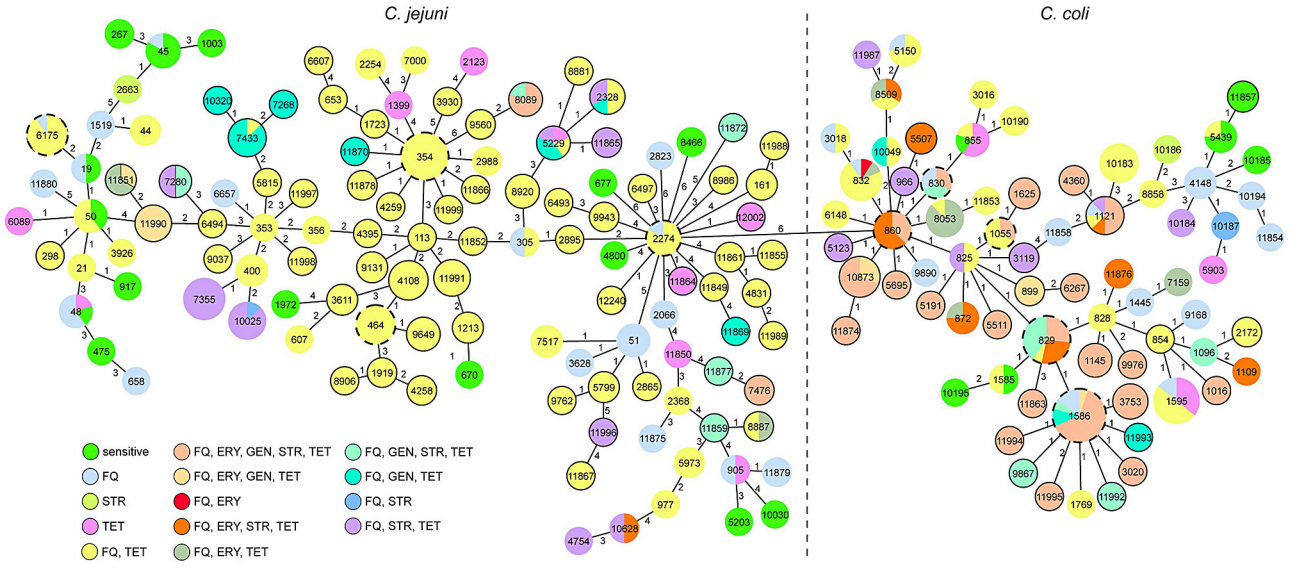

Fig. 2 Test strains showed phylogenetical diversity, with AMR patterns distributed all over the identified MLST types. Minimum spanning tree (MST) based on MLST analysis. Colors indicate different phenotypic resistance profiles obtained with EUCAMP2 plate format. Nodes with numbers represent ST types; node size corresponds to the number of isolates (e.g. ST-267 is only represented by one isolate). Closed circles, Vietnamese isolates; open circles, German isolates; dashed-lined circles, isolates from both countries. FQ, (fluoro-)quinolone resistant; STR, streptomycin resistant; ERY, erythromycin resistant; TET, tetracycline resistant; GEN, gentamicin resistant. Numbers between nodes indicate numbers of allele difference based on 7 housekeeping genes (cgMLST differences are depicted in Table S2). MST was created with Ridom SeqSphere + software.

with AMR were identified (Fig. 3 and Table S1). The resistance determinants were differently distributed among *Campylobacter* populations from Germany and Vietnam and fewer AMR genes were found in *C. jejuni* compared to *C. coli* (Fig. 3). We first checked whether the identified genes could be associated with the phenotype obtained by the EUCAMP2 plate format (Table 2). In case other resistance genes were identified via WGS analysis, custom plate microdilution for characterization of antimicrobial susceptibility was performed. Hence, the expected phenotypic resistance based on the presence of each AMR gene was experimentally tested. Table 3 summarizes the concordances and discrepancies of phenotypic and genotypic resistance characteristics of the isolates sorted by antibiotic class (detailed in Table S1), which we address in the following sections. As proof of principle, a selection of 14 isolates was also subjected to long-read ONT sequence analysis.

Resistance to (fluoro-)quinolones

The mutation T86I in the gyrase A subunit was the most prominent mutation found to be associated with resistance to (fluoro-)quinolones. The T86I was found in 98.4% (n=436), while the T86V mutation was identified in only 1.6% (n=7) of the ciprofloxacin resistant isolates. Nearly all (97%, n=246) isolates from Vietnam and 79% (n=189) of the isolates from Germany contained this specific resistance mechanism (Fig. 3). Only five isolates from Vietnam and two from Germany showed the mutation T86V and displayed resistance to nalidixic acid and ciprofloxacin. Three isolates from Vietnam and seven isolates from Germany with the T86I mutation in GyrA were resistant to ciprofloxacin (MIC_{CIP} = 4–16 mg/L) but sensitive to nalidixic acid. Interestingly, six of the seven isolates from Germany susceptible to nalidixic acid had MIC values ≤ 2 mg/L, while being resistant to ciprofloxacin.

Resistance to macrolides and lincosamides

In all macrolide resistant isolates from Germany (n=22/22) and in 59% of the isolates from Vietnam (n=55/93) the single point mutation A2075G in the 23S rRNA gene was found, conveying erythromycin resistance. However, 38 *C. coli*$_{VN}$ isolates harbored the gene *erm*(B), encoding an rRNA adenine N-6-methyltransferase, modifying the target binding site for macrolides in the 23S rRNA, thus conferring resistance to macrolides [66]. The MIC distribution of isolates carrying the 23S rRNA A2075G point mutation or the *erm*(B) gene was comparable, ranging from 64 mg/L (n_{ermB} = 6; n_{23S_A2075G} = 5) to 128 mg/L (n_{ermB} = 5; n_{23S_A2075G} = 4) and exceeding 128 mg/L (n_{ermB} = 27; n_{23S_A2075G} = 68) (Figure S3). The translated *erm*(B) genes shared 99–100% amino acid identity to the reference Erm(B) protein WP_002321849.1, with maximally one conservative mutation (I125V) in three *C. coli* isolates from Vietnam (BfR-CA-16073, BfR-CA-16297, BfR-CA-18879), displaying MIC values > 128 mg/L to erythromycin. The resistance gene *lnu*(C), which codes for a lincosamide nucleotidyltransferase (100% identity shared with

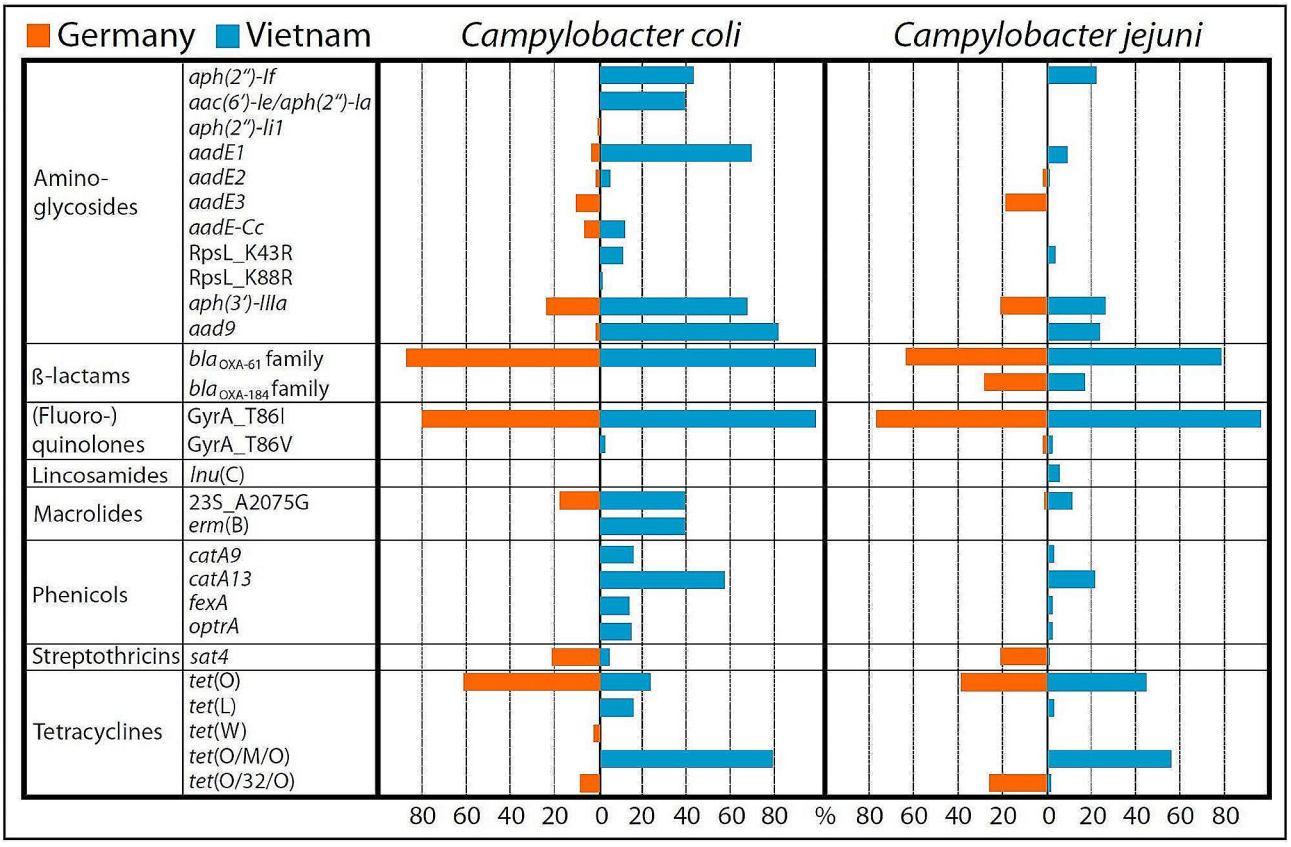

Fig. 3 Distribution and prevalence of resistance determinants identified by whole genome sequencing in *Campylobacter* spp. Fraction (%) of German (orange bars) and Vietnamese (blue bars) *C. jejuni* ($n = 280$) and *C. coli* ($n = 214$) isolates, carrying the respective resistance determinant are depicted. Resistance determinants are sorted according to antibiotic class. Partial and full-length genes are considered

WP_002837187.1) was found in eight *C. jejuni* isolates from Vietnam. In four of the eight isolates, the point mutation A2075G in 23S rRNA was also present, which is sufficient for resistance to lincomycin. However, the other four isolates, harboring the *lnu*(C) gene in absence of the 23S rRNA A2075G point mutation, were sensitive to erythromycin but resistant to lincomycin (MIC of 64 to >128 mg/L), indicating *lnu*(C) as the determinant for lincomycin resistance in these isolates. The point mutation A103V in the L22 ribosomal protein was identified in 124 macrolide sensitive isolates, from which 103 isolates displayed MICs of ≤1 mg/L erythromycin. Furthermore, the point mutation was identified in three lincomycin sensitive isolates. Hence, this mutation alone did not confer resistance to macrolides nor lincomycin.

Resistance to tetracyclines

Tetracycline resistance of *Campylobacter* isolates was associated with the presence of either the ribosomal protective protein-encoding genes *tet*(O), mosaic variants (*tet*(O/M/O), *tet*(O/32/O), the latter missing in the AMRFinder database) or *tet*(W), or the efflux transporter-encoding gene *tet*(L). ResFinder enabled the detection of the Tet(O) protein variants, which share ≥92.3% identity with each other, while Tet(W) shows ~67% identity to the Tet(O) proteins (Fig. 4).

In some resistant isolates, *tet*(O) and/or its mosaic variants were either partially found at the end of contigs ($n = 54$) or were falsely absent ($n = 8$). These isolates were reanalyzed by mapping raw reads to reference tetracycline resistance genes using Geneious Prime software (exampled in Figure S4). As a result the presence of multiple different variants of *tet*(O), including isolates exhibiting unique variants of *tet*(O/M/O) with varying degree and localisation of *tet*(M) sequence introgression, could be detected (Figure S5, visualized using [67], Table S1). However, as expected, mapping of reads to template *tet*(O) gene variants did not provide information about the presence of multiple identical full-length and/or partial gene copies. We confirmed the presence of multiple copies of identical or *tet*(O) variants by employing AMRFinderPlus on hybrid assemblies obtained from long-read sequencing of selected isolates. Consistently, except for one isolate (BfR-CA-17105), only long-read sequencing was capable of identification of multiple identical copies of *tet*(O) genes. Long-read sequencing also detected different truncated versions of *tet*(O) variants (in BfR-CA-15991, BfR-CA-18842, BfR-CA-16077,

Table 3 Correlation and discrepancies between genotype and phenotype of *Campylobacter* spp. resistance profile using AMR FinderPlus

Antibiotic class	Antibiotic tested	#Isolates tested	#Isolates resistant	Resistance determinant	Correlation between pheno- and genotype	Reason for discrepancy†
Aminoglycosides	GEN	494	114	*aph(2")-Ii*$_1$, *aph(2")-If*, bifunctional *aac(6')-Ie/aph(2")-Ia*	99.1% (113/114)	isolate with yet unknown resistance determinant (MIC > 16 mg/L; GEN-R; *n* = 1),
	STR	494	143	*aadE1-3*, *aadE-Cc*, RpsL_K43R, RpsL_K88R	78.1% (114/146)	*aadE*3 gene not found (missing in database (WP_057035408.1); STR-R; *n* = 29), partial *aadE*1 genes (STR-R; *n* = 2), isolate slightly resistant (MIC = 8 mg/L), but harboring none of the known resistance determinants (*n* = 1)
	KAN	157	139	*aph(2")-If*, bifunctional *aac(6')-Ie/aph(2")-Ia*, *aph(3')-IIIa*	100% (139/139)	n.a.
	SPC	139	118	*aad9*	30.5% (36/118)	partial genes found due to frame-shift within poly-C tract (SPC-R; *n* = 82)
β-Lactams	AMP	139	134	bla_{OXA-61} and $_{-184}$ family genes	98.5% (132/134)	Isolate susceptible (MIC = 16 mg/L), but harboring $bla_{OXA-193}$ (*n* = 1); isolate slightly resistant (MIC = 32 mg/L), but harboring no bla_{OXA} gene (*n* = 1)
(Fluoro-) Quinolones	CIP	494	442	GyrA_T86I, GyrA_T86V	100% (442/442)	n.a.
	NAL	494	432	GyrA_T86I, GyrA_T86V	97.7% (432/442)	CIP-R/NAL-S phenotype, yet unknown mechanism (*n* = 10)
Lincosamides	LCM	44	35	*lnu*(C), 23S_A2075G, *erm*(B)	88.6% (31/35)	isolates slightly resistant (MIC = 16 mg/L), but harboring none of the known resistance determinants (*n* = 4)
Macrolides	ERY	494	115	23S_A2075G, *erm*(B)	100% (115/115)	n.a.
				50S_L22_A103V	20% (31/155)	point mutation not associated with resistance to erythromycin; 20% correlation due to additional presence of either 23_A2075G or *erm*(B)
Nourseothricin	NTC	98	56**	*sat4*	100% (56/56)	n.a.
Phenicols	CHL	130	93	*catA9*, *catA13*, *fexA*, *optrA*	100% (94/94)	n.a.
	FLO	53	29	*fexA*, *optrA*	62.1% (18/29)	isolates slightly resistant (MIC = 8–16 mg/L) in absence of known phenicol resistance determinants (*n* = 11)
Tetracyclines	TET	494	412	*tet*(O), *tet*(O/32/O), *tet*(W), *tet*(O/M/O), *tet*(L)	84.6% (351*/415)	partial (mosaic-) *tet*(O) genes found (TET-R; *n* = 54), (mosaic-) *tet*(O) genes not found, but phenotypic resistance expressed (under coverage threshold; TET-R; *n* = 8), *tet*(W) with two point mutations (G511A/G1736A leading to D171N/G579D; TET-S; *n* = 2)

AMP, ampicillin; CHL, chloramphenicol; CIP, ciprofloxacin; ERY, erythromycin; FLO, florfenicol; GEN, gentamicin; KAN, kanamycin; LCM, lincomycin; NAL, nalidixic acid; NTC, nourseothricin; SPC, spectinomycin; STR, streptomycin; TET, tetracycline; n.a., not applicable (100% correlation); * *tet*(O/32/O) found as *tet*(O) with reduced identity (93.4%; missing in database; TET-R; *n* = 41) not depicted here, since pheno- and genotype were consistent with only incorrect nomenclature; **Considering a cut-off value of > 4 mg/L as resistant; †Based on the prediction of resistance determinants obtained via the BakCharak pipeline (comprises the AMRFinderPlus tool and its corresponding database version 2023-08-08.2)

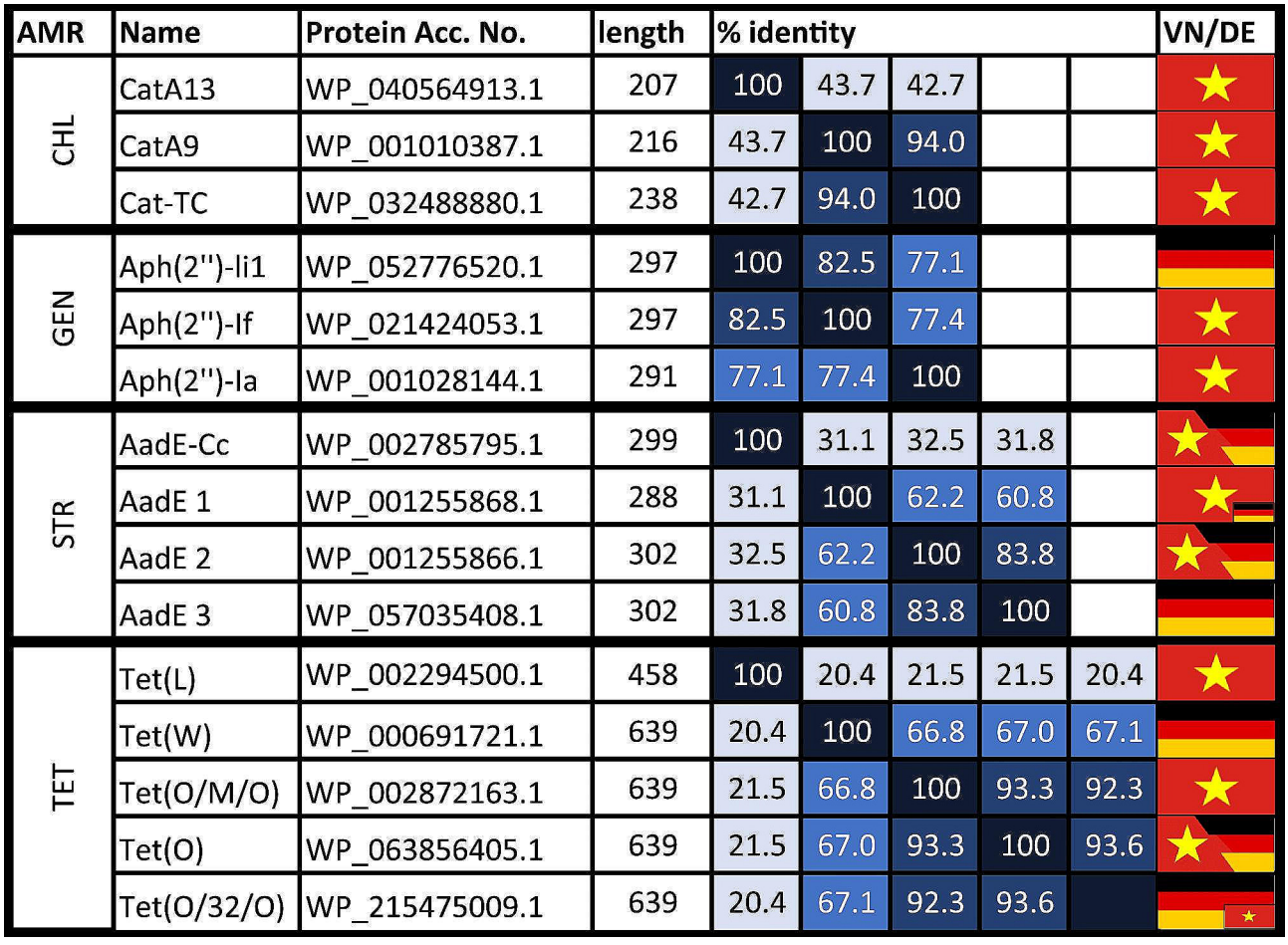

Fig. 4 Visualization of the protein variants found in thermotolerant *Campylobacter* spp. Closest NCBI matches with accession number (Acc. No.), amino acid length and percentage of protein identity to each other are depicted (computed with UniProt Align tool (Release 2023_02, [56])). Country-specific prevalence is highlighted with national flags, whose sizes correspond to the magnitude of prevalence (detailed in Fig. 3). CHL, chloramphenicol; GEN, gentamicin; STR, streptomycin; TET, tetracycline; VN, Vietnam; DE, Germany. Percent sequence identity is colored as follows: 100%, black; 80–99%, dark blue; 60–79%, blue; ≤ 59%, light blue

BfR-CA-16088, BfR-CA-16297 and BfR-CA-19087) or a mutated *tet*(O) leading to a premature stop codon and a truncated protein (BfR-CA-16040) (Table 4). Those seven isolates with tetracycline resistance also harbored one or two additional copies of *tet*(O) or gene variants.

Within the tested concentration range (0.5–64 mg/L), we did not find differences in the degree of resistance associated with a single copy of *tet*(O) or its variant genes or with multiple copies of *tet* genes. The predominant resistance gene (full-length and/or partial) among the isolates tested was *tet*(O) (119 and 91 isolates from Germany and Vietnam, respectively). *tet*(O/M/O) was exclusively found in isolates from Vietnam ($n=164$) and *tet*(O/32/O) predominantly in isolates from Germany ($n_{DE}=42$, $n_{VN}=2$). Thus, different *Campylobacter* populations harbored distinct gene variants. One of the *C. coli*$_{DE}$ isolates (BfR-CA-17078) carrying the *tet*(O/32/O) gene was sensitive to tetracycline and carried a point mutation introducing a stop codon (G1475A; p.W492Ter). The correlation of *tet*(L) presence and tetracycline resistance in *Campylobacter* was only shown in isolates also carrying *tet*(O). Three isolates from Germany harbored the *tet*(W) gene, yet two of them were sensitive to tetracycline and showed the same amino acid substitutions (D171N and G579D) (Figure S6).

Resistance to the aminoglycosides gentamicin and kanamycin

Gentamicin resistance in *Campylobacter* was rare in Germany, with only two identified resistant *C. coli*. One of the two isolates harbored the resistance gene *aph(2")-li*$_1$, which encodes an aminoglycoside phosphotransferase [68]. For the second isolate, the genetic determinant for gentamicin resistance was not detected but phenotypic resistance was repeatedly observed by microdilution assays (MIC>16 mg/L). Here, further studies are needed to decipher the underlying mechanism of gentamicin resistance. In 112 gentamicin resistant isolates

Table 4 Long-read sequencing found AMR genes often near transposase genes and on the chromosome

Isolate No.	VN/DE	Spec	predictions short-read assembly				predictions based on ONT/hybrid assembly			
			plasmids contigs	plasmids circular	plasmids mobilization elements	plasmids conjugation elements	circular contigs	plasmid contigs	Point mutations and AMR genes on chromosome (in bold indicates location in proximity to transposase genes)	AMR genes on plasmid
BfR-CA-15687	DE	Cc	**1** (-)	0	**1**	**6**	2	1	*bla*$_{OXA}$-489;*tet*(O);GyrA_T86I	*tet*(O)
BfR-CA-15991	VN	Cc	**0**	**0**	**0**	**0**	1	0	***tet*(O/M/O)-*catA9*-*tnp*$_{IS1216\ family}$-*fexA*-*optrA*-*tnp*$_{IS1216family}$-*tet*(L)**;*aac(6')-Ie/aph(2")-Ia-aadE*1-*tet*(O)x$_{\Delta C-terminus}$;*bla*$_{OXA}$-193;23S_A2075G; 23S_A2075G; 23S_A2075G;GyrA_T86I	
BfR-CA-16040	VN	Cc	1 (-)	**0**	**0**	**0**	1	0	***tnp*$_{ISCco2\ family}$-*catA13*-*aph(3')-IIIa*-*aad9***;*tet*(O/M/O)-*aad9-erm*(B)-*aadE*1;*aac(6')-Ie/aph(2")-Ia-aadE*1-*tet*(O)x$_{\Delta C-terminus}$; *bla*$_{OXA}$-489;GyrA_T86I	
BfR-CA-16046	VN	Cc	**2** (-)	**1**	**1**	**6**	2	1	***tnp*$_{ISCco2\ family}$-*catA13*-*aph(3')-IIIa*-*aad9*-*aph(2")-If*-*bla*$_{OXA}$-193**;*tet*(O/M/O)-*aad9-erm*(B)-*aadE*1;*aadE-Cc*;GyrA_T86I	
BfR-CA-16077	VN	Cj	1 (-)	**0**	**0**	**0**	1	0	***tnp*$_{ISCco2\ family}$-*catA13*-*aph(3')-IIIa*-*aad9*-*aph(2")-If***;*tet*(O/M/O)-*aadE*1-*tet*(O)x$_{\Delta N-terminus}$;***aph(3')-IIIa*-*tnp*$_{ISCaje6\ family}$**;*bla*$_{OXA}$-184 family; ***tnp*$_{ISCco2\ family}$-*lnu*(C)**;GyrA_T86I	
BfR-CA-16088	VN	Cj	1 (-)	**0**	**0**	**0**	1	0	***tnp*$_{ISCco2\ family}$-*catA13*-*aph(3')-IIIa*-*aad9*-*aph(2")-If***;*tet*(O/M/O)-*aadE*1-*tet*(O)x$_{\Delta N-terminus}$;***aph(3')-IIIa*-*tnp*$_{ISCaje6\ family}$**;*bla*$_{OXA}$-184 family; ***tnp*$_{ISCco2\ family}$-*lnu*(C)**;GyrA_T86I;23S_A2075G;23S_A2075G;23S_A2075G	
BfR-CA-16110	VN	Cc	**0**	**0**	**0**	**0**	1	0	*tet*(O)-*aad9-erm*(B)-*aadE*1;*bla*$_{OXA}$-193;GyrA_T86I	
BfR-CA-16201	VN	Cc	0	0	0	0	2	1	*tet*(O)-*aad9-erm*(B)-*aadE*1; ***tnp*$_{ISCco2\ family}$-*catA13*-*aph(3')-IIIa*-*aad9*-*aph(2")If*-*bla*$_{OXA}$-193**;*tet*(O);GyrA_T86I	
BfR-CA-16258	VN	Cc	**1** (+)	**1**	0	0	2	1	*tet*(O)-*aad9-erm*(B)-*aadE*1;*tet*(O);*bla*$_{OXA}$-193;GyrA_T86I	
BfR-CA-16297	VN	Cc	**0**	**0**	**0**	**0**	1	0	*tet*(O/M/O)-*aad9-erm*(B)-*aadE*1;***aph(2")-If*-*aph(3')IIIa*-*tnp*$_{ISCaje6\ family}$**; *aac(6')-Ie/aph(2")-Ia-aadE*1-*tet*(O)x$_{\Delta C-terminus}$;***tet*(O)-*tnp*$_{IS607\ family}$**;*bla*$_{OXA}$-193;GyrA_T86I	
BfR-CA-16737	DE	Cj	**2** (+)	0	**1**	**6**	2	1	*bla*$_{OXA}$-185 like;*tet*(O);GyrA_T86I	*tet*(O/32/O)-*aadE2*_Δ1-415-*sat4-aph(3')-IIIa*
BfR-CA-18842	VN	Cc	**0**	**0**	**0**	**0**	1	0	*aac(6')-Ie/aph(2")-Ia-aadE*1-*tet*(O)x$_{\Delta C-terminus}$; *tet*(O/M/O);*bla*$_{OXA}$-193;GyrA_T86I	
BfR-CA-19087	DE	Cc	**3** (+)	0	0	0	2	1	***tnp*$_{IS607\ family}$-*tet*(O/32/O)-*aph(2")-Ii*$_1$-*aph(3')-IIIa*-*aad9*-*aadE*1-*tet*(O)**x$_{\Delta N-terminus}$;*tet*(O/32/O);*aadE-Cc*;GyrA_T86I	
BfR-CA-19301	VN	Cj	**0**	**0**	**0**	**0**	1	0	***aadE*3-*sat4*-*aph(3')IIIa*-*tnp*$_{IS1216\ family}$**;*tet*(O/32/O);*bla*$_{OXA}$-193; GyrA_T86I	

Bold numbers, plasmid predictions based on short-read sequence data are consistent with ONT data; (+), true; (-), false prediction of AMR gene localization on plasmids compared to ONT data. Genes in bold depict AMR determinants located on the chromosome in proximity to transposase genes. 50S_L22_A103V mutation was omitted due to absence of resistance phenotype; VN, Vietnam; DE, Germany; Spec, Species; Cj, *C. jejuni*; Cc, *C. coli*

from Vietnam, the aminoglycoside phosphotransferase gene *aph(2")-If* (n=76) and the gene *aac(6')-Ie/aph(2")-Ia* (n=38) were found, the latter coding for a bifunctional enzyme combining a phosphotransferase with an N-acetyltransferase. Both resistance determinants also confer resistance to kanamycin.

Kanamycin resistance was further associated with the presence of the aminoglycoside phosphotransferase *aph(3')-IIIa*. In total 160 isolates contained this gene (n_{VN}=106, n_{DE}=54) and were phenotypically resistant to kanamycin. Among them were 97 isolates (n_{VN}=96, n_{DE}=1) with a combination of *aph(3')-IIIa and* either *aph(2")-If* (n_{VN}=73) or the bifunctional gene (n_{VN}=21), both conferring gentamicin and kanamycin resistance, or *aph(2")-li*$_1$ (n_{DE}=1). Furthermore, two additional *C. coli*$_{VN}$ (BfR-CA-16297, BfR-CA-18728) harbored a combination of *aph(3')-IIIa, aph(2")-If* and the bifunctional gene and, thus, acquired two genetic determinants redundantly encoding a gentamicin and kanamycin modifying enzyme and a further enzyme for kanamycin inactivation. Intriguingly, long-read sequencing even revealed two isolates (BfR-CA-16077, BfR-CA-16088) with two copies of *aph(3')-IIIa* in combination with *aph(2")-If*. Within the test ranges of gentamicin (0.12–16 mg/L) and kanamycin (2–1024 mg/L), we could not observe increased MIC values for isolates containing multiple redundant resistance determinants compared to isolates only harboring a single gene.

Resistance to the aminoglycoside streptomycin

Four variants of *aadE* genes (*aadE-Cc* and *aadE* 1, 2, 3, Fig. 4), coding for aminoglycoside 6-adenylyltransferases and two additional point mutations in the *rpsL* ribosomal gene were associated with streptomycin resistance in the *Campylobacter* spp. isolates. The predominant streptomycin resistance gene in Vietnam was *aadE*1 (WP_001255868.1, n_{VN}=82, n_{DE}=2). AMRFinderPlus identified a partial *aadE*1 gene (88.9% protein sequence coverage) in two of these isolates from Vietnam (BfR-CA-19112, BfR-CA-19119), which displayed resistance to streptomycin. Mapping of raw reads to reference gene *aadE*1 revealed the presence of the full-length gene, thus indicating an assembly error. Both isolates additionally carried a partial *aadE*2 (Δ1-109 bp) as verified by extraction of the Bakta annotated coding sequences and subsequent alignment to a reference gene (NG_047393.1, Table S3). This observation explained streptomycin resistance in these two isolates. Hence again, the presence of redundant homologous genes resulted in contig breaks during the assembly process, impeding the accurate reconstruction of genes from short-read sequences. In total, mapping of reads to template *aadE2* revealed eight isolates displaying truncated non-functional AadE2 (WP_001255866.1), among them three streptomycin sensitive isolates from Germany (BfR-CA-16737, BfR-CA-16834, BfR-CA-19311), confirming loss of function of AadE2 due to truncation (*aadE2*_Δ1-415). The five isolates from Vietnam also contained full length *aadE*1, consistent with their streptomycin resistant phenotype. The AadE3 variant (WP_057035408.1), exclusively found in isolates from Germany (n=29), is missing in the AMRFinderPlus database and was, thus, only found by manual ABRicate search using the *aadE*3 reference nucleotide sequence (Table S3). The AadE-Cc variant (WP_002785795.1) was detected in *C. coli*$_{VN}$ (n=11) and *C. coli*$_{DE}$ (n=8). While three isolates from Vietnam and one from Germany in addition contained the *aadE*1, one isolate from Germany displayed streptomycin sensitivity, corresponding to a *aadE-Cc* with a point mutation (ΔA558; p.A187LfsTer188) leading to early termination of translation, correctly annotated by AMRFinderPlus.

A point mutation in the RpsL ribosomal protein was rare and only observed in isolates from Vietnam. The RpsL K43R point mutation was present in 10 *C. coli* and 5 *C. jejuni* isolates, while one *C. coli* harbored the RpsL K88R mutation (BfR-CA-18880). Isolates carrying either RpsL K43R or RpsL K88R were resistant to streptomycin (MIC>16 mg/L). One of these isolates (BfR-CA-18738) additionally carried the *aadE*1 gene.

Resistance to the aminoglycoside spectinomycin

Spectinomycin resistance was widespread among isolates from Vietnam (n=116) and rare among isolates from Germany (n=2). In our study, the presence of a gene encoding the spectinomycin adenyltransferase Aad9 (WP_002578722.1) was associated with high-level resistance (MIC of 256 to >512 mg/L) and was carried by 80.8% *C. coli*$_{VN}$ and 23.2% *C. jejuni*$_{VN}$ isolates, as well as by the two *C. coli*$_{DE}$ isolates (Fig. 3).

In the majority of spectinomycin resistant isolates (n=82/118), the AMRFinderPlus identified the presence of a truncated version of *aad9* (69.8 to 88.0% gene coverage to WP_002578722.1). Again, this was partially due to an inability of correct identification of full-length *aad9* genes from short-read sequence data caused by the presence of multiple copies of *aad9*, confirmed by long-read sequencing (e.g. BfR-CA-16040 and BfR-CA-16046). Additionally, we observed frameshifts within a putative poly-C tract present in the resistance gene, leading to a truncated Aad9 protein. However, all isolates, carrying *aad9* showed phenotypic resistance. We wondered whether *aad9* inactivation by poly-C was only present in a subpopulation of the bacterial suspension and/or whether frame-shifting can lead to restoration of a full-length protein. Indeed, when we mapped raw reads to an *aad9 C. coli* reference gene linked to the reference protein WP_057031337.1 (Acc. NZ_CP091310.1:1,750,066–1,750,845), we detected a variable number of cytosines

in the frame shift region in some of the sequences, suggesting that *aad9* undergoes phase variation. To identify potential reversal of the correct number of cytosines in the poly-C tract associated with phenotypic resistance, we subjected one of the isolates, BfR-CA-15987, to selection pressure on ColbA plates supplemented with 128 mg/L spectinomycin, followed by whole genome sequencing analysis. Analysis of sequence data before and after selection on spectinomycin showed that spectinomycin selected for BfR-CA-15987 clones with one additional cytosine within the poly-C tract, restoring the full-length gene (Figure S7).

Resistance to chloramphenicol and florfenicol

Resistance to antibiotics from the phenicol group was only observed in the isolates from Vietnam. About 58% (n=57 of the *C. coli* and 23% (n=36) of the *C. jejuni* isolates carried one or multiple phenicol modifying enzymes and showed resistance to chloramphenicol (MIC 32 to >128 mg/L) (Fig. 3 and Table S1). The most common resistance determinant was a gene (*catA13*) coding for a type A-13 chloramphenicol O-acetyltransferase (WP_040564913.1; Fig. 4). This resistance gene was present in all except five chloramphenicol resistant isolates, either alone or in combination with *catA9* (n=14), encoding a type A-9 chloramphenicol O-acetyltransferase (WP_001010387.1). The *catA9* determinant was also present in the residual five chloramphenicol resistant isolates. The point mutation in *catA9* observed in two chloramphenicol resistant *C. coli* isolates (BfR-CA-16261, BfR-CA-18728), leading to a single amino acid substitution (p. A197T) in CatA9, was falsely annotated as *catTC* gene with an internal stop codon by AMRFinderPlus.

One sensitive *C. coli* (BfR-CA-16259) displayed a *catA* gene, which corresponded to a protein of 262 amino acids and was N-terminally identical to CatA13 until P179 (CatA13_p.L180-K207delins180-262). The C-terminus was different from CatA proteins. The gene was "correctly" found as a partial *catA13* gene by AMRFinderPlus.

Furthermore, 15.2% *C. coli* (n=15) and 1.9% *C. jejuni* (n=3) were highly resistant to florfenicol (MIC values of >16 mg/L; Table S1). The two resistance genes coding for a **f**lorfenicol **ex**porter protein **A** (*fexA*) and an ABC-F type ribosomal protection protein (*optrA*), respectively, were found to be associated with high level florfenicol resistance. In the majority of highly resistant isolates, both genes were present ($n_{C.coli}$=12, $n_{C.jejuni}$=3); just three *C. coli* isolates either harbored *fexA* (BfR-CA-15989) or *optrA* (BfR-CA-16261, BfR-CA-18728), indicating that either gene might be sufficient for high level florfenicol resistance. Medium-level resistance (MIC 8–16 mg/L) could not be attributed to the presence of a genetic determinant (n=11; Table 3 and S1).

Resistance to β-Lactams

Genes encoding oxacillinases (class D β-lactamases) of the OXA-61- or -184-like family were identified in 215 (89.6%) and 244 (96.1%) isolates from Germany and Vietnam (Table S1 and S3) by AMRFinderPlus, respectively. The predominant variant found was $bla_{OXA-193}$, which accounted for 61.2% of identified bla_{OXA} genes (281/459). Other variants that were found more frequently were $bla_{OXA-489}$, $bla_{OXA-184}$, and $bla_{OXA-460}$. Overall, 21 different bla_{OXA} genes were identified and further variants with yet unknown point mutations, belonging to either bla_{OXA-61} or $bla_{OXA-184}$ family genes. Genes of the OXA-184-like family were only detected in *C. jejuni* isolates. Susceptibility to ampicillin was tested in approximately 30% of the isolates, demonstrating resistance to ampicillin with MIC values ranging from 32 to >512 mg/L in the presence of a bla_{OXA} gene, except for one strain. This *C. jejuni* from Germany (BfR-CA-14940) displayed a MIC of 16 mg/L ampicillin, just below the ECOFF for resistance, but carried a $bla_{OXA-193}$ gene. We analyzed the promoter of the bla_{OXA} gene in this isolate using the Geneious software. It was found previously that a transversion (G to T) at position −57 restored the Pribnow box, leading to upregulation of bla_{OXA} and high-level ß-lactam resistance [69]. Indeed, this point mutation was missing in BfR-CA-14940, thus potentially explaining the low observed MIC for ampicillin. Consistently, isolates carrying bla_{OXA} with lower MIC values between 32 and 64 mg/L also did not harbor the optimal Pribnow box for increased bla_{OXA} transcription. There was one exception to the rule (BfR-CA-16023), carrying a bla_{OXA} gene with the non-optimal Pribnow box but displaying a MIC value of 256 mg/L. Furthermore, one *C. coli*$_{VN}$ isolate was detected, which did not harbor a bla_{OXA} gene, but showed slight ampicillin resistance just above the ECOFF (MIC=32 mg/L).

Resistance to Nourseothricin

The resistance determinant *sat4*, encoding a streptothricin N-acetyltransferase, accounted for resistance to nourseothricin, a mixture of streptothricins C, D, E and F. Isolates carrying *sat4* showed MIC values between 8 and 512 mg/L nourseothricin, while the respective sensitive isolates without *sat4* had MICs of ≤1–2 mg/L. Although an ECOFF value is not yet officially published, we defined >4 mg/L as elevated non-wildtype MICs for our study to categorize sensitive and resistant isolates (Table 1). The *sat4* resistance determinant was more common in Germany with 21.7% *C. coli* (n=25/115) and 20.8% *C. jejuni* (n=26/125) harboring *sat4* compared to only five isolates from Vietnam. The translated protein sequences showed high similarity to the reference protein WP_000627290.1.

Prediction of localization and mobilization of AMR genes

The tool Platon v1.6 was used for annotation of plasmid localization of AMR genes based on short-read data. For verification, selected isolates were also processed by Oxford Nanopore long-read technology (n = 14). All fourteen genomes could be closed using the Unicycler hybrid assembler and the chromosomes displayed a size between 1.62 and 1.82 Mb, while six isolates carried an additional circular plasmid of 3.3 kb to 52 kb (Table 4). AMR genes in these isolates were mostly found on the chromosome. Only two plasmids carried either a *tet*(O) gene (BfR-CA-15687) or an operon containing *tet*(O/32/O) – *aadE*2_Δ1-415 – *sat4* – *aph(3')-IIIa* (BfR-CA-16737). We asked whether the current plasmid prediction from short-read data using the Platon tool corresponded to the closed genomes/plasmids upon long-read sequencing within our dataset. We observed that the annotation of "plasmid contigs" by Platon overestimated plasmid existence in three isolates (false positives), while missing the plasmid in one isolate (false negative, Table 4). The prediction of the presence of either/and (i) a circular plasmid, (ii) mobilization or (iii) conjugation elements (Table S1, column BC, BD, BE) led to missing two plasmid-containing isolates. However, false positive results were lacking. If this conservative filter was applied for all short-read data (Table S1, column BF > 0), 183 of the total 494 isolates were predicted to carry one or multiple plasmid/s. However, prediction of plasmid-location of AMR genes seemed to be inaccurate based on the Platon tool optimized for other bacteria such as *Escherichia coli*: only one out of the two plasmids, which contained AMR gene/s, was detected by Platon and a further four isolates were falsely annotated as carrying AMR genes on plasmids based on short-read data.

Based on long-read sequencing data and hybrid assemblies using Unicycler, we further investigated the localization of AMR gene clusters and their mobilization potential using AMRFinderPlus. In principle, we found three types of AMR gene localizations that suggest different mobilization of AMR genes (Fig. 5). As mentioned

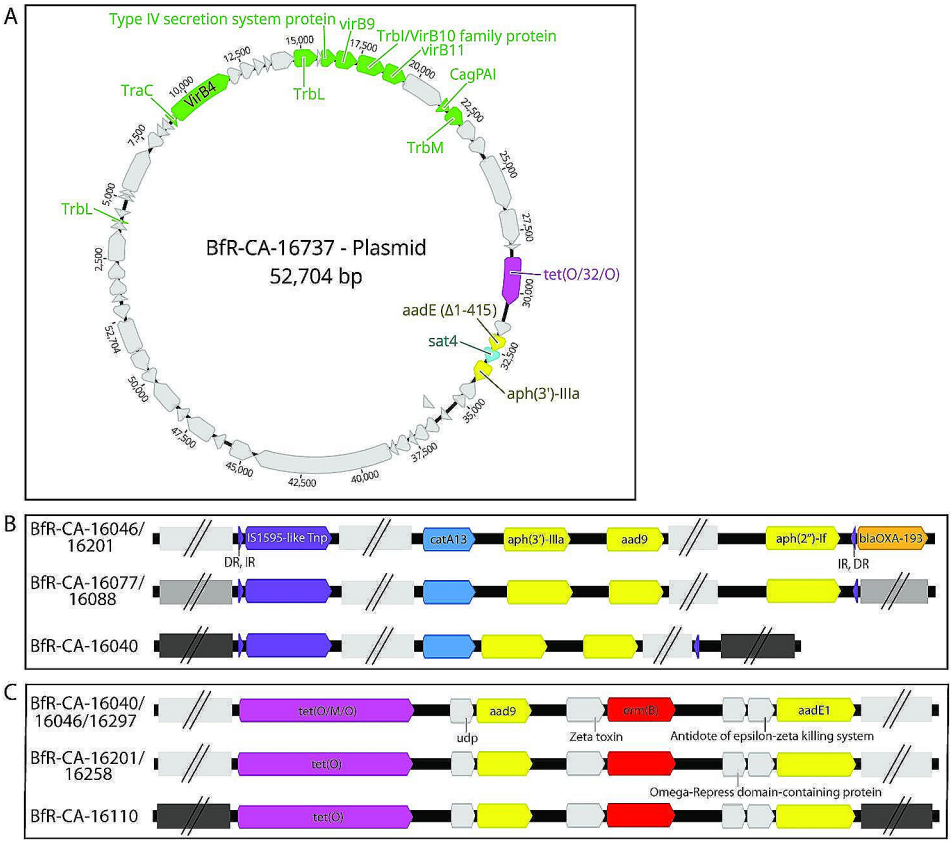

Fig. 5 Mobilizable MDRI clusters and AMR genes in *Campylobacter* spp. identified by long-read sequencing. Localization of AMR clusters on **A**, plasmid, **B** and **C**, the chromosome, with **B** in proximity to transposase genes. All elements are mobilizable by natural transformation in *Campylobacter* spp. In addition, conjugative transfer (**A**) and transposition (**B**) is likely to occur. In **A**, genes associated with type IV secretion/conjugation are depicted in green; in **B**, transposase genes and associated direct (DR) and inverted repeats (IR) are marked in purple. AMR genes from different antimicrobial classes are depicted in different colors; blue, *catA* genes, yellow, aminoglycoside resistance genes; orange, bla_{OXA} gene; light purple, *tet*(O) variant genes; red, *erm*(B) genes. Grey arrows, non-AMR related genes; grey boxes with two vertical lines indicate clusters of non-AMR related genes, with homology indicated using identical shading

above, plasmid localization of AMR genes was rare. Only one *tet*(O) gene in a *C. coli* isolate and the operon structure *tet*(O/32/O) – *aadE*2_Δ1-415 – *sat4*– *aph(3')-IIIa* in a *C. jejuni* were plasmid-located within the long-read sequenced isolates (Fig. 5A), thus, being transferable via conjugation. Chromosomal AMR genes, like e. g. the gene cluster *tet*(O) – *aad9* – *erm*(B) – *aadE*1 can be transferred by natural transformation, depending on homologous recombination. Likewise, we observed that the gene context of this MDRI was rather stable in the analyzed long-read sequenced isolates, with five out of six isolates displaying homologous gene context flanking the MDRI (Fig. 5C). Also the chromosomal *aac(6') -Ie/aph(2") -Ia*– *aadE*1 – *tet*(O)$x_{\Delta C-terminus}$ gene cluster was embedded in a highly conserved genomic region in the analyzed four isolates, which is expected for mobilization via natural transformation. However, we frequently found chromosomal MDRI in proximity to a transposase gene. For example the *catA13* – *aph(3') -IIIa* – *aad9* MDRI was situated in three different chromosomal contexts with and without additional adjacent AMR genes in five analyzed isolates (Fig. 5B). Hence, this MDRI was putatively disseminated by natural transformation and transposition, thereby enhancing the movement within a bacterial chromosome but also among the bacterial population. A similar mechanism of transfer might be predicted for other MDRIs as well as for single AMR genes in proximity to transposase genes, e. g. *aph(2") -If*– *aph(3') -IIIa* in *C. coli* BfR-CA-16297, *aadE*3 – *sat4*– *aph(3') -IIIa* in *C. jejuni* BfR-CA-19301, *lnu*(C) or a second copy of *aph(3') -IIIa* in *C. jejuni* BfR-CA-16077 and BfR-CA-16088, *tet*(O/M/O) – *catA9* – *fexA* – *optrA* – *tet*(L) in *C. coli* BfR-CA-15991 and *tet*(O/32/O) *-aph(2") -li*$_1$ – *aph(3') -IIIa* – *aad9* – *aadE*1 – *tet*(O)$_{\Delta N-terminus}$ in *C. coli* BfR-CA-19087 (Figure S8).

Discussion

The study aimed to improve AMR diagnostics of thermotolerant *Campylobacter* spp. by elucidating the reliability of predictions for antimicrobial resistances from whole genome sequence data. Within nearly 500 investigated isolates, whole genome cgMLST results suggested a broad diversity of isolates, constituting a suitable data source for in-depth AMR analysis. We detected 14 different resistance genes and genes with point mutations in isolates from Germany and 22 different AMR determinants associated with antibiotic resistance in the *Campylobacter* spp. population from Vietnam. Each identified resistant determinant was correlated to phenotypic resistance against the respective antimicrobial. Any discrepancies were re-analyzed. Our study showed high rates of aminoglycoside, (fluoro-)quinolone, macrolide, phenicol and tetracycline resistance in isolates from Vietnam, which is likely related to the extensive use of antibiotics on farms [24] and comparable to those previously reported in other Asian countries such as China, Malaysia, and the Philippines [69–72]. Resistance to (fluoro-)quinolones and tetracycline was also frequent in isolates from Germany, while resistances to aminoglycosides and macrolides were comparably low, which is in line with recent data from Germany [73].

Our main question was whether current next generation sequence data analysis pipelines are prepared for appropriate detection of potential worldwide spread of multi-resistant *Campylobacter* spp. With our systematic approach we observed five principle discrepancies between pheno- and genotype in thermotolerant *Campylobacter* spp.

Missing or falsely annotated AMR genes in databases

First, certain AMR genes were either missing in the AMRFinderPlus and ResFinder databases (*aadE*3), although previously published [74] or falsely annotated to confer resistance in *Campylobacter* spp. in the AMRFinderPlus database (ribosomal L22 protein A103V mutation). Despite the previous suggestion that the point mutation A103V in the ribosomal protein L22 may confer resistance to macrolides [66], our findings do not show a correlation between this mutation and erythromycin resistance. This is consistent with the conclusion reached by others, who also found no association between A103V and resistance to macrolides [30, 75]. Furthermore, the mosaic gene variant *tet*(O/32/O) is also missing in the AMRFinderPlus database (version 2023-08-08.2) and was identified by the pipeline as *tet*(O) with reduced identity (~93%), thus, at least not causing a pheno-/genotype discrepancy. However, ResFinder database 2.1.0 includes this variant. The above mentioned inconsistencies can be easily addressed by curation and harmonization of the databases.

Detection of *tet*(O), *aadE* genes and *aad9* partially failed due to frequently observed presence of multiple copies or variant genes

Second, short-read sequencing eventually failed or falsely detected partial (inactive) AMR genes, if multiple copies and/or homologous mosaic genes were present. This was, in particular, the case for *tet*(O) but also for *aadE* gene variants and multiple copies of *aad9*. In the *Campylobacter* population from Vietnam, there was a high prevalence of isolates with either two identical or two distinct variants of the (mosaic) tetracycline resistance genes (Table S1). The assembler used may have encountered difficulties in generating complete resistance gene sequences from raw reads due to regions of ambiguity within the assembly process. Consequently, either incomplete genes were identified in these isolates, or the sequencing reads were inadequate in length and did not

meet the pipeline's coverage threshold, which resulted in "absence" of AMR gene detection (Table 3). As proof of principle SKESA as alternative assembler was used for the assembly of short-read sequencing data of 10 isolates, for which detection of some AMR genes failed using the shovill assembler (Table S2). However, the results were similar, except that in one isolate the full-length copy of *aad*9 was, in addition, falsely detected as "partial" upon SKESA assembly. In another isolate, in which *tet*(O) was missing upon shovill assembly, SKESA assembly led to the detection of a partial *tet*(O). In a study with commensal *E. coli*, short-read sequencing was capable of detecting only one copy of each duplicated resistance gene, yet the authors did not observe partial or unidentified genes arising from allelic variants [76].

Under our test conditions, we did not observe any functional differences between the *tet*(O) or *aadE* variants, nor enhanced resistance levels were detected, if isolates carried multiple copies of resistant gene variants (verified by long-read sequencing). Thus, so far the impact or purpose for redundant genetic determinants in *Campylobacter* spp. remains unknown. It might be speculated that redundant genes are located in a gene context with essential/other AMR genes, thereby, being co-transferred. Most initial discrepancies from AMRFinder with its default thresholds were resolved by manual search of missing genes via ABRicate and by mapping of raw reads to reference genes using Geneious Prime (as exampled in Figure S4). Mosaic tetracycline genes such as *tet*(O/M/O) and *tet*(O/32/O) variants were previously found [77, 78] and in this study, we showed differential distribution of these variant genes in different *Campylobacter* populations. Yet, the complexities arising from the diverse recombinant forms of *tet*(O) within *Campylobacter* isolates from Vietnam could not be conclusively resolved unless long-read sequencing was applied. Long-read sequencing by Oxford Nanopore Technology deciphered multiple copies of AMR genes (including multiple identical genes and or partial genes) and, furthermore, revealed AMR gene localization (Table 4), which was frequently inconsistent with predictions from short-read sequencing. Hence, a combination of short- and long-read sequencing may circumvent inconsistencies caused by the presence of multiple AMR gene (variants) with the additional benefit of identification of AMR gene location.

Novel point mutations in *tet*(W) led to AMR gene inactivation, while *aad9* was identified as phase variable gene

Third, while some partial genes harboring point mutations were correctly identified by the pipeline, we identified novel point mutations D171N/G579D in Tet(W), leading to a tetracycline sensitive phenotype (BfR-CA-16942 and BfR-CA-18353). Furthermore, in case of the *aad9* gene, around 70% of the isolates were annotated to display a truncated inactive version of *aad9*, but those isolates were indeed resistant to spectinomycin. Next to assembly problems due to multiple copies of *aad9*, we revealed weakness of the assembling process to correctly identify the poly-C tract variant of functional *aad9*. This was probably due to a mixture and ambiguity of raw reads with different number of cytosines within this novel phase variable gene (Figure S7). As proof of principle we reselected an isolate annotated as harboring an inactive *aad9* gene on spectinomycin and after re-sequencing, we were able to correctly identify the full-length *aad9* gene. This observation is in agreement with reversion to a functional gene by insertion/deletion of cytosines, explaining the phenotypic resistance observed in the antimicrobial sensitivity tests. Thus, we concluded that *aad9* is frequently inactivated by frameshifting, but the isolates keep resistance to spectinomycin as a bacterial population due to the reversion of the frameshift. Phase variation was proposed an important mechanism for regulation of several genes in *Campylobacter* spp., in particular for host response, like e.g. the *flgR/S* system, essential for motility [79, 80]. Here, it might balance the cost for AMR gene carriage and suggests prolongation of persistence of the AMR gene.

MIC values just above the cut-off probably display non-specific resistance due to enhanced efflux and/or decreased inward diffusion

Fourth, discrepancies were identified for isolates with MIC values close to the cut-off value. Most frequently, we found isolates without any known resistance determinant but with slight resistance according to the current ECOFF or elevated non-wildtype MICs. This was the case for four lincosamide and eleven florfenicol resistant isolates and for one isolate resistant to ampicillin (Table 3). Low level resistance without known gene determinants might be promoted by increased efflux or decreased influx mechanisms [80–83]. It has been previously reported that inactivation of the ABC-efflux transporter CmeABC led to increased sensitivity to a variety of antimicrobials such as (fluoro-)quinolones, macrolides, phenicols and tetracyclines [84, 85]. Low level ampicillin resistance was due to the presence of the non-optimal Pribnow box in the promotor region, if bla_{OXA} genes were present (see above and [69, 86]). We identified a further exceptional isolate (BfR-CA-16023) carrying a bla_{OXA} gene with the non-optimal Pribnow box but displaying a MIC value of 256 mg/L. As for the slightly ampicillin resistant isolate BfR-CA-19104 without bla_{OXA}, there might be additional efflux and/or decreased influx mechanisms, which await further investigations.

Unknown resistance mechanisms in *Campylobacter* spp. remain elusive

Fifth, we found isolates harboring unknown resistance mechanisms. One gentamicin resistant isolate from German turkey cecum (BfR-CA-15687) did not harbor any of the known resistance determinants but repeatedly showed high level resistance to gentamicin (MIC>16 mg/L). The isolate was also resistant to (fluoro-)quinolones (GyrAT86I) and tetracycline (*tet*(O)) and carried a $bla_{OXA-489}$ gene. Further studies are needed to identify the unknown gentamicin resistance mechanism.

As previously confirmed by other studies and reiterated by our WGS results, the single point mutation T86I in the "quinolone resistance determining region" (QRDR) of the gyrase subunit A confers resistance to (fluoro-) quinolones in *Campylobacter* spp. [33, 87, 88]. This widespread resistance in *Campylobacter* isolates is likely due to the demonstrated fitness advantage that it confers at least in some *C. jejuni* isolates [89]. However, we found several isolates, harboring the point mutation GyrA T86I and displaying high-level resistance to ciprofloxacin but complete sensitivity to nalidixic acid (Table 3 and S1). This phenomenon was previously found by others [29, 90] but the underlying mechanism is yet unsolved. We conclude that the point mutation alone is not sufficient for both resistances to ciprofloxacin and nalidixic acid and the overall (fluoro-)quinolone resistance mechanism in *Campylobacter* remains enigmatic.

Fitness costs of AMR and Impact of AMR gene localization on transfer and spread

ONT sequencing and hybrid assembly of long- and short-reads led to closure of circular contigs, the chromosome and potential plasmids. Hybrid assembly data resulted in improved identification of multiple AMR gene(s) variants, which were non-resolvable by only short-read analysis. Interestingly, *Campylobacter* populations in Germany and Vietnam showed distinct patterns of gene variants, e.g. *tet*(O/M/O) in Vietnam and *tet*(O/32/O) in Germany. The reason for the acquisition of redundant resistance mechanisms by the isolates is uncertain. In our analysis we could not find enhanced levels of resistance due to multiple resistance determinants, since the presence of one copy already led to high level resistance of the AMR investigated. However, if selection is exerted on AMR genes situated within AMR gene clusters, also neighboring AMR genes are co-selected and transferred from one isolate to another. We conclude that AMR genes in *C. jejuni* and *C. coli* were frequently organized in mobilizable MDRIs next to transposase genes and different MDRIs harbored multiple AMR genes with analogous function. Hence, these isolates appear to be perfectly prepared for a changing selective environment and additionally harbored transiently non-functional AMR genes, which might be restored under selection pressure.

Interestingly, most AMR genes appeared to be chromosomally located, frequently in association with transposase genes (Fig. 5). Plasmid prediction from short-read data was limited, while long-read data identified 43% strains carrying a plasmid (n=6/14). From these isolates, only two plasmids were identified with AMR genes, one harbored *tet*(O), the other *tet*(O/32/O) – *aadE*2_Δ1-415 – *sat4*– *aph(3')-IIIa*. This is consistent with previous findings in the literature, where plasmids containing tetracycline resistance genes were reported in *Campylobacter*, such as the self-transferable plasmid pTet and *tet*(O) associated AMR gene clusters [91, 92]. Previous research has demonstrated the existence of the resistance gene cluster *aadE* – *sat4* – *aph(3') -IIIa*, located on both the chromosome and plasmids, in *C. jejuni* and *C. coli* isolates [74, 92–95]. These findings align with our results from long-read sequencing. It is noteworthy that the use of streptothricin was restricted to the former German Democratic Republic, and ceased by 1989 at the latest, while therapeutic use in humans has been halted due to its nephrotoxicity [96]. It is possible that the *sat4* gene is conserved to some degree as it is co-flanked within the aminoglycoside resistance conferring genes *aadE* and *aph(3')-IIIa*, that might provide an advantage to *Campylobacter* in Germany and explain the observed preferential presence of *sat4* in isolates from Germany.

Spread of macrolide resistance is of great concern, since in particular macrolides are the drug of choice to treat campylobacteriosis in humans [9]. The point high level resistance conferring mutation A2075G in the 23S rRNA was shown to result in a substantial decrease in bacterial fitness among *C. jejuni* [97, 98]. This fact may explain its low prevalence in areas with a comparably low selection pressure. In regions with high selection pressure, such as Vietnam [25, 99] this mutation was more frequently found (Fig. 3). Additionally, high-level resistance to macrolides and/or lincosamides is also conferred by the emerging resistance gene *erm*(B), which was first described in a *C. coli* strain isolated from swine in China [100]. We showed in our study that phenotypic resistance testing with erythromycin cannot distinguish the presence of the 23S rRNA point mutation from that of *erm*(B), since the MIC distribution of both resistant determinants was comparable (Figure S3). As also observed in our study (Fig. 5), *erm*(B) has already been shown to be part of different MDRIs [98, 101, 102] and probably derived from Gram-positive bacteria [103]. In the ONT-analyzed isolates, *erm*(B) was located on the chromosome with a rather conserved gene context, suggesting mobilization via natural transformation (Fig. 5).

We previously showed that natural transformation in *C. jejuni* was a highly efficient process and occurred most frequently under microaerobic conditions at neutral pH, found in the natural hosts [104].

The *catA13– aph(3')-IIIa– aad9* cluster was one of the AMR clusters found in proximity to transposase genes (Fig. 5; Table 4). As expected for transposable elements, the AMR cluster context was rather diverse, with occasional acquisition of additional nearby located AMR genes, like *aph(2") -If* and $bla_{OXA-193}$. Interestingly, in another study from China the two resistance genes *fexA* and *optrA* were found together as part of an MDRI, which aligns with the data we collected [105]. Given that the two genes were also identified in close proximity to transposases within operon structures among isolates from Vietnam, it is highly probable that they will continue to disseminate. Although chloramphenicol is not commonly used in human medicine due to its bone marrow toxicity, it is still reserved for the treatment of severe infections such as certain types of meningitis, rickettsiae, or typhoid fever [105–109].

The high prevalence and frequent redundant presence of multiple homologous and analogous resistance genes, e. g. *aph(2")-If*, *aac(6')-Ie/aph(2")-Ia*, *aph(3')-IIIa* and *aadE* in particular, in the isolates from Vietnam, may reflect regular selection of MDRI, resulting in AMR accumulation. In general, high resistance to aminoglycosides should be regarded as concerning as they are considered a high-priority critically important antimicrobial class according to the World Health Organization [110].

Conclusion

Our results highlight the extensive presence of various AMR genes and gene variants, as well as point mutations associated with AMR in the investigated *Campylobacter* population. The approach corroborated the necessity for continuous update of databases with respect to novel AMR gene (variants), point mutations leading to (transient) inactivation of AMR and for including long-read sequencing for improved detection of redundant AMR genes and AMR gene locations. Limitations of gene detection from short-read assemblies can partially be dealt with by lowering required coverage thresholds and complementing analysis with read mapping approaches. Furthermore, yet unknown mechanisms for gentamicin and (fluoro-)quinolone resistance, transiently inactive AMR genes and mobilization of MDRI await further investigation. The findings showed elevated levels of resistance depending on the origin of isolation, emphasizing the need for improved surveillance and diagnostics of AMR in thermotolerant *Campylobacter* spp. along the food production chain globally.

Abbreviations

AMR	Antimicrobial Resistance
CAMHB/FCS	Cation-supplemented Mueller-Hinton broth with 5% fetal calf serum
CC	Clonal Complex
CI	Confidence Interval
ColbA	Columbian Blood Agar
ECOFF	Epidemiological Cut Off
EDTA	Ethylenediaminetetraacetic Acid
FCS	Fetal Calf Serum
mCCDA	Modified Charcoal-Cefoperazone Deoxycholate Agar
MDRI	Multidrug Resistance Island
MIC	Minimum Inhibitory Concentration
MLST	Multi-locus sequence typing
MST	Minimum Spanning Tree
ONT	Oxford Nanopore Technology
OR	Odds Ratio
QRDR	Quinolone resistance determining region
SRA	Sequence Read Archive
WGS	Whole-Genome Sequencing
WHO	World Health Organization

Supplementary Information

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Supplementary Material 1

Supplementary Material 2

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Author contributions

Conceptualization: KS; Methodology, MZ, MK, MT; Investigation, MZ, HQL, HTTH, MK, MT; software, CD; formal analysis, MZ, NB, KS, IH; Writing– original draft, MZ, KS; Writing– review and editing, HQL, CD, PTN, IH; Funding acquisition, HQL, KS. All authors reviewed and agreed upon the final version of the manuscript.

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Data availability

Raw read sequences and either complete annotated genomes or draft genomes were published within the BioProjects No. PRJNA562653, PRJNA595957, PRJNA648048 and PRJNA872862. All data supporting the findings of this study are provided within the paper and its supplementary information. All additional information are available upon request from the authors.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests
The authors declare no competing interests.

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6.5 Publication 4: The point mutation A1387G in the 16S rRNA gene confers aminoglycoside resistance in *C. jejuni* and *C. coli*

The point mutation A1387G in the 16S rRNA gene confers aminoglycoside resistance in *Campylobacter jejuni* and *Campylobacter coli*

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Running Title: Novel aminoglycoside resistance in *Campylobacter* spp.

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Abstract

Thermotolerant *Campylobacter* spp. are the most frequent cause of foodborne bacterial diarrhea and high-priority antibiotic-resistant pathogens according to the World Health Organization (WHO). Monitoring revealed current low prevalence of gentamicin resistance in European *Campylobacter* spp. isolates but substantial presence of gentamicin-modifying genes circulating globally.

Using a combined approach of natural transformation and whole genome sequencing, we revealed a novel gentamicin resistance mechanism, namely the point mutation A1387G in the 16S rRNA gene, originally identified in a *C. coli* isolate from turkey caecal content. The

transformation rate of the resistance using genomic DNA of the resistant donor to sensitive recipient *C. jejuni* and *C. coli* was ~2.5 $\log_{10}$ lower compared to the control *rpsL*-A128G point mutation conferring streptomycin resistance. Antimicrobial susceptibility tests showed cross-resistance to apramycin, kanamycin and tobramycin, with transformants exhibiting more than 4- to 8-fold increased MICs to apramycin and tobramycin and over 64-fold higher MICs to kanamycin compared to wildtype isolates. Although transformants showed 177-1235 variations relative to the recipient, only the A1387G point mutation in the 16S rRNA was in common. This mutation was causal for resistance, as transformation of a 16S rRNA_A1387G PCR fragment into susceptible isolates also led to resistant transformants. Sanger sequencing of the 16S rRNA genes and Oxford nanopore whole genome sequencing of transformants identified clones harboring either all three copies with A1387G or a mixed population of wildtype and mutated 16S rRNA gene alleles. Within 15 passages on non-selective medium, transformants with mixed populations of the 16S rRNA gene copies partially reverted to wildtype, both geno- and phenotypically. In contrast, transformants harboring the A1387G point mutation in all three 16S rRNA gene copies kept full resistance within at least 45 passages. We speculate that partial acquisition and rapid loss of the point mutation limited its spread among *C*. spp. isolates. In-depth knowledge on resistance mechanisms contributes to optimal diagnosis and preventative measures.

Introduction

In 2022, the leading cause of bacterial gastroenteritis in the European Union was again *Campylobacter* spp. with 137,000 reported Campylobacteriosis cases, i. e. more than twice the number of reported *Salmonella* infections (1). Patients with acute campylobacteriosis show symptoms like watery and/or bloody diarrhea, abdominal cramps, fever and nausea (2).

Furthermore, there is a potential for the development of long-term autoimmune sequelae following an acute infection, such as Guillain-Barré syndrome, reactive arthritis and irritable bowel syndrome (3). While antibiotic therapy may not be required for the majority of cases of food-borne campylobacteriosis, patients with severe or persistent infections necessitate antimicrobial treatment (4). Fluoroquinolones and macrolides are the preferred pharmaceutical agents applied in clinics for the treatment of campylobacteriosis (5, 6). However, globally emerging antimicrobial resistances (AMR) are impeding the effectiveness in treatment with these agents, in particular for (fluoro-)quinolones (7-9). Thus, in cases of systemic infection, aminoglycoside antibiotics, specifically gentamicin, persist as the recommended therapeutic option given the susceptibility of *Campylobacter* isolates to this particular class of antibiotics (10).

Aminoglycosides are a class of potent broad-spectrum antibiotics derived from actinomycetes, which have been in use since the 1940s (11). Their primary mode of action involves inhibition of bacterial protein synthesis via blocking elongation or directly inhibiting initiation, with the exact mechanism varying by chemical structure (12-15). Aminoglycosides can be subdivided into two main classes based on the core structure of the aminocyclitol moiety: those derived from streptidine (e.g. streptomycin) and those derived from 2-deoxystreptamine (e.g. gentamicin, kanamycin). The 2-deoxystreptamine-derived aminoglycosides further divide into subclasses based on the specific substitution pattern of their side chains. These structural differences are crucial for their mechanisms of action and susceptibility to various aminoglycoside-modifying enzymes (16). Resistance to gentamicin is rare in Europe (17, 18) but more frequently encountered in China (19, 20), Vietnam (21) and the Philippines (22). Aminoglycoside resistance in *Campylobacter* spp. is mainly attributed to enzymatic inactivation of the aminoglycoside by enzymes. These enzymes include aminoglycoside *N*-

acetyltransferases (AAC), *O*-phosphotransferases (APH), and *O*-nucleotidyltransferases (ANT), which are the predominant mechanisms of resistance (23-25). Resistance to gentamicin, kanamycin and tobramycin is conveyed by the presence of aminoglycoside 2''-phosphotransferase genes (*aph(2'')*) with several distinct variants identified in *Campylobacter* (19, 26-31). Kanamycin resistance is also attributed to the presence of 3'-phosphotransferase genes, like *aph(3')-IIIa* (32) and *aph(3')-VIIa* (33). A recent study found the presence of the resistance gene *apmA* in a *C. coli* isolate which may encode an acetyltransferase for inactivating apramycin (30).

In this study, we report the identification of a novel point mutation in the bacterial A-site of the 16S rRNA in a German *C. coli* isolate that causes resistance to aminoglycosides with a 2-deoxystreptamine structure. We investigated the transferability of this mutation among thermotolerant *Campylobacter* spp. through natural transformation and evaluated its stability under non-selective conditions. Our results highlight the importance of in-depth investigation of the mechanisms of antimicrobial resistance in food-borne pathogens in order to evaluate their spread and persistence. This will improve prediction of resistances using current diagnostics of whole genome sequencing.

Results

Identification of a *C. coli* isolate from turkey caecum with an unknown gentamicin resistance mechanism

Routine resistance monitoring of thermotolerant *Campylobacter* spp. isolated from German turkey in 2018 revealed the presence of a *C. coli* isolate (BfR-CA-15687) displaying gentamicin

resistance with a MIC value >16 mg/L (21). This isolate displayed ST type 10049, which is not yet assigned to a clonal complex. The antimicrobial microdilution assay using the EU-wide harmonized EUCAMP3 plate format was conducted in three independent experiments, all confirming high level gentamicin resistance. In addition, the isolate was resistant to ciprofloxacin and tetracycline (Table 1, Suppl. Figure S1A). Whole genome sequencing based on Illumina short-reads was carried out to identify known resistance determinants. However, no known resistance determinant associated with gentamicin resistance was detected in the assembly or in trimmed reads. As expected for ciprofloxacin and tetracycline resistant *C*. spp., the presence of the T86I point mutation in gyrase subunit A and two copies of the *tet*(O) resistance gene - one located on the chromosome and the other on the plasmid - were detected. The isolate additionally harbored a $bla_{\text{OXA-489}}$ gene with a G to T transversion at position -57 in the promoter region, expected to restore the Pribnow box and to confer resistance to ampicillin (34), which was not phenotypically characterized. The short-read sequencing was repeated, again leading to lack of any known resistance determinants for the observed gentamicin resistance.

Table 1. MIC values of BfR-CA-15687, including test ranges and resistance evaluation

Antimicrobial	**Plate format**	**Test range (mg/L)**	**resistant > MIC (mg/L)**	**MIC of BfR-CA-15687**	**Evaluation (R, S)**
Apramycin	custom	0.03-32	16*	>32	R
Chloramphenicol	EUCAMP3	2-64	16	4	S
Ciprofloxacin	EUCAMP3	0.12-32	0.5	32	R
Ertapenem	EUCAMP3	0.12-4	0.5	0.12	S
Erythromycin	EUCAMP3	1-512	4 (Cj), 8 (Cc)	2	S
Gentamicin	EUCAMP3	0.25-16	2	>16	R
Kanamycin	custom	1-1024	16*	>1024	R
Streptomycin	custom	0.25-16	4	1	S
Tetracycline	EUCAMP3	0.5-64	1 (Cj), 2 (Cc)	>64	R
Tobramycin	custom	0.06-64	16*	>64	R

For resistance evaluation ecological cut-off values (ECOFF) were used, if available or – indicated with * - elevated non-wildtype MIC. R, resistant; S, sensitive; MIC, minimal inhibitory concentration; Cj, *C. jejuni*; Cc, *C. coli*.

The known gentamicin phosphorylating Aph(2'') enzyme variants not only confer resistance to gentamicin but also to the aminoglycosides kanamycin (KAN) and tobramycin (TOB) (21, 25). Hence, BfR-CA-15687 was also tested for susceptibility to these two aminoglycosides as well as to apramycin (APR) and streptomycin (STR) using custom created plates (Table 1, Suppl. Figure S1B, C). BfR-CA-15687 additionally demonstrated elevated non-wildtype MIC values for APR (>32 mg/L), KAN (>1024 mg/L) and TOB (>64 mg/L) (Table 2). In comparison, the tested wildtype isolates (*C. jejuni* BfR-CA-14430; *C. coli* BfR-CA-14856) and reference strains (81-176; NCTC 11168) displayed sensitivity to GEN and notably lower MIC values for the aminoglycosides APR (4-8 mg/L), KAN (8-16 mg/L) and TOB (4-8 mg/L). Given the absence of determinants linked to APR, KAN or TOB resistance, these results indicated that the unidentified gentamicin resistance determinant might be a potential factor also contributing to the observed elevated MIC values to APR, KAN and TOB (Table 2).

Table 2. MIC values of the donor *C. coli* BfR-CA-15687, wildtype recipient isolates and transformant strains to aminoglycosides

			MIC [mg/L]				
	Species	**Sample**	**APR**	**GEN**	**KAN**	**STR**	**TOB**
Donor	*C. coli*	BfR-CA-15687	>32	>16	>1024	1	>64
Wildtype recipient isolates	*C. coli*	BfR-CA-11057	4	0.5	16	1	8
		BfR-CA-14856	8	0.5	16	1	8
	C. jejuni	BfR-CA-14430	4	0.5	8	1	4
		NCTC 11168	4	0.25	8	0.5	8
		81-176	4	0.25	8	1	8
TF using gDNA$_{BfR\text{-}CA\text{-}15687}$	*C. coli*	BfR-CA-11057-TF15687	>32	>16	>1024	1	>64
		BfR-CA-14856-TF15687	>32	>16	>1024	2	>64
	C. jejuni	81-176-TF15687	>32	>16	>1024	1	>64
TF using 16SrRNA fragment$_{BfR\text{-}CA\text{-}15687}$	*C. coli*	BfR-CA-11057-TF16S	>32	>16	>1024	1	>64
		BfR-CA-14856-TF16S	>32	>16	>1024	2	>64
	C. jejuni	BfR-CA-14430-TF16S	>32	>16	>1024	0.5	>64
		NCTC 11168-TF16S	>32	>16	>1024	1	>64
		81-176-TF16S	>32	>16	>1024	1	>64

MIC, minimal inhibitory concentration; TF, transformant; TF16S, transformant after transformation of the 16S rRNA PCR fragment; APR, apramycin, GEN, gentamicin, KAN, kanamycin, STR, streptomycin, TOB, tobramycin.

Natural transformation experiments showed that the unknown APR-GEN-KAN-TOB resistance is transferable among isolates

To explore the transferability of the observed APR-GEN-KAN-TOB resistance through natural transformation, genomic DNA from isolate BfR-CA-15687 was used to naturally transform different recipient strains, which were sensitive to gentamicin and displayed low MICs for apramycin, kanamycin and tobramycin (Table 2). The *C. coli* and *C. jejuni* transformants were selected on 16 and 8 mg/L TOB, respectively, in order to provide a selective pressure at the MIC or maximally 2-fold MIC of the respective recipient strains. As a control, genomic DNA from a streptomycin-resistant *Campylobacter jejuni* transformant BfR-CA-14430-strep, harboring the *rpsL*$_{A128G}$ point mutation, was used and transformants were selected on 16 mg/L STR (35). This allowed for the quantification of natural transformation capacity and normalization of the transformation rate.

When transforming gDNA of BfR-CA-15687 into recipient strains *C. jejuni* 81-176, *C. coli* BfR-CA-11057 and *C. coli* BfR-CA-14856, we observed transformation rates of approximately 10^{-7} per CFU after 48 hours of incubation (Figure 1). As control, transformation of the *rpsL*$_{A128G}$ point mutation in the same recipient strains was around 2.5 $\log_{10}$ more efficient, with transformation rates ranging from 2.23 x 10^{-5} to 1.26 x 10^{-4} per CFU (Figure 1). Additionally, when using a PCR fragment of the 16S rRNA_A1387G as substrate, transformation rates were in mean 4.51 x 10^{-6} ± 1.48 x 10^{-6} per CFU (overall mean of the strains, n=5).

Whole-genome sequencing analysis elucidates a correlation between aminoglycoside resistance and a novel 16S rRNA gene mutation

In order to gain insight into the genetic determinant of the APR-GEN-KAN-TOB resistance in BfR-CA-15687, whole genome sequencing of the sensitive BfR-CA-11057 recipient and nine of its isogenic APR-GEN-KAN-TOB resistant transformants derived from two independent transformation experiments using gDNA of BfR-CA-15687 were compared. For this purpose, the donor isolate BfR-CA-15687 and the recipient isolate BfR-CA-11057 also underwent Oxford Nanopore long-read sequencing in addition to short-read sequencing to obtain a closed genome upon Unicycler hybrid assembly. Mapping of trimmed reads derived from each transformant to the hybrid assembly of BfR-CA-11057 revealed 177 to 1235 sequence nucleotide variants (SNPs) relative to the recipient strain (Table S1B). “Unused reads”, which did not map to the recipient, were subsequently mapped to the donor strain BfR-CA-15687 hybrid assembly sequence. However, those reads did not map to any sequence region common to all transformants (Table S2). Moreover, the transformants exhibited no similarities among genetic regions with low coverage, putatively representing deleted regions compared to the recipient (Table S3). Intriguingly, the consensus of all examined variations in transformants relative to the recipient was a mutation in all three copies of the 16S rRNA gene, located in the aminoacyl tRNA decoding A-site (A1387G; *E. coli* numbering A1408G; Table S1A, B and Figure 2), which was also present in the donor strain BfR-CA-15687 (NCBI; Genome Accession CP126367-CP126368, BioSample Accession SAMN34728731).

In vitro* transformation experiments using a PCR fragment of the 16S rRNA of BfR-CA-15687 verified A1387G point mutation in 16S rRNA gene as a novel mechanism for aminoglycoside resistance in *C. jejuni* and *C. coli

In order to ascertain that the phenotypic resistance was indeed solely attributed to this novel point mutation, we amplified the majority of the 16S rRNA gene (10-1514 bp) of BfR-CA-15687 by PCR (Figure 2A). In order to render the PCR fragment mobilizable via natural transformation in *C. jejuni* and *C. coli*, a 5'-*Eco*RI motif was introduced at both ends of the PCR fragment and the fragment was methylated by an *Eco*RI methylase before use as DNA substrate in the natural transformation experiments (35, 36).

For all five aminoglycoside sensitive recipient strains, BfR-CA-11057, BfR-CA-14856, BfR-CA-14430, NCTC 11168 and 81-176, APR-GEN-KAN-TOB resistant transformants were obtained by transformation of the 16S rRNA PCR fragment of BfR-CA-15687 (Table 2). Subsequent short-read sequencing unveiled the A1387G mutation within the 16S rRNA gene of all five analyzed transformants (one per parental strain), providing corroborative evidence for the causal association between this specific mutation in the 16S rRNA gene and phenotypic resistance to APR-GEN-KAN-TOB in *C. jejuni* and *C. coli*.

We investigated whether the 16S rRNA gene point mutation could be found in previously published sequences of *C. coli*. Using the Basic Local Alignment Search Tool (BLAST) at NCBI, we screened over 32,000 publicly available *C. coli* whole-genome sequences. However, we did not find any instance of this mutation.

Transformants harbor different numbers of 16S rRNA_A1387G gene copies per chromosome

We intended to know, whether all three 16S rRNA gene copies, present in *C. jejuni* and *C. coli* chromosomes, displayed the A1387G point mutation in the transformants, leading to TOB resistance. Hence, just after natural transformation with gDNA, single TOB resistant transformant colonies of BfR-CA-11057-TF15687 and 81-176-TF15687 were once subcultured on ColbA. Subsequently, DNA was extracted from this first passage and the 16S rRNA fragment

comprising position 1387 was Sanger sequenced. We observed two different genotypes of transformants on non-selective ColbA – either a G was detected at position 1387 (Figure 3, CFU 2, no selection) or a double peak in the chromatogram of the Sanger sequence, corresponding to a mixed population of A and G at position 1387 was identified (Figure 3, CFU 1, no selection).

Furthermore, single colonies just after transformation were streaked on plates with varying concentrations of TOB (4, 8 and 16 mg/L) and without TOB supplementation (Figure 3). The colonies from non-selective plates with only G at position 1387 maintained this genotype independent of the TOB concentration the colony was characterized from. However, colonies from non-selective plates, showing a mixed population of A and G at position 1387 in the 16S rRNA gene, switched to a "pure" G at position 1387 at either 8 or 16 mg/L TOB (Figure 3). Hence, the relative ratio of transformants with a distinct number of 16S rRNA gene copies with A1387G appeared to be dynamic, unless all three copies displayed the resistance determining mutation.

We further wanted to decipher, whether the mixed A/G population of 16S rRNA gene sequences at position 1387 was caused by a mixture of 16S rRNA gene variants in the same bacterium. For this purpose, Oxford Nanopore Technologies (ONT) sequencing was performed on a freshly obtained transformant of 81-176-TF15687 only once passaged on non-selective ColbA and displaying a mixed population of A/G at position 1387 in the Sanger sequence. The same DNA was subjected to Illumina short-read sequencing. Using long-read and short-read sequences a hybrid assembly was created using Unicycler, leading to a closed chromosome and one plasmid of 44.8 kb. To rule out assembly errors, the trimmed long-reads of the 81-176-TF15687 transformant were mapped to its hybrid assembly. All three copies of the 16S rRNA gene located in the three ribosomal RNA (rrn) operons at positions 39,157 - 44,986 bp

(rrn I), 395,917 – 401,610 bp (rrn II) and 693,077 – 698,770 bp (rrn III) of the chromosome were visualized (Figure S2). Indeed, in this transformant, the 16S rRNA gene at rrn I and rrn II displayed the A1387G point mutation, whereas the copy at position rrn III maintained wildtype base A at position 1387.

The copy number of 16S rRNA genes with A1387G is important for persistence of aminoglycoside resistance

Furthermore, we intended to evaluate the stability of the newly acquired resistance. For this purpose, fresh transformant colonies of 81-176-TF15687 were first serially diluted to form new single colonies. Subsequently, representative colonies were repeatedly subcultured on non-selective ColbA. Upon passage 1 the genotype at position 1387 in the 16S rRNA genes was initially analyzed by Sanger sequencing (Figure 4). As mentioned above, either a mixed A/G genotype at position 1387 in 16S rRNA or only G at this position was observed (81-176-TF15687$_{16SrRNA_A/Gmix1387}$ or 81-176-TF15687$_{16SrRNA_G1387}$, respectively). After 15 passages on non-selective ColbA, the resistance to tobramycin was reassessed in transformants by agar dilution, that had initially been shown to harbor the mixed A/G genotype. Colonies of the subcultured transformants, that were stamped, i. e. transferred by velvet cloth on ColbA plates with different concentrations of TOB, revealed loss of resistance to 8 and 16 mg/L TOB after passaging. Thus, colonies were only observed on non-selective medium and, in a smaller quantity, in the presence of 4 mg/L TOB (Figure 4A). The reversion to a sensitive genotype (only A at position 1387 in the 16S rRNA gene) was confirmed by Sanger sequencing for a colony, which only grew on non-selective ColbA (Figure 4A). After passaging 81-176-TF15687$_{16SrRNA_G1387}$ for 45 times, which initially only displayed G at position 1387, the phenotypic assay revealed stability of resistance to TOB. In particular, the number of colonies

with and without TOB was stable, independent on the concentration of TOB (Figure 5B). Here, Sanger sequencing of a representative colony showed that the G base at position 1387 was still the only base present after passaging, thus, suggesting stable G1387 presence in all three copies of the 16S rRNA gene.

Discussion

According to regular zoonosis surveillance of thermotolerant foodborne *Campylobacter* spp., resistance to gentamicin remains rare in Europe (17). In 2022, gentamicin resistance was observed in 2 % of the *C. coli* isolates and 0.1 % of *C. jejuni* isolates from broiler, and in 3 % of *C. coli* and 0.5 % of *C. jejuni* isolates from infected humans. Thus, this antibiotic substance can still be considered effective for treatment of campylobacteriosis. However, in China, 15.6 % of *C. jejuni* and 79.9 % of *C. coli* isolates from chicken and swine collected in 2014 and 13 % of *C. jejuni* as well as 50 % of *C. coli* isolated from humans in 2017-2018 showed gentamicin resistance (19, 20). Likewise, a high proportion of *C*. spp. isolates from chicken were gentamicin resistant in Vietnam (21.9 % and 78.8 % in *C. jejuni* and *C. coli* isolated from broiler, respectively (21)) and on the Philippines (65.2 %, (22)). Although point mutations in the 16S rRNA gene have been linked with 2-deoxystreptamine aminoglycoside resistance in other organisms (37-40), this has never been observed before in *C*. spp.. In this study, we have demonstrated that the A1387G mutation occurring at the bacterial A-site (aminoacyl tRNA binding site; Figure 2) confers resistance to the aminoglycosides APR, GEN, KAN and TOB in *C. coli* and *C. jejuni*. Target site modifications, involving genetic mutations and enzymatic methylation predominantly occur at the bacterial A-site, which serves as the binding site for most aminoglycosides (36, 41, 43).

The aminoglycosides used in this study, except streptomycin, all have a 2-deoxystreptamine backbone in common. While GEN, KAN and TOB belong to the 4,6-disubstituted class with an ammonium group (NH_3^+) at position 6' of ring I, APR differs in its structural appearance by belonging to the 4-monosubstituted subclass, while having a hydroxy group (OH) at position 6' of ring I. Nevertheless, these four aminoglycosides have rings I and II in common and either residue (NH_3^+, OH) of ring I is able to build a Watson-Crick pseudo pair with 16S rRNA A1408 (numbering in *E. coli*, corresponding to A1387 in *C.* spp.), thereby inhibiting the decoding step of protein biosynthesis of the bacterium (16).

We wondered, why we were the first to describe this point mutation in *Campylobacter* and if there were sequences published that harbor this specific 16S rRNA gene point mutation. Thus, we conducted analyses utilizing the NCBI BLAST tool and screened the database of whole genome sequences publicly available. However, we could not find the point mutation in any of the more than 32,000 whole-genome sequencing datasets of *C. coli*, suggesting that the resistance determinant identified in the field isolate from caecum of a turkey in Germany during routine monitoring is rare. Likewise, its transferability via horizontal gene transfer was inefficient, with a ~2.5 $\log_{10}$ lower transformation rate compared to the control *rpsL*$_{A128G}$ point mutation. In addition, we only observed transformants when using relatively low initial concentrations of selective aminoglycoside, just above the MIC of the respective wild-type recipients. If transformant colonies were picked initially and streaked on increasing concentrations of selective aminoglycoside, we observed adaptation of colonies with initial mixed 16S rRNA gene copies with and without A1387G mutation to only G at position 1387 at higher concentrations (Figure 3). This likely stems from a gradual transition from a sensitive to a fully resistant phenotype. Hence, we concluded that colonies that have undergone only partial transition are still impeded in growth due to the selective pressure at higher

concentration of aminoglycoside, potentially resulting in a reduced growth rate. Likewise, loss of resistance was observed upon few passages on non-selective medium (Figure 4A), while the resistance was stable if all three copies of the 16S rRNA genes harbored G at position 1387 (Figure 4B). The combined results suggest that complete resistance is only evident when all three copies of the 16S rRNA gene have acquired the A1387G point mutation but that acquisition might be the limiting factor. Interestingly, previous studies reported that thermotolerant *C*. spp. carry aminoglycoside modifying enzymes, such as Aph(2'') phosphotransferase variants (19, 28, 29). Thus, we speculate that although the presence of all three copies of the 16S rRNA gene provides high level gentamicin resistance in *C*. spp., the gradual acquisition of mutated 16S rRNA gene(s) with a low level of resistance may not provide sufficient advantage under selection pressure. In Germany, gentamicin resistance in *C*. spp. is very low, with the isolation of only single isolates per year during zoonosis monitoring. From our analysis, it is tentative to speculate that the 16S rRNA_A1387G gene in the *C. coli* from caecal content of turkey may have emerged by sublethal concentrations of selective agent over time, which remains to be further investigated for potential future practical consequences. A similar phenomenon of gradual acquisition of point mutations in multiple copies of the 16S rRNA gene was observed in *Nocardia farcinica* exposed to amikacin for 24 hours (38). Here, the three 16S rRNA genes showed increasing copy number containing the A1408G point mutation, leading to all copies with a G at position 1408 after prolonged incubation under selective conditions.

In the absence of selective pressure, we did not detect any growth deficiencies on blood agar in transformants, which stably acquired G in all copies of the 16S rRNA gene. However, easy loss of the point mutation upon passage on non-selective blood agar in transformants with mixed copies of A and G at position 1387 indicated fitness costs *in vitro* in *C*. spp.. In other

bacterial pathogens like *Mycobacteria* (41, 42) and in *Borrelia burgdorferi* (43) the point mutation in the 16S rRNA gene is frequently found as resistance determinant for gentamicin in clinical isolates, demonstrating principle toleration and full function of the mutated 16S rRNA gene *in vivo* at least in some bacterial species.

Macrolide resistance in *Campylobacter* is primarily attributed to the A2075G point mutation in the 23S rRNA gene (44). In contrast to the 16S rRNA_A1387G gene mutation, the macrolide resistance conferring mutation was stable upon passaging on non-selective medium, even in isolates harboring only 2 out of 3 copies of the 23S rRNA gene with A2075G (45). This enhanced stability might be a factor contributing to its frequent occurrence in macrolide resistant *Campylobacter*, while antibiotic resistant mutations in the 16S rRNA gene have not been observed before. However, also the macrolide conveying 23S rRNA mutations have been shown to lead to fitness costs in *C. jejuni* in chicken (46). Nevertheless, further investigations are required to evaluate the potential loss of fitness of the 16S rRNA_A1387G gene mutation also *in vivo*. Here, strains with all three 16S rRNA gene copies harbouring the A1387G mutation might be tested over time for colonization capacity in a chicken model. In particular, it would be interesting to challenge the resistant strain in competition with an isogenic strain, carrying all three wildtype 16S rRNA gene copies with A1387.

Conclusion

The novel point mutation A1387G in the 16S rRNA gene of *C. jejuni* and *C. coli* was revealed as novel causative determinant for APR, GEN, KAN and TOB resistance. However, acquisition in less than all three copies of the three 16S rRNA genes in *C.* spp. led to rapid loss and return to a sensitive phenotype. This phenomenon putatively contributed to *C. coli* BfR-CA-15687 being the first and to our knowledge yet only isolate, harboring this resistance. Understanding the

molecular mechanism of resistances as well as their acquisition and persistence in pathogens is crucial for combatting the spread of resistances globally.

Methods

Strains and growth conditions

Campylobacter coli BfR-CA-11057, BfR-CA-14856 and BfR-CA-15687 were isolated in Germany in the years 2012, 2016 and 2018 from raw cow milk, raw goat milk and caecum of turkey, respectively. *Campylobacter jejuni* isolate BfR-CA-14430 was obtained from fresh chicken meat in Germany in 2016 (47). Isolation was conducted by the federal state laboratories according to EN ISO 10272-1 valid in the respective year (48, 49). In addition, reference strains *C. jejuni* NCTC 11168 (50), 81-176 (51) and DSM 4688 (DSMZ - German Collection of Microorganisms and Cell Cultures GmbH, Braunschweig, Germany) as well as *C. coli* strain 2012-70-443-2 (Technical University of Denmark, Lyngby, Denmark) were used. If not stated otherwise, incubation of all cultures was performed under microaerobic conditions with 5 % O_2, 10 % CO_2 and 85 % N_2 (Binder, Tuttlingen, Germany). Cultures derived from -80 °C stock cultures (MAST Group Ltd., Bootle, UK) were cultivated on Columbia blood agar plates containing 5 % defibrinated sheep blood (ColbA, Oxoid, Thermo Fisher Scientific Inc., Waltham, MA, USA) at a temperature of 42 °C for 24 h. Subsequently, the bacteria were subcultured on ColbA for 20 ± 2 h before use. For the selection of transformants, ColbA was supplemented with either tobramycin (8 - 16 mg/L) or streptomycin (16 mg/L) (Sigma Aldrich, St. Louis, MO, USA, respectively).

PCR Amplification and methylation of 16S rRNA

For the amplification of the 16S rRNA of target sequence BfR-CA-15687, forward primer C127 (5'-CTA GCG AAT TCA GAG TTT GAT CCT GGC TCA G-3') and reverse primer C128 (5'-GGA CTG

AAT TCA AGG AGG TGA TCC AAC CGC A-3') were used, carrying each an *Eco*RI motif at the 5' end. The PCR amplification was performed using a Q5 High Fidelity DNA Polymerase (New England Biolabs, Ipswich, MA, USA), following PCR fragment purification using the QIAquick PCR Purification Kit (Qiagen, N.V., Venlo, The Netherlands). Subsequently, the PCR fragment was methylated using an *Eco*RI methyltransferase (New England Biolabs, Ipswich, MA, USA) for 1 h at 37 °C, followed by heat inactivation at 65 °C for 15 min. This procedure is mandatory for mobilization of the PCR fragment for DNA uptake by *C.* spp. (36, 52).

Sanger sequencing analysis of 16S rRNA genes

The primers 16SrRNA-F1 (5'-AGA GTT TGA TCC TGG CTG AG-3') and 16SrRNA-R1 (5'-AAG GAG GTG ATC CAG CCG CA-3') (53) were used for amplification applying the Q5 High Fidelity DNA Polymerase (New England Biolabs, Ipswich, MA, USA). The PCR fragment was purified using the QIAquick PCR Purification Kit (Qiagen, N.V., Venlo, The Netherlands) and 1.5 µg of the DNA was supplemented with the sequencing primer 16SrRNA-S4 (5'-AGT CCC GCA ACG AGC GCA AC-3') (54) for Sanger sequencing at Eurofins Scientific SE, Luxembourg City, Luxembourg.

DNA uptake assay and transformation

Recipient strains from a 20 h $\pm$ 2 h preculture on ColbA was resuspended in 5 mL of brain heart infusion (BHI, Oxoid, Thermo Fisher Scientific Inc., Waltham, MA, USA) and adjusted to an optical density (OD) at 600 nm of 0.3. Subsequently, the strains were cultured at 140 rpm and 37 °C in an atmosphere containing 3.5 % H_2, 6 % O_2, 7 % CO_2 and rest N_2 for 6 hours. Cultures were passaged to fresh BHI and grown over night at the same conditions (16-18 h), using a suitable inoculum assuming doubling times of 1-1.5 hours. Cells were harvested in exponential growth phase at OD_{600nm} = 0.05-0.6 by centrifugation at 14,000 x g for 5 min. The pellet was resuspended in fresh BHI supplemented with 1 µg/mL DNA, either genomic DNA of

BfR-CA-15687, BfR-CA-14430-strep (35) or methylated 16S rRNA gene fragment. DNA uptake, recombination and outgrowth of phenotypic resistance was accomplished by incubation for 4 h at 37 °C. After incubation, cell suspensions were serially diluted in BHI, plated on ColbA with and without tobramycin or streptomycin and incubated for 48 h at 37 °C. The transformation rate was calculated as the ratio of the number of transformants grown on ColbA supplemented with the respective antimicrobial and the total number of colonies on non-selective plates.

Antimicrobial susceptibility testing using microdilution

The susceptibility testing using broth microdilution method followed the guidelines outlined in M45-A and VET06 (55, 56). Isolates subcultured on ColbA at a temperature of 42 °C for 20 ± 2 h were inoculated into cation-supplemented Mueller-Hinton broth (Thermo Fisher Scientific Inc., Waltham, MA, USA) with 5 % fetal calf serum (PAN-Biotech, Aidenbach, Germany) (CAMHB/FCS) at a bacterial concentration ranging from 2 to 8 × 10^5 CFU/ml. The minimum inhibitory concentrations (MICs) were determined using the European standardized EUCAMP3 plate (Thermo Fisher Scientific Inc., Waltham, MA, USA). In addition, custom plate formats were prepared, incorporating the subsequent antimicrobial agents (Sigma Aldrich, St. Louis, MO, USA) and their concentration ranges depicted in Table 1. Stock solutions of the antimicrobials were dissolved in H_2O. The U-bottom microtiter plates (Greiner Bio-One International GmbH, Frickenhausen, Germany) were prepared by adding 50 µL of CAMHB/FCS supplemented with the corresponding double-concentrated antimicrobial agent per well. Before use, the sealed plates were stored at 4 °C for 24 h. The isolates were prepared following the described method above, with the exception that the inoculum was double concentrated in a volume of 50 µL, which was added to each well of the pre-prepared customized plates. Samples were incubated at 37 °C for 48 h. The determination of minimal inhibitory

concentrations (MICs; in mg/L) was performed using the semi-automated Sensititre™ Vizion™ system (Thermo Fisher Scientific Inc., Waltham, MA, USA) and the Sensivizion V2.0 software (MCS Diagnostics BV, Swalmen, The Netherlands). The determination of antimicrobial resistance in *Campylobacter* was based on the guidelines established by the European Committee on Antimicrobial Susceptibility Testing (EUCAST) for Epidemiological cutoff Values (ECOFFs) (57). "Elevated non-wildtype MICs" were previously defined for kanamycin resistance (21). For apramycin and tobramycin "elevated non-wildtype MICs" were defined as >16 mg/L. All ECOFFS and elevated non-wildtype MICs are depicted in Table 1. For quality control, *C. jejuni* strain DSM 4688 and *C. coli* strain 2012-70-443-2 were included, which displayed sensitive phenotypes.

Assessment of stability of acquired antibiotic resistance

To assess the stability of the acquired resistance determinant, fresh transformant colonies were first serially diluted to form new single colonies on non-selective ColbA plates. Subsequently, representative colonies were repeatedly subcultured on non-selective ColbA at 42 °C for 20 ± 2 h. Following the indicated number of passages, bacteria were resuspended in 1 mL buffered peptone water (10 g/L peptone, 5 g/L NaCl, 9 g/L Na_2HPO_4 x 12 H_2O, 1.5 g/L KH_2PO_4, pH 7.0 ± 0.2 at 25 °C), serially diluted to approximately 200 colonies in 100 µL and plated on ColbA. After incubation at 37 °C for 48 hours under microaerobic conditions, colonies were transferred by stamping with velvet cloth on a series of ColbA plates containing 4, 8, and 16 mg/L tobramycin and, as the last plate, ColbA without antimicrobial. The orientation of the plates during stamping was carefully marked, ensuring comparison of plate images, which were taken after 48 h of incubation at 37 °C using the G:BOX CHEMI XX6 imaging system (Synoptics Ltd, Beacon House, Nuffield Road, Cambridge) controlled by the Genesys V1.8.5.0 software (Synoptics Ltd, Beacon House, Nuffield Road, Cambridge).

Whole genome sequencing

Campylobacter isolates were subcultured on ColbA for 20 ± 2 h at 42 °C. Bacteria were harvested from 1 ml cells at OD_{600nm} of 2 by centrifugation at 14,000 x g for 5 min. DNA extraction for short-read sequencing was performed using either the Maxwell RSC Cultured Cells DNA Kit (Promega Corporation, Fitchburg, WI, USA) or the PureLink Genomic DNA Mini Kit (Thermo Fisher Scientific, Waltham, MA, USA). For long-read sequencing, DNA extraction was performed using either the MagAttract HMW Genomic Extraction Kit (Qiagen N.V., Venlo, The Netherlands) according to the protocol but with a 1.5 h of 56 °C incubation step or the MasterPure Complete DNA & RNA Purification Kit (Biozym Scientific GmbH, Hessisch Oldendorf, Germany) following the manufacturer's protocol but using a more concentrated RNase A solution (100 mg/mL; Qiagen N.V., Venlo, The Netherlands).

The DNA quality was assessed through spectral analysis using a NanoDrop Spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA), while the concentration was determined using a Qubit 3.0 Fluorometer with the dsDNA BR Assay Kit (4–2000 ng; Thermo Fisher Scientific, Waltham, MA, USA). DNA libraries for short-read sequencing were prepared using the Illumina DNA Prep, (M) Tagmentation Kit (Illumina, Inc., San Diego, CA, USA), with the modification of using half the volume of all reagents. The Illumina MiSeq benchtop sequencer, equipped with the MiSeq reagent kit v3 (600 cycle, Illumina, Inc., San Diego, CA, USA), or the Illumina NextSeq 500 sequencer utilizing the NextSeq 500/550 mid output kit v2.5 (300 cycle, Illumina, Inc., San Diego, CA, USA) were employed for paired-end sequencing. The read lengths were set from 2 x 149 to 2 x 301, depending on the instrument used.

DNA libraries for long-read sequencing were prepared using the Rapid Barcoding Kit 96 (SQK-RBK110.96, Oxford Nanopore Technologies Limited, Oxford, United Kingdom). The sequencing

process was performed on the MinION Mk1C instrument, using either the MinION R9.4.1 or R10.4.1 FlowCell (Oxford Nanopore Technologies Limited, Oxford, United Kingdom). To process the Oxford Nanopore Technology sequencing data, the Guppy basecaller v. 6.4.8 (Oxford Nanopore Technologies, Oxford, UK) was used in the "super-accuracy" mode.

Bioinformatic analysis

The Illumina paired-end reads were subjected to trimming and *de novo* assembly using the AQUAMIS pipeline, version 1.3.8 (58). For data quality assessment, reads were considered satisfactory if they exhibited a base accuracy of Q30 (error rate 1:1000) for over 80 % of the reads, and if the minimum read coverage was at least 40. For ONT reads, quality control and assembly was conducted using the MiLongA Pipeline v1.0.1 (59). This pipeline includes various tools, such as porechop v0.2.4 (60) for trimming and Unicycler v0.4.8 (61) for hybrid assembly. Quality was considered sufficient if the filtered median fragment length (N50 value) was >10,000 and the read coverage exceeded the minimum of 30.

The assembled contigs underwent analysis using the BakCharak pipeline v3.0.4 (62), which incorporates the antimicrobial resistance gene finder module. This module utilizes AMRFinderPlus v3.10.45 (63) and the corresponding AMRFinder database 2023-04-17.1 to identify resistance determinants, applying default thresholds. Furthermore, ResFinder v4.1 (64) was employed on assembled and trimmed read data with lowest thresholds applied (30 % identity, 20 % coverage) to complement AMRFinderPlus results. Assembled genome contigs were annotated with Bakta (65).

Geneious Prime 2023.2.1 (Biomatters Ltd., New Zealand) was employed to conduct mapping of trimmed reads to assemblies and to analyse sequence variations of the transformants relative to the recipient (Figure 5). In detail, the trimmed short-reads obtained from the

resistant transformants were mapped to the bakta annotated Unicycler hybrid assembly of the recipient isolate. Deletions in the transformants relative to the recipient were identified by displaying low coverage regions (maximum coverage of 5 reads). Variations/SNP's were identified using a minimum coverage of 40 and a minimum variant frequency of 0.8. The paired unused reads were subsequently mapped to the bakta annotated Unicycler hybrid assembly sequences of the donor isolate, which had been concatenated (chromosome and plasmid), to investigate the transfer of larger sequences, such as putative genes or antimicrobial resistance islands (minimum coverage regions (≥ 20 reads)). Finally, the consensus of the SNPs was found using the "Compare Annotations" function (Table S1). Putative deletions in common among the various resistant transformants were detected by tracking "low coverage" regions in the recipient (Table S2). Potential insertions were identified by detection of "high coverage" regions of "unused reads" in the donor, which did not map to the recipient (Table S3). Nucleotide sequences of 16S rRNA genes were aligned using Geneious Prime software with the Geneious Alignment algorithm.

The results retrieved from Sanger sequencing were analyzed with SeqMan Pro 17 (DNASTAR Lasergene 17, DNASTAR, Inc., Madison, WI, USA).

A small fragment (position 1357-1433) of the 16S rRNA of BfR-CA-15687 comprising the A1387G transition was used to search against NCBIs Nucleotide collection (nr/nt) and Whole-genome shotgun contigs (wgs) databases using BLASTN 2.15.0+ (66). Limitations were set for the latter database as *Campylobacter coli* (taxid:195).

Data availability

The complete sequence of the BfR-CA-15687 genome (incl. plasmid) can be found at the National Center for Biotechnology Information (NCBI; Genome Accession CP126367-

CP126368, BioSample Accession SAMN34728731). The 16S ribosomal RNA gene sequence of BfR-CA-15687 is additionally published as GeneBank file, Accession No. PQ227239.

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Author contributions

Conceptualization: K.S. and M.Z.; Formal analysis: M.Z. and K.S.; Investigation: M.Z. and C.W. Methodology: M.Z. and J.G. Writing—original draft: M.Z. and K.S. Writing—review & editing: J.G. and C.W. All authors reviewed and agreed upon the final version of the manuscript.

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Figure Legends

Figure 1. The transformation rates of APR^R-GEN^R-KAN^R-TOB^R resistance determinant using gDNA of BfR-CA-15687 was ~2.5 $\log_{10}$ lower (blue bars) than transformation of the control *rpsL*$_{A128G}$ point mutation using gDNA of BfR-CA-14430-strep leading to STR^R (turquoise bars). The sensitive wildtype strains *C. jejuni* 81-176, *C. coli* BfR-CA-11057 and *C. coli* BfR-CA-14856 were transformed with 1 µg/ml gDNA. Transformation rates were assessed from the ratio of resistant transformants relative to CFU on non-selective Columbia blood agar. The data stem

from at least three independent experiments, with error bars representing standard deviation.

Figure 2. Primary sequence of the 16S rRNA of *C. coli* BfR-CA-15687 (A) and proposed secondary structure of *Campylobacter* spp. 16S rRNA (B, modified from (67)) with the location of the point mutation highlighted with blue frames in A and B, leading to APR^R-GEN^R-KAN^R-TOB^R resistance phenotype. Blue frame in B, sequence of the aminoacyl tRNA decoding region (A-site) of sensitive (1387A in green) and resistant (1387G in red) phenotypes. Numbers indicate positions in the *C.* spp. 16S rRNA sequence. Forward and reverse primers (grey boxes) flanked with 5'-*Eco*RI motifs are depicted in A, which were used for amplification of a 16S rRNA gene fragment of BfR-CA-15687, transformed into sensitive recipient strains.

Figure 3. Single colonies of transformants switched from a mixed A/G genotype at position 1387 in 16S rRNA to only G at higher TOB concentrations. Two representative transformant colonies (CFU 1 and CFU 2) of each *C. jejuni* 81-176-TF15687 and *C. coli* BfR-CA-11057-TF15687 after transformation were transferred to different concentrations of TOB and in parallel on non-selective ColbA. Sanger sequencing revealed two populations of resistant transformants – either harboring base G upon transformation or a mixture of bases A and G at position 1387 in the 16S rRNA genes (marked with black arrows), which changed to only G under higher TOB concentrations. The base color code of the Sanger sequences is indicated below the chromatograms. TOB, tobramycin; wt, wildtype.

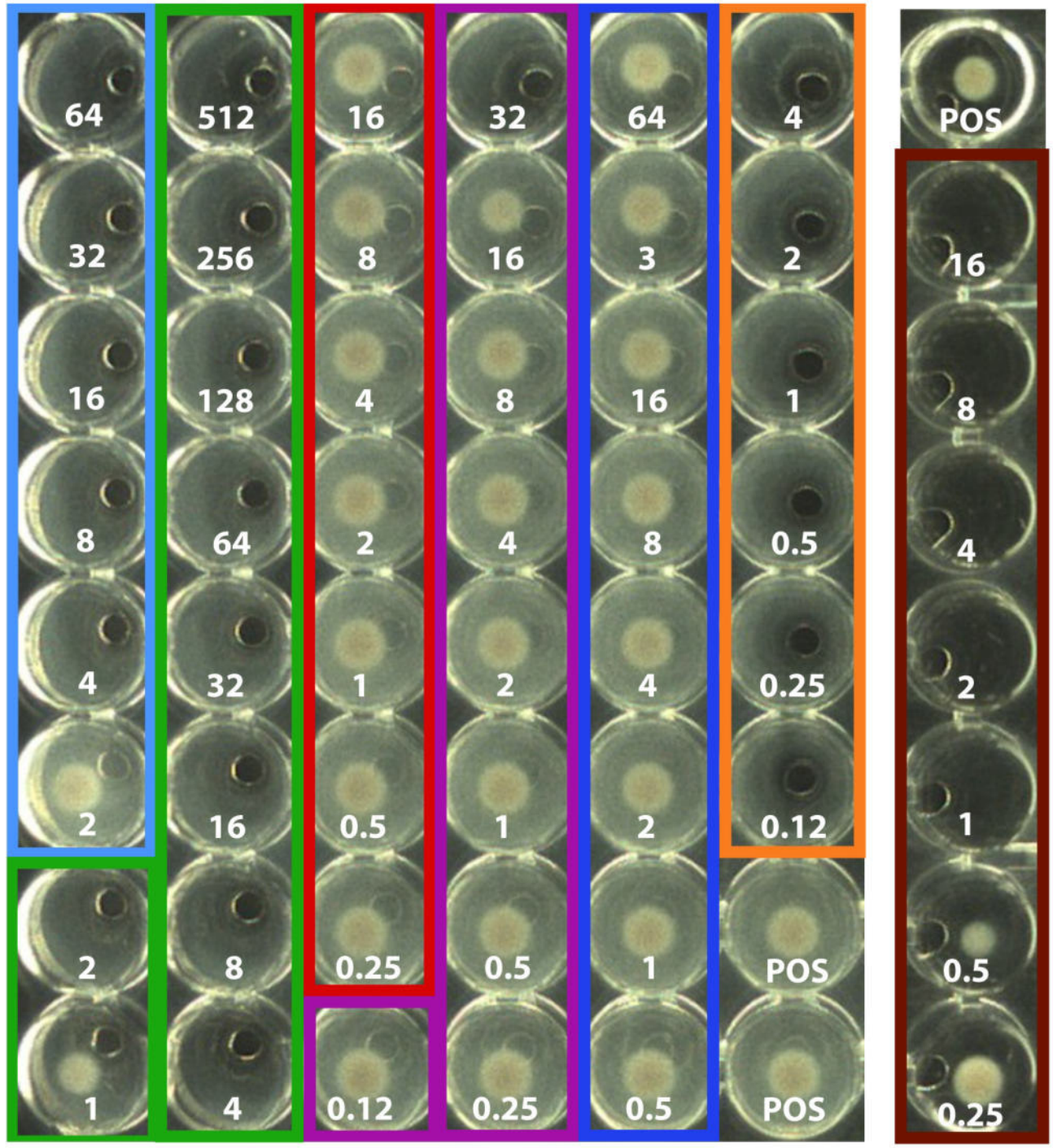
Figure 4. A transformant harboring a mixed A/G genotype at position 1387 in 16S rRNA reverted to a sensitive phenotype after 15 passages (A). In contrast, a transformant with only G at position 1387 maintained resistance even after 45 passages (B). Transformants of *C. jejuni* 81-176-TF15687 were passaged on non-selective ColbA. After the indicated number of

passages, the transformant culture was diluted and spread on non-selective ColbA plates in order to obtain single colonies. Subsequently, colony material was transferred on plates with different concentrations of TOB by stamping with velvet cloth. Photographs of colony patterns on each plate were captured after the indicated number of passages. Sanger sequences are shown after passage 1 (fresh transformant) and after repeated subculturing. A colony, which did not grow on TOB supplemented plates, was taken from non-selective ColbA for Sanger sequencing after passaging.

Figure 5. Schematic illustration of the strategy for identification of the novel resistance determinant. Trimmed short-reads from resistant transformants were mapped to the Unicycler hybrid assembly of the recipient. Variants/SNPs and deletions were revealed per transformant. For each transformant, unused reads were subsequently mapped to the Unicycler hybrid assembly of the donor isolate in order to find AMR gene transfer. The consensus of SNPs, deletions and or insertions of all transformants was verified to be present in the donor, but absent in the recipient isolates.

A

B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ERY S
GEN R
CIP R
TET R
ETP S
STR S
64
32
16
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4
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32
16
16
8
4
2
1
0.5
32
16
8
4
2
1
64
3
1
0.5
0.25
0.12
4
2
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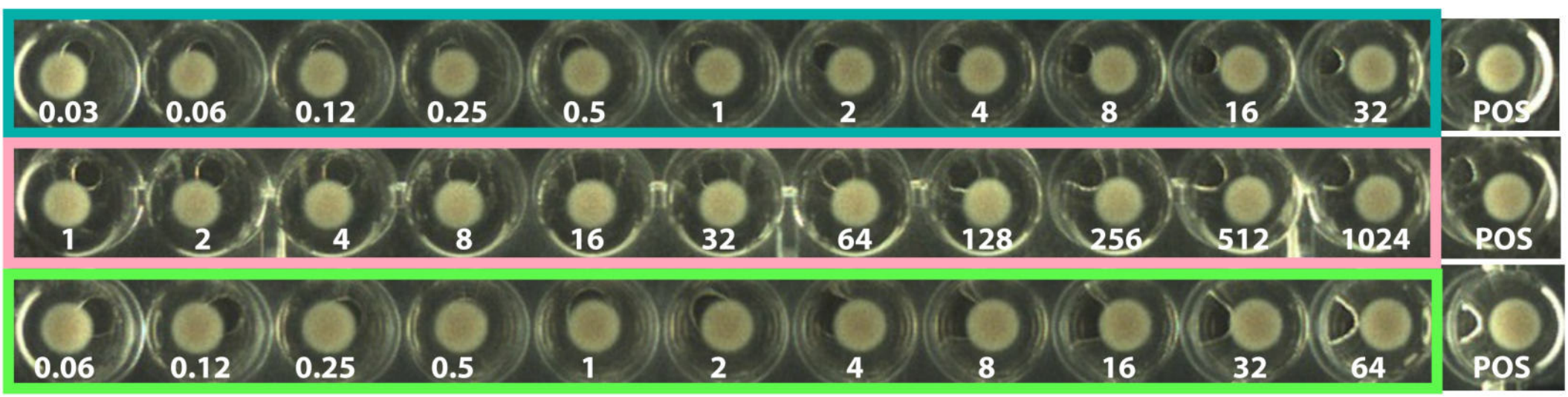
0.5
0.25
0.12
POS
POS
POS
16
8
4
2
1
0.5
0.25

C


APR R
KAN R
TOB R
0.03
0.06
0.12
0.25
0.5
1
2
4
8
16
32
POS
1
2
4
8
16
32
64
128
256
512
1024
POS
0.06
0.12
0.25
0.5
1
2
4
8
16
32
64
POS

APR^R-GEN^R-KAN^R-TOB^R

STR^R

transformation rate (log_{10} /CFU)

-2
-3
-4
-5
-6
-7
-8

81-176

BfR-CA-11057

BfR-CA-14856

A

*Eco*RI- Primer C127

```
TTTTTATGGAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAGCTTC   80
TAGCTTGCTAGAAGTGGATTAGTGGCGCACGGGTGAGTAAGGTATAGTTAATCTGCCCTACACAAGAGGACAACAGTTGG  160
AAACGACTGCTAATACTCTATACTCCTGCTTAACACAAGTTGAGTAGGGAAAGTTTTTCGGTGTAGGATGAGACTATATA  240
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ACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGGAAACCCTGACGCAGCAACGC  400
CGCGTGGAGGATGACACTTTTCGGAGCGTAAACTCCTTTTCTTAGGGAAGAATTCTGACGGTACCTAAGGAATAAGCACC  480
GGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTACTCGGAATCACTGGGCGTAAAGGGCGCGTAG  560
GCGGATTATCAAGTCTCTTGTGAAATCTAATGGCTTAACCATTAAACTGCTTGGGAAACTGATAGTCTAGAGTGAGGGAG  640
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CTCAACTGACGCTAAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCCTAAACGATGTAC  800
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GTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTATTTAGTTGCTAACGGTTCGGC 1120
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GCGACACACGTGCTACAATGGCATATACAATGAGACGCAATACCGCGAGGTGGAGCAAATCTATAAAATATGTCCCAGTT 1280
CGGATTGTTCTCTGCAACTCGAGAGCATGAAGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTT 1360
CCCGGGTCTTGTACTCACCGCCCGTCGCACCATGGGAGTTGATTTCACTCGAAGCCGGAATACTAAACTAGTTACCGTCC 1440
                          A1387G
ACAGTGGAATCAGCGACTGGGGTGAAGTCGTAACAAGGTAACCGTAGGAGAACCTGCGGTTGGATCACCTCCTT       1514
```
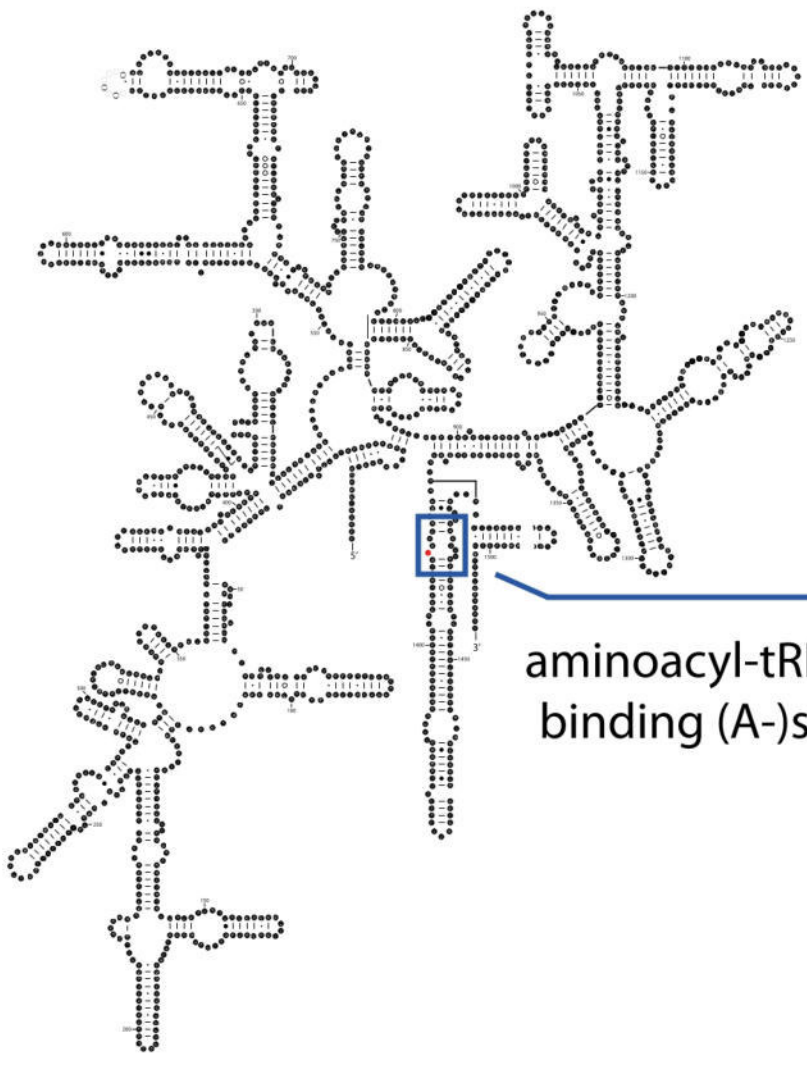
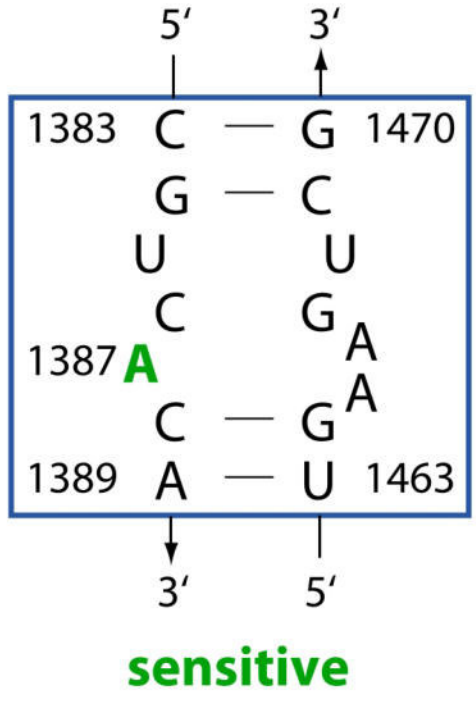

Primer C128 -*Eco*RI

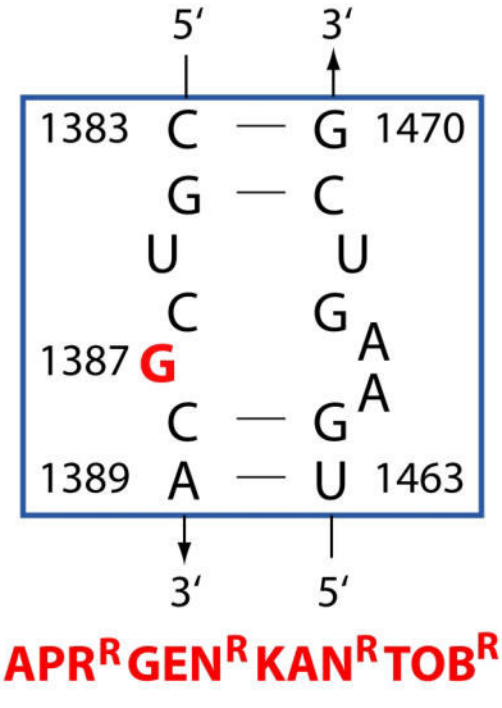
B



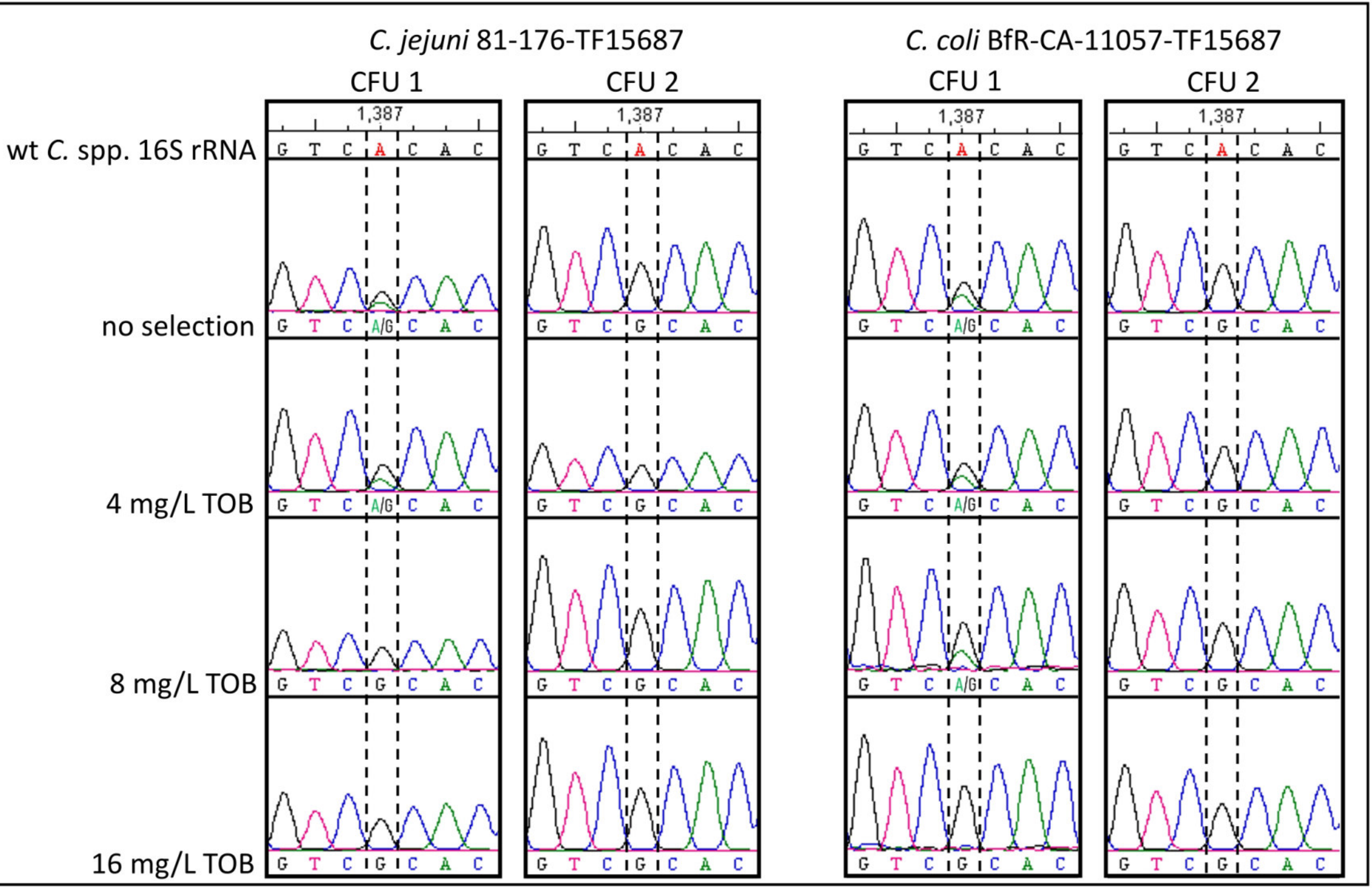
aminoacyl-tRNA binding (A-)site



sensitive

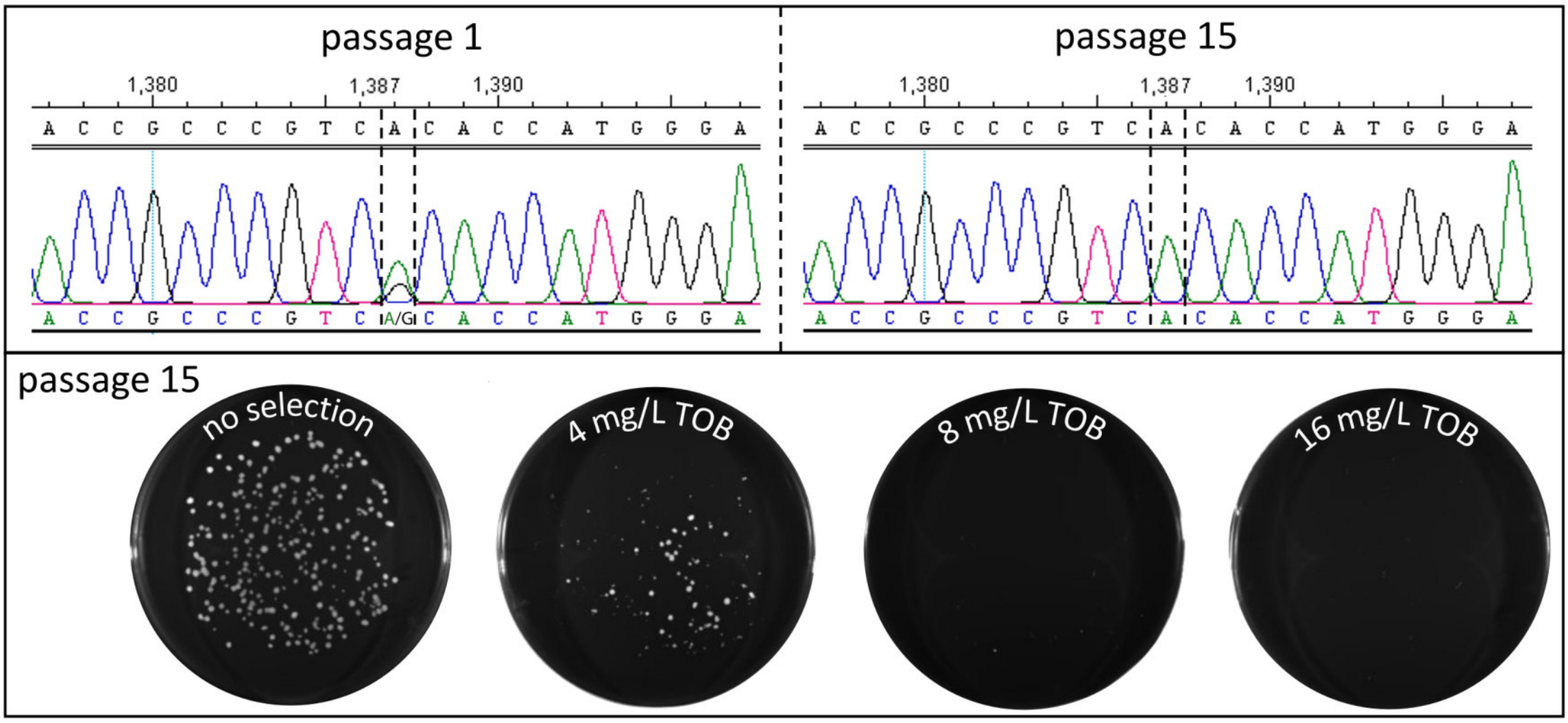


APR^R GEN^R KAN^R TOB^R


C. jejuni 81-176-TF15687
C. coli BfR-CA-11057-TF15687
CFU 1
CFU 2
CFU 1
CFU 2
wt C. spp. 16S rRNA
no selection
4 mg/L TOB
8 mg/L TOB
16 mg/L TOB
1,387
G T C A C A C
G T C A/G C A C
G T C G C A C

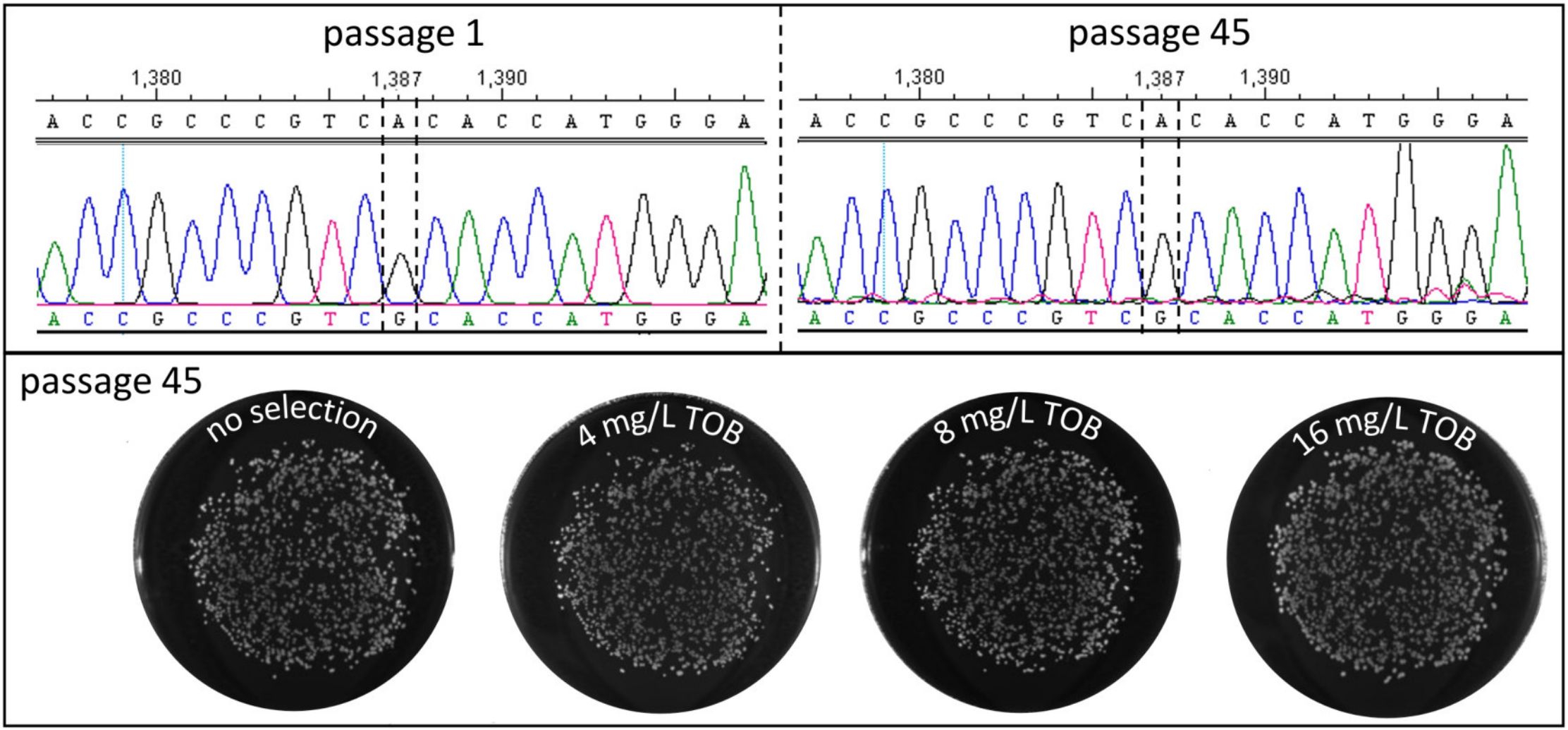
81-176-TF15687$_{16SrRNA_A/G_{mix}1387}$

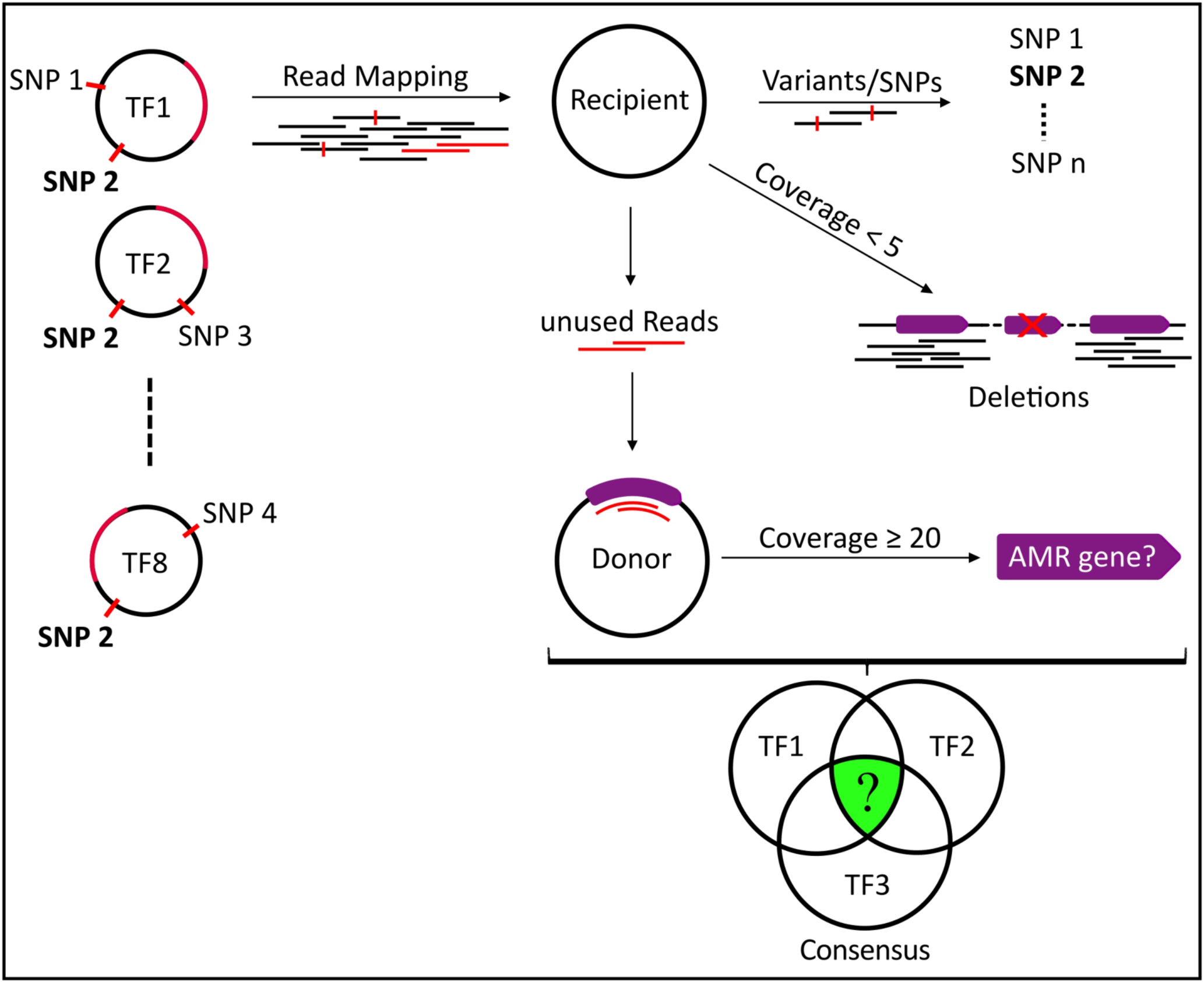
A



81-176-TF15687$_{16SrRNA_G1387}$

B




SNP 1
TF1
SNP 2
TF2
SNP 2
SNP 3
TF8
SNP 4
SNP 2
Read Mapping
Recipient
Variants/SNPs
SNP 1
SNP 2
SNP n
Coverage < 5
unused Reads
Deletions
Donor
Coverage ≥ 20
AMR gene?
TF1
TF2
TF3
?
Consensus

7 Discussion

C. jejuni and *C. coli* stand out as the primary agents associated with campylobacteriosis in humans and thus have a major impact on public health globally. Although antibiotics are crucial for treatment in human and veterinary medicine, their use have led to resistances arising and circulating in bacterial populations. This poses a serious threat as it limits antibiotic treatment options. Hence, The European Centre for Disease Prevention and Control (ECDC) and the World Health Organization (WHO) have emphasized on the need for better surveillance of antimicrobial resistance (AMR) worldwide (159). *Campylobacter* was classified as a high-priority resistant bacterium regarding its fluoroquinolone resistance (58) and was identified by the Centers for Disease Control and Prevention (CDC) as a serious threat to public health (57).

7.1 Phenotypic evaluation reveals regional variation of resistance profiles in *Campylobacter* spp.

The conducted studies comprising *Campylobacter jejuni* and *C. coli* isolates from different geographical regions within Europe and Asia showed that antimicrobial resistance and associated resistance determinants vary depending on origin of isolation. Our study on *Campylobacter* spp. in Georgia provided the first data on antimicrobial resistance for this pathogen in the country (89). Likewise, prevalence of antimicrobial resistance in *Campylobacter* from Vietnam was scarce. Although there are some studies regarding antimicrobial resistance among Vietnamese *Campylobacter* isolates, there are either only a limited number of isolates tested (149, 195) or the study does not reflect the recent situation (153). Hence, our study comprising 254 *Campylobacter* spp. isolates from the poultry production chain and retail markets in Vietnam is the most comprehensive evaluation of antimicrobial resistance in *Campylobacter* in Vietnam to date.

The antibiotic resistance profiles of *Campylobacter* spp. isolates from poultry in Georgia and Germany showed similarities with the antimicrobial resistance data profiles of *Campylobacter* spp. in EU member states. In particular, both *C. jejuni* and *C. coli* from poultry sources in the EU displayed notable resistance to fluoroquinolones and tetracycline, aligning with the findings of our studies (121). Resistance to the aminoglycoside gentamicin was similarly low in isolates from both countries. It was also intriguing to find that all human and chicken isolates from Georgia were sensitive to macrolides, whereas German *C. coli* isolates from chicken meat from retail had a prevalence of 12.8% macrolide resistance in 2022 (160). Similarly, our study of *C. coli* isolates from poultry obtained in Germany from 2013 to 2021 found an 18.3% prevalence of macrolide resistance (67). In Germany, the implementation of mitigation strategies has mandated farmers to reduce antibiotic use (144, 145). This was reflected by a decrease of antibiotic use in poultry by 11.5% in chickens and a 13.1% in turkeys from 2017 to 2021. Although the overall use of antimicrobials has decreased, there has been a shift from the use of polypeptide antibiotics, sulfonamides, and fluoroquinolones toward a preference for aminoglycosides and lincosamides. Additionally, lincosamides are gradually replacing some of the macrolides used. As a result, the use of lincosamides in chickens increased by 2.3%, while macrolide use decreased by 2.2% between 2017 and 2021 (161). The continued use of macrolides and lincosamides in German poultry farming may be a factor contributing to the occurrence of macrolide-resistant isolates. Nevertheless, temporal trends from 2014 to 2022 showed a significant decrease in macrolide resistance at least in *C. jejuni* from broilers and fattening turkeys (121). Meanwhile, due to the lack of data on macrolide use in veterinary settings in Georgia, no conclusions can be drawn, and it remains unclear why all tested isolates were susceptible.

The Vietnamese *Campylobacter* isolates differed as they were comparably more resistant for all tested substances, except that German *C. jejuni* were more frequently

resistant to streptomycin compared to Vietnamese *C. jejuni* (18.4% vs. 12.9%). Next to both *C. jejuni* and *C. coli* being nearly fully or fully resistant to fluoroquinolones and tetracyclines, respectively, especially the *C. coli* isolates also showed high-level resistance to aminoglycosides, macrolides and phenicols (67). This is probably due to the large quantities of antibiotics used for rearing of food animals in Vietnam. For instance, in 2015, Vietnam utilized a total of 3,838 t of antimicrobials, with 71.7% allocated for veterinary purposes. Compared with EU data from 2014, Vietnam's use of antimicrobials for animals was 1.72 times higher (162). Moreover, among the used antimicrobials in Vietnam there are substances that are regarded “highest priority critically important” for human health as stated by the WHO (163-167). This was also reflected in a questionnaire that was handed to farmers where they stated that they used e.g. tetracyclines, tylosin (macrolide), colistin (polymyxin), amoxicillin (ß-lactam) and gentamicin during rearing of chicken. A study on antimicrobial use in household, semi-industrialized, and industrialized pig and poultry farms in Vietnam found that farmers with higher education levels and larger farm sizes were more likely to follow recommended dosages, withdrawal times, and manufacturer guidelines. Consequently, household farmers were less likely to adhere to these recommended guidelines (168). In 2013, Vietnam was the first country from WHOs Western Pacific region to approve a national action plan to fight antimicrobial resistance (169). This action plan is thought to establish better surveillance of resistances circulating in bacterial populations and to improve laboratory capacity. Furthermore, the addition of antimicrobials to animal feed for growth promotion has been banned since 2018 (168).

Macrolides and fluoroquinolones are the preferred pharmaceuticals to treat severe and persisting campylobacteriosis (27, 51, 53). Hence, combined resistance to both substance classes is regarded critically important for treatment. As there were no erythromycin resistant isolates obtained in Georgia, treatment with macrolides would still be applicable. From our study comparing antimicrobial resistance in

Campylobacter isolates from Germany and Vietnam (67), 9.2% (22/240) of the *Campylobacter* spp. isolates derived from poultry between 2013 and 2021 exhibited resistance to both ciprofloxacin and erythromycin; however, all 22 isolates were still susceptible to gentamicin, making this antimicrobial a suitable treatment option. In contrast, 11.0% and 76.8% of *C. jejuni* and *C. coli* isolates from Vietnam, respectively, showed resistance to both macrolides and fluoroquinolones, with isolates collected from fresh chicken feces and chicken meat from retail between 2016 and 2018. Furthermore, 84.4% of the Vietnamese *C. coli* resistant to both substances were also resistant to gentamicin, leaving only few treatment options in case of severe outcomes of the disease.

Surveillance of the carbapenem ertapenem is mandatory in Europe for *C.* spp isolates from food and food animals since the Commission Implementing Decision (EU) 2020/1729 (170) came into force. Hence, the microdilution panel EUCAMP2 was updated to include ertapenem as substance for testing in the latest EUCAMP3 microtiter plate format. The current epidemiological cut-off value (ECOFF) of ertapenem for *Campylobacter* is 0.5 mg/L, defining isolates with MIC values above this value as resistant (171). However, as this antibiotic was introduced for monitoring thermotolerant *Campylobacter* spp. in 2021, there is only limited data on minimum inhibitory concentrations in the current EUCAST database (172). Therefore, adjustments of the ECOFF are likely. According to the current ECOFF, German *Campylobacter* isolates from humans and food obtained between 2018 and 2023 exhibited moderate resistance (6.8–40.0%), while Georgian human and chicken-derived isolates showed moderate to high-level resistance (37.0–82.0%) to the carbapenem antibiotic ertapenem (89, 173). Most recent results from zoonosis monitoring in chicken from retail in 2022 show even higher prevalences, with 6.4% of *C. jejuni* and 66.0% of *C. coli* being resistant to ertapenem (160). Carbapenems, like ertapenem and meropenem have already been used in humans for treating persistent

campylobacteriosis, resulting in the development of resistance to these antimicrobials in previously susceptible strains (174, 175). Vietnamese *Campylobacter* phenotype was only assessed with the EUCAMP2 plate, so that data on carbapenem resistance is still lacking and might be collected in the future.

Concerning species distribution of *C.* spp. isolated from chicken samples, it was intriguing to find that *C. coli* had a substantially higher prevalence of 74% compared to *C. jejuni* in Georgian backyard chickens and a prevalence of 90% in industrial chickens, which contrasts with other studies (176, 177). Meanwhile, the species distribution in human isolates from Georgia, with 82.0% being *C. jejuni* and 18.0% being *C. coli*, reflected a typical distribution, which is commonly observed among human isolates. A study from China showed a species shift from the previously predominant *C. jejuni* to more resistant *C. coli* over the course of seven years. The authors suggested that this species shift might have been likely induced by extended antimicrobial use, especially macrolides (178). Macrolide resistance associated with the point mutations in the 23S rRNA, is linked to a substantial fitness loss in *C. jejuni* (68), whereas *C. coli* does not seem to encounter the same fitness costs (69). However, in the Georgian isolates, none of the *Campylobacter* strains exhibited macrolide resistance, so the high prevalence of *C. coli* is unlikely to be attributed to this factor. In a study by Luangtongkum et al., conventional farms using antimicrobials were associated with a higher prevalence of *C. jejuni* and a lower prevalence of *C. coli* in broilers, but a higher prevalence of *C. coli* and a lower prevalence of *C. jejuni* in turkeys. Conversely, organic farms without antimicrobial use showed the opposite trends for both broilers and turkeys (179). Therefore, there appeared to be no causal relationship between antimicrobial use and the predominance of *C. coli*. Another study from Italy has also indicated that seasonality influences the prevalence of *C.* spp., demonstrating a higher occurrence of *C. coli* during the spring and summer seasons (180). Furthermore, the usage of selective agars and enrichment broth seemed to favor the presence of *C. coli*

(181). Likewise, it was shown by Kramer et al. that *C. coli* was more likely to be isolated after enrichment if multispecies contamination was present (182).

7.2 In-depth analysis of antimicrobial resistance determinants resulted in identification of knowledge gaps in AMR prediction based on WGS

In one of our studies, we analyzed nearly 500 *Campylobacter* isolates from Germany and Vietnam to identify and resolve discrepancies between short-read derived Whole-Genome Sequencing (WGS) and phenotypic data, and to evaluate the reliability of antimicrobial resistance prediction based on WGS. The findings showed regional differences in occurrence of resistance determinants, with substantially more resistance determinants being identified in *Campylobacter* isolates from Vietnam. Interestingly, distinct variants of certain genes, such as *tet*(O) and its mosaic variants, as well as *aadE*, were preferentially harbored by isolates from different geographical regions.

Although, several studies have already published whole-genome sequencing data alongside some phenotypic analysis of thermotolerant *Campylobacter* spp. (65, 66, 90, 104, 107, 108, 116), they did not provide in-depth analyses specifically focused on identifying and resolving discrepancies between whole-genome sequencing data and phenotypic resistance profiles. With our comprehensive and systematic approach, we were able to identify five principle discrepancies between pheno- and genotype in German and Vietnamese *Campylobacter* spp.. These five discrepancies were i) missing or falsely annotated AMR genes, ii) detection issues due to multiple copies or variant genes, iii) AMR gene inactivation by novel mutations and phase variability, iv) non-specific resistance indicated by MIC values just above the cut-off, and v) unknown resistance mechanisms in *Campylobacter* spp..

Certain antimicrobial resistance genes were either missing or inaccurately annotated

in databases. For example, the *aadE*3 gene was absent from both the AMRFinderPlus and ResFinder databases. Yet, this gene had already been described prior (105). Additionally, the ribosomal L22 protein A103V mutation, falsely identified as conferring resistance in the AMRFinderPlus database, lacked correlation with erythromycin resistance. Suggestions that mutations in ribosomal proteins L4 and L22 play a role in macrolide resistance are largely drawn from observed resistances in other bacteria (86, 183), or based on the presence of specific mutations, although without establishing direct causation between a sole mutation and a particular phenotype (184). Several studies have shown that, at least for the proposed resistance mechanism of the point mutation A103V in ribosomal protein L22, there is no correlation with macrolide resistance (65, 67, 185). The mosaic tetracycline resistance gene *tet*(O/32/O) was not yet part of the AMRFinderPlus database (version 2023-08-08.2). Instead, it was identified as *tet*(O) with a reduced identity of approximately 93%. Gene alignments involving *tet*(32) and *tet*(O) demonstrated that the identified gene was indeed the mosaic resistance determinant *tet*(O/32/O). Nevertheless, these issues can be easily addressed by curation of the AMRFinderPlus and ResFinder databases.

We encountered another inconsistency with antimicrobial resistance genes, which appeared either as multiple copies or variant genes. Short-read sequencing methods frequently struggled to precisely assign single reads to specific copies or variants of the genes, causing the assembler to struggle in creating complete sequences of resistance genes from the raw reads. This led to the generation of incomplete genes or lack of the resistant gene in the assemblies. Such assembly errors arising from repetitive regions are known and can be circumvented using long-read sequencing (186). We frequently observed lack of tetracycline resistance genes, especially in tetracycline resistant Vietnamese *Campylobacter* isolates, which harbored up to three copies or variant genes. The assembly process was further complicated due to the presence of the mosaic tetracycline resistance genes *tet*(O/32/O) and *tet*(O/M/O), with

the latter exclusively present in Vietnamese *Campylobacter* spp.. Furthermore, among Vietnamese *Campylobacter* isolates, we detected tetracycline resistance genes exhibiting varying levels of *tet*(M) introgression into the *tet*(O) gene. It is known that ribosomal protection proteins (RPPs) like *tet*(O), *tet*(M), and *tet*(W) are likely to form chimeric structures where they can undergo diverse rearrangements (119). Whether these mosaic-like genes have advantageous traits in bacteria remains uncertain. From our phenotypic analysis we did not observe any differences in resistance to tetracycline arising from these genes. To address issues arising from multiple copies or variant genes, read mapping was performed using an artificial template consisting of three reference genes (*tet*(O), *tet*(O/M/O), and *tet*(O/32/O)), to which the trimmed short reads were aligned. True evidence was then achieved via long-read sequencing, which aligned well with results from read-mapping. Similarly, this phenomenon was noted with other resistance genes such as *aadE*, which existed in various variants, resulting in truncated genes being reported by AMRFinderPlus. The acquisition of multiple genes conferring the same resistance phenotype likely stems from the transfer of multidrug resistance islands, which harbor both the necessary resistance determinants and other resistance genes already present in the genome. Similarly, multiple genes conferring redundant phenotypes, including resistance to tetracycline and phenicol, were observed in isolates from food animals in China (187).

Another issue was the occurrence of point mutations. Mutations in the tetracycline resistance gene *tet*(W) apparently led to inactivation of *tet*(W), since the isolate was tetracycline sensitive, despite the presence of a full-length gene. Likewise, we observed point mutations in the gene *aad9*, which led to annotation of truncated resistance genes by AMRFinderPlus in over two-thirds of all isolates harboring this gene. Yet, phenotypic resistance was always detected in these isolates. From our sequencing data we identified mutations in a poly-C tract within the gene, which led to frameshifts and thus early termination of translation. Through application of selection

pressure with the antimicrobial spectinomycin, the gene reverted to a functional full-length *aad9* capable of inactivating the antibiotic substance. This led to the conclusion that *aad9* is a phase-variable gene able to undergo frameshifting but quickly reverting to a functional gene in presence of spectinomycin. Such phase variation might be important to reduce the cost of carrying AMR genes. Likewise, phase variation has been shown to be important in adaptation and in compensating for fitness costs in pathogenic bacteria (188, 189). In *Campylobacter* phase variation has been proposed e.g., a key mechanism regulating various genes crucial for host response (190-192).

Furthermore, we identified isolates with unknown resistance mechanisms. For instance, some isolates displayed resistance to ciprofloxacin without concurrent resistance to nalidixic acid, indicating unresolved aspects of (fluoro-)quinolone resistance in *Campylobacter*. Additionally, we identified a gentamicin resistant *C. coli* isolated in Germany in 2018 from turkey. Here, initial whole-genome sequencing and analysis approaches utilizing AMRFinderPlus and ResFinder led to absence of any known resistance determinant. Antimicrobial susceptibility testing using customized plate formats revealed that the isolate exhibited cross-resistance to the aminoglycosides apramycin, kanamycin, and tobramycin. Through a combined approach of natural transformation and whole-genome sequencing we were able to identify a novel point mutation within the 16S rRNA gene in the aminoacyl-tRNA binding (A-)site, where gentamicin is known to bind (193). This novel mutation in *Campylobacter* spp. has previously been described in other bacteria as the A1408G mutation (using *E. coli* numbering) (194-197). From our findings we could conclude that the resistance was transferrable via natural transformation in *Campylobacter* spp. but with a comparably low transformation rate. Additionally, Sanger sequencing revealed resistant transformants with different genotypes, which impacted the stability of the acquired resistance. Hence, the presence of the mutation A1387G in all three copies of the 16S rRNA gene was associated with stable resistance even after 45

passages, while presence of 1 or 2 copies led to rapid reversion to a sensitive phenotype after 15 passages. Likewise, in co-cultures of *Borrelia burgdorferi*, where resistant and sensitive strains were mixed, it was observed that the resistant strains were eventually outcompeted. This was evidenced by the absence of colonies from the cocultures on plates with the corresponding antibiotics after 100 generations (194). This study also observed no growth deficiencies in absence of selection pressure, which aligns with our findings. Hence, it can be concluded that, despite no growth deficiency is observable in absence of selection pressure, still the mutation leads to a fitness loss, and that a reversion to a sensitive phenotype was favored.

Additionally, we witnessed that transformants with a mixed population of 16S rRNA gene copies adapted to having only G at position 1387 at higher concentrations of tobramycin. This is probably due to a gradual transition from a sensitive to a fully resistant phenotype. Consequently, we concluded that colonies undergoing only partial transition still experience impeded growth due to the selective pressure at higher aminoglycoside concentrations, leading to a reduced growth rate. This also suggests that complete resistance is only apparent when all copies of 16S rRNA have undergone transition. Similar observations were made for isolates of *Nocardia farcinica* that were exposed to the aminoglycoside amikacin for an extended period (195).

To further elucidate the genetic basis of resistance, we employed Oxford Nanopore long-read sequencing technology. This approach enabled us to pinpoint the exact location of resistance genes within the genome. Our sequencing results revealed that resistance genes were predominantly located on the chromosome, particularly near transposase genes, while they were less frequently found on plasmids. Hence, we concluded that primary mobilization of resistance determinants in *Campylobacter* is likely through natural transformation and transposition and to a lesser extent through conjugation. For instance, the *lnu*(C) gene, found exclusively in Vietnamese *C. jejuni*

isolates, was located near a transposase gene. Similarly, literature from China reported this resistance gene in *C. coli* isolates from chickens, also positioned adjacent to a transposase gene, aligning with our findings (198). Additionally, *fexA* and *optrA* were found next to *IS1216* family transposase genes in *C. jejuni* and *C. coli* from poultry and swine in China, which corresponds with our long-read sequencing data (187). We observed the resistance cluster *aadE-sat4-aph(3')-IIIa* to be located either within the bacterial chromosome or on plasmids. When situated on the chromosome, it was found in close proximity to transposase genes, as reported by other researchers as well (199). Likewise, its presence on plasmids has also been described before (105, 200). Next to the *aadE-sat4-aph(3')-IIIa* gene cluster, both plasmids harboring resistance genes carried either the resistance gene *tet*(O) or *tet*(O/32/O). Transmissible plasmids with tetracycline resistance genes are frequently encountered in *Campylobacter* spp., such as the plasmid pTet (201-203). We also observed genes encoding the Type IV Secretion system, which is crucial for conjugative DNA transfer in *Campylobacter* spp. (204).

Since macrolides are the preferred antimicrobials in treatment of severe and prolonged campylobacteriosis (27, 51, 53), high resistances and spread of associated resistance determinants should be viewed critically. It was intriguing to find that some *Campylobacter coli* isolates from Vietnam harbored the methyltransferase *erm*(B), which also leads to high-level macrolide resistance. Our results from long-read sequencing showed that the gene was situated in a MDRI on the chromosome and that this MDRI was quite conserved throughout the investigated isolates. Likewise, other studies from China also found the gene to be part of different multidrug resistance genomic islands (76, 78). Additionally, a novel *erm* class methyltransferase, subsequently named *erm*(N), was identified in five French and one Canadian clinical strain. Its consistent presence within the CRISPR-*cas9* operon suggested potential dissemination of this resistance determinant between France and Canada, aided by

travel (77, 205). Due to the transferability of the *erm*(B) gene via natural transformation (206), the rapid spread of macrolide resistance is particularly concerning. An indicator of its dissemination is that it has already been identified in many countries globally (72-78).

7.3 Novel pentaplex Real-Time PCR shows rapid and reliable detection of clinically important resistance determinants in *Campylobacter* spp.

The findings from our genomic investigations into resistance determinants circulating globally in the zoonotic pathogen *Campylobacter* were used to develop a novel pentaplex real-time PCR system for routine detection. This novel Real-Time PCR system was specifically designed to target the most commonly encountered and clinically important resistance determinants relevant to the treatment of campylobacteriosis (121). Therefore, we decided to incorporate the detection of the GyrA_T86I point mutation linked to fluoroquinolone resistance, the A2075G point mutation within the 23S rRNA gene, along with the *erm*(B) gene associated with macrolide resistance, and finally, the ribosomal protection protein *tet*(O) responsible for tetracycline resistance. Our aim was to identify resistance determinants without relying on time-consuming and labor-intensive phenotypic characterization, providing rapid tools for utilization in European monitoring surveys of circulating resistance determinants.

While there have been PCR detection systems described for identifying resistance determinants in *Campylobacter*, ours integrates a broader range of resistance determinants than those typically covered by existing systems. For instance, singleplex systems were previously utilized to assess the presence of point mutations, such as in the 23S rRNA gene using mismatch amplification mutation assay (MAMA) PCR (207). A real-time PCR assay, based on amplifying a fragment of the 23S rRNA gene was

designed to detect macrolide-associated mutations (64). Additionally, Hadiyan and colleagues used conventional endpoint PCR to detect the resistance genes *tet*(O), *aph(3')*, *bla*$_{OXA}$ and *cmeB* in *Campylobacter* isolates from poultry meat samples (208). A duplex PCR system was also used to detect fluoroquinolone resistance associated with the T86I point mutation within the *gyrA* gene (209). The novel pentaplex PCR System for detection of four different resistance determinants (*tet*(O), *erm*(B), *gyrA*_T86I and 23S rRNA_A2075G) integrates the detection of the most frequent resistant determinants in *C.* spp. simultaneously.

Although MAMA PCR is commonly used for point mutation detection (210), the pentaplex PCR opted to use Locked Nucleotide Acid (LNA) oligonucleotides instead (211), due to their advantage in providing high specificity by thermally stabilizing the probes (212, 213). Furthermore, unlabeled LNA probes were added, containing the wild-type nucleotide sequence, to enhance the specificity of detecting *gyrA* and 23S rRNA point mutations. The developed multiplex assay does not detect the point mutations A2074G, A2074C, and A2074T (60-62), which may slightly constrain its range of application. Nevertheless, these mutations are rarely observed, while the A2075G mutation is the most frequent encountered mutation associated with macrolide resistance in *Campylobacter* (66, 67, 90, 124).

The comparison between phenotypic and genomic results obtained from EUCAMP3 and PCR, respectively, demonstrated 100% agreement, confirming the specificity of the system. Therefore, the pentaplex PCR system is well-suited as an alert tool for routine resistance monitoring. In future, there might be a need to develop an additional multiplex PCR system capable of detecting other circulating resistance determinants in *Campylobacter* worldwide. Notably, it might be crucial to include aminoglycoside and carbapenem resistance determinants in this expanded system for comprehensive monitoring.

7.4 Conclusion

Our studies have provided valuable insights into the occurrence of resistances in *Campylobacter* isolates from a global perspective. We successfully correlated phenotypic resistance with the presence of genomic determinants. In-depth analysis of whole-genome sequencing data revealed knowledge gaps in the prediction of AMR based on genomic information, emphasizing the need for ongoing refinement and validation of predictive tools. This includes improvements in database curation and sequencing methodologies. Furthermore, the development of a novel pentaplex Real-Time PCR system will enhance routine resistance monitoring in the near future. Our findings highlight the importance of comprehensive surveillance strategies to address ongoing dissemination and adaptation of AMR in thermotolerant *Campylobacter*, particularly in the context of global health.

8 References

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9 Appendix

9.1 List of Abbreviations

2-DOS	2-deoxystreptamine
AMR	antimicrobial resistance
ATP	adenosine triphosphate
BfR	German Federal Institute for Risk Assessment
BVL	German Federal Office of Consumer Protection and Food Safety
CDC	Centers for Disease Control and Prevention
CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats
DALY	Disability Adjusted Life Years
DART	German Antimicrobial Resistance Strategy
ECDC	European Centre for Disease Prevention and Control
ECOFF	Epidemiological Cut-Off
EFSA	European Food Safety Authority
EIA	Enzymatic Immunoassay
EUCAST	European Committee on Antimicrobial Susceptibility Testing
FDA	U.S. Food and Drug Administration
FERG	Foodborne Disease Burden Epidemiology Reference Group
LNA	Locked Nucleic Acid
MAMA	Mismatch Amplification Mutation Assay
MDRI	Multidrug Resistance Island
MIC	Minimum Inhibitory Concentration
NAP	National Action Plan

NARMS	National Antimicrobial Resistance Monitoring System
QRDR	Quinolone Resistance Determining Region
RPP	Ribosome Protection Protein
rRNA	ribosomal Ribonucleic Acid
RT-PCR	Real-Time Polymerase Chain Reaction
SAM	S-adenosylmethionine
tRNA	transfer Ribonucleic Acid
WGS	Whole-Genome Sequencing
WHO	World Health Organization

9.2 Supplementary material of own publications

9.2.1 Publication 1: Comparison of Antimicrobial Susceptibility Profiles of Thermotolerant *Campylobacter* spp. Isolated from Human and Poultry Samples in Georgia (Caucasus)

TabS1_Complete_sample list

data export 10.03.2022

strain No.	source	original No.	Isolation date	Species	NGS_Species	CHL	CIP	ERY	ETP	GEN	TET	Res profile	Res type
BfR-CA-19789	broiler, feces	BY 5	12.02.2020	Campylobacter coli	Campylobacter coli	4	32	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19797	human stool	H8	06.07.2020	Campylobacter jejuni	Campylobacter jejuni	4	16	2	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19798	human stool	H5	08.07.2020	Campylobacter jejuni	Campylobacter jejuni	<=2	8	<=1	<=0,12	0,5	64	CIP, TET	2-fold
BfR-CA-19799	human stool	H9	13.07.2020	Campylobacter coli	Campylobacter coli	4	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19802	human stool	H12	20.08.2020	Campylobacter coli	Campylobacter coli	4	32	<=1	0,5	1	>64	CIP, TET	2-fold
BfR-CA-19804	human stool	H18	29.09.2020	Campylobacter coli	Campylobacter coli	<=2	8	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19805	human stool	H19	29.09.2020	Campylobacter jejuni	Campylobacter jejuni	<=2	16	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19806	human stool	H20	13.10.2020	Campylobacter jejuni	Campylobacter jejuni	<=2	16	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19807	human stool	H27	10.12.2020	Campylobacter coli	Campylobacter coli	4	16	2	<=0,12	0,5	>64	CIP, TET	2-fold
BfR-CA-19808	human stool	H28	15.12.2020	Campylobacter coli	Campylobacter coli	4	16	2	2	0,5	<=0,5	CIP, ETP	2-fold
BfR-CA-19812	human stool	H34	05.03.2021	Campylobacter jejuni	Campylobacter jejuni	<=2	16	<=1	<=0,12	<=0,25	>64	CIP, TET	2-fold
BfR-CA-19817	human stool	H39	13.05.2021	Campylobacter jejuni	Campylobacter jejuni	<=2	16	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19820	human stool	H13	20.08.2020	Campylobacter jejuni	Campylobacter jejuni	<=2	<=0,12	<=1	<=0,12	0,5	<=0,5	sensitive	sensitive
BfR-CA-19827	broiler, feces	BY 15	03.07.2020	Campylobacter coli	Campylobacter coli	<=2	<=0,12	<=1	0,5	0,5	<=0,5	sensitive	sensitive
BfR-CA-19828	broiler, feces	BY 18	03.07.2020	Campylobacter jejuni	Campylobacter jejuni	<=2	16	<=1	<=0,12	0,5	64	CIP, TET	2-fold
BfR-CA-19831	broiler, feces	BY 33	11.02.2021	Campylobacter jejuni	Campylobacter jejuni	<=2	8	<=1	<=0,12	<=0,25	>64	CIP, TET	2-fold
BfR-CA-19833	broiler, feces	BY 37	11.02.2021	Campylobacter coli	Campylobacter coli	4	16	<=1	0,5	1	>64	CIP, TET	2-fold
BfR-CA-19839	broiler, feces	BY 45	23.02.2021	Campylobacter jejuni	Campylobacter jejuni	<=2	<=0,12	<=1	<=0,12	0,5	<=0,5	sensitive	sensitive
BfR-CA-19845	human stool	H30	11.01.2021	Campylobacter jejuni	Campylobacter jejuni	4	32	2	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19846	broiler, feces	BY 27	17.07.2020	Campylobacter jejuni	Campylobacter jejuni	<=2	8	<=1	<=0,12	0,5	32	CIP, TET	2-fold
BfR-CA-19851	human stool	H41	08.06.2021	Campylobacter jejuni	Campylobacter jejuni	4	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19853	human stool	H43	16.06.2021	Campylobacter jejuni	Campylobacter jejuni	<=2	<=0,12	<=1	<=0,12	0,5	64	TET	1-fold
BfR-CA-19854	human stool	H44	16.06.2021	Campylobacter coli	Campylobacter coli	<=2	16	<=1	2	1	>64	CIP, ETP, TET	3-fold
BfR-CA-19857	human stool	H47	01.07.2021	Campylobacter coli	Campylobacter coli	<=2	32	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19863	human stool	H53	30.07.2021	Campylobacter jejuni	Campylobacter jejuni	<=2	16	<=1	<=0,12	<=0,25	<=0,5	CIP	1-fold
BfR-CA-19866	human stool	H56	23.09.2021	Campylobacter jejuni	Campylobacter jejuni	<=2	16	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19874	broiler, feces	BY 46	23.02.2021	Campylobacter coli	Campylobacter coli	4	16	<=1	4	1	<=0,5	CIP, ETP	2-fold
BfR-CA-19876	broiler, feces	BY 48	26.02.2021	Campylobacter jejuni	Campylobacter jejuni	4	32	<=1	<=0,12	0,5	>64	CIP, TET	2-fold
BfR-CA-19902	human stool	H29	25.12.2020	Campylobacter coli	Campylobacter coli	<=2	8	<=1	1	0,5	64	CIP, ETP, TET	3-fold
BfR-CA-19906	broiler, feces	BY 80	07.04.2021	Campylobacter coli	Campylobacter coli	4	8	<=1	1	0,5	<=0,5	CIP, ETP	2-fold
BfR-CA-19911	broiler, feces	BY 66	01.04.2021	Campylobacter jejuni	Campylobacter jejuni	<=2	8	<=1	<=0,12	<=0,25	>64	CIP, TET	2-fold
BfR-CA-19922	broiler, feces	BY 86	07.04.2021	Campylobacter coli	Campylobacter coli	<=2	32	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19931	broiler, feces	BY 95	07.04.2021	Campylobacter jejuni	Campylobacter jejuni	<=2	4	<=1	<=0,12	0,5	16	CIP, TET	2-fold
BfR-CA-19951	broiler, feces	BY 115	15.04.2021	Campylobacter jejuni	Campylobacter jejuni	<=2	16	<=1	<=0,12	0,5	>64	CIP, TET	2-fold
BfR-CA-19952	broiler, feces	IndChi 1	03.06.2021	Campylobacter coli	Campylobacter coli	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19961	broiler, feces	IndChi 10	17.06.2021	Campylobacter coli	Campylobacter coli	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19967	broiler, feces	IndChi 16	17.06.2021	Campylobacter jejuni	Campylobacter jejuni	4	16	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19989	broiler, feces	IndChi 38	09.07.2021	Campylobacter coli	Campylobacter coli	<=2	16	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19995	broiler, feces	IndChi 44	09.07.2021	Campylobacter jejuni	Campylobacter jejuni	4	16	<=1	<=0,12	0,5	>64	CIP, TET	2-fold
BfR-CA-19996	broiler, feces	IndChi 45	09.07.2021	Campylobacter coli	Campylobacter coli	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19786	broiler, feces	BY 1	28.10.2020	Campylobacter coli	n.a.	4	32	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19787	broiler, feces	BY 3	12.02.2020	Campylobacter coli	n.a.	4	32	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19788	broiler, feces	BY 4	12.02.2020	Campylobacter coli	n.a.	4	>32	<=1	0,5	1	>64	CIP, TET	2-fold
BfR-CA-19790	broiler, feces	BY 6	18.06.2021	Campylobacter coli	n.a.	8	>32	<=1	1	1	>64	CIP, ETP, TET	3-fold
BfR-CA-19791	broiler, feces	BY 7	18.06.2021	Campylobacter coli	n.a.	4	>32	<=1	1	1	>64	CIP, ETP, TET	3-fold
BfR-CA-19792	broiler, feces	BY 9	21.02.2020	Campylobacter coli	n.a.	4	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19793	human stool	H2	21.06.2020	Campylobacter jejuni	n.a.	4	8	<=1	<=0,12	0,5	>64	CIP, TET	2-fold
BfR-CA-19794	human stool	H3	21.06.2020	Campylobacter coli	n.a.	<=2	16	2	2	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19795	human stool	H1	21.06.2020	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	<=0,25	64	CIP, TET	2-fold
BfR-CA-19796	human stool	H7	06.07.2020	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	0,5	>64	CIP, TET	2-fold
BfR-CA-19800	human stool	H10	15.07.2020	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19801	human stool	H11	20.07.2020	Campylobacter jejuni	n.a.	4	16	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19803	human stool	H14	04.09.2020	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19809	human stool	H31	18.01.2021	Campylobacter jejuni	n.a.	<=2	8	<=1	<=0,12	1	>64	CIP, TET	2-fold
BfR-CA-19810	human stool	H32	11.02.2021	Campylobacter jejuni	n.a.	<=2	<=0,12	<=1	<=0,12	0,5	<=0,5	sensitivee	sensitive
BfR-CA-19811	human stool	H33	02.03.2021	Campylobacter jejuni	n.a.	<=2	8	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19813	human stool	H35	21.04.2021	Campylobacter jejuni	n.a.	<=2	<=0,12	<=1	<=0,12	<=0,25	<=0,5	sensitive	sensitive
BfR-CA-19814	human stool	H36	21.04.2021	Campylobacter jejuni	n.a.	<=2	<=0,12	<=1	<=0,12	1	<=0,5	sensitive	sensitive
BfR-CA-19815	human stool	H37	26.04.2021	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	1	<=0,5	CIP	1-fold
BfR-CA-19816	human stool	H38	07.05.2021	Campylobacter jejuni	n.a.	<=2	4	<=1	<=0,12	0,5	16	CIP, TET	2-fold
BfR-CA-19818	human stool	H4	06.07.2020	Campylobacter jejuni	n.a.	4	**32**	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19819	human stool	H6	06.07.2020	Campylobacter jejuni	n.a.	4	16	2	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19821	human stool	H15	11.09.2020	Campylobacter jejuni	n.a.	<=2	8	<=1	<=0,12	<=0,25	<=0,5	CIP	1-fold
BfR-CA-19822	human stool	H16	11.09.2020	Campylobacter jejuni	n.a.	<=2	<=0,12	<=1	<=0,12	0,5	<=0,5	sensitive	sensitive
BfR-CA-19823	human stool	H17	24.09.2020	Campylobacter jejuni	n.a.	4	16	4	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19824	broiler, feces	BY 2	28.10.2020	Campylobacter coli	n.a.	4	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19825	broiler, feces	BY 8	18.06.2021	Campylobacter coli	n.a.	<=2	4	<=1	<=0,12	0,5	16	CIP, TET	2-fold
BfR-CA-19826	broiler, feces	BY 14	03.07.2020	Campylobacter coli	n.a.	<=2	16	<=1	1	1	>64	CIP, ETP, TET	3-fold
BfR-CA-19829	broiler, feces	BY 31	11.02.2021	Campylobacter coli	n.a.	<=2	8	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19830	broiler, feces	BY 32	11.02.2021	Campylobacter coli	n.a.	<=2	8	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19832	broiler, feces	BY 35	11.02.2021	Campylobacter coli	n.a.	<=2	8	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19834	broiler, feces	BY 39	11.02.2021	Campylobacter coli	n.a.	4	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19835	broiler, feces	BY 40	11.02.2021	Campylobacter coli	n.a.	8	32	<=1	**0,5**	0,5	<=0,5	CIP	1-fold
BfR-CA-19836	broiler, feces	BY 41	11.02.2021	Campylobacter coli	n.a.	<=2	16	2	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19837	broiler, feces	BY 42	11.02.2021	Campylobacter coli	n.a.	4	32	4	0,5	1	<=0,5	CIP	1-fold
BfR-CA-19838	broiler, feces	BY 43	23.02.2021	Campylobacter coli	n.a.	<=2	8	<=1	1	0,5	64	CIP, ETP, TET	3-fold
BfR-CA-19840	human stool	H22	13.10.2020	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	0,5	>64	CIP, TET	2-fold
BfR-CA-19841	human stool	H23	16.10.2020	Campylobacter jejuni	n.a.	<=2	8	<=1	<=0,12	<=0,25	64	CIP, TET	2-fold
BfR-CA-19842	human stool	H24	23.10.2020	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19843	human stool	H25	20.11.2020	Campylobacter jejuni	n.a.	<=2	16	<=1	0,25	0,5	<=0,5	CIP	1-fold
BfR-CA-19844	human stool	H26	08.12.2020	Campylobacter jejuni	n.a.	<=2	8	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19847	broiler, feces	BY 29	17.07.2020	Campylobacter coli	n.a.	4	16	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19848	broiler, feces	BY 36	11.02.2021	Campylobacter coli	n.a.	4	0,5	<=1	1	0,5	<=0,5	ETP	1-fold
BfR-CA-19849	broiler, feces	BY 44	23.02.2021	Campylobacter coli	n.a.	4	16	<=1	1	1	>64	CIP, ETP, TET	3-fold
BfR-CA-19850	human stool	H40	20.05.2021	Campylobacter jejuni	n.a.	<=2	16	2	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19852	human stool	H42	10.06.2021	Campylobacter jejuni	n.a.	<=2	8	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19855	human stool	H45	01.07.2021	Campylobacter jejuni	n.a.	<=2	32	<=1	<=0,12	0,5	>64	CIP, TET	2-fold
BfR-CA-19856	human stool	H46	01.07.2021	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	0,5	16	CIP, TET	2-fold
BfR-CA-19858	human stool	H48	02.07.2021	Campylobacter jejuni	n.a.	4	32	<=1	<=0,12	0,5	32	CIP, TET	2-fold
BfR-CA-19859	human stool	H49	05.07.2021	Campylobacter jejuni	n.a.	<=2	8	<=1	<=0,12	0,5	16	CIP, TET	2-fold
BfR-CA-19860	human stool	H50	07.07.2021	Campylobacter coli	n.a.	8	<=0,12	4	0,5	1	<=0,5	sensitive	sensitive
BfR-CA-19861	human stool	H51 No cult	09.07.2021	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19862	human stool	H52	30.07.2021	Campylobacter jejuni	n.a.	<=2	8	<=1	<=0,12	<=0,25	<=0,5	CIP	1-fold
BfR-CA-19864	human stool	H54	30.07.2021	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19865	human stool	H55	23.09.2021	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19867	human stool	H57	23.09.2021	Campylobacter jejuni	n.a.	<=2	8	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19868	human stool	H21	13.10.2020	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19869	broiler, feces	BY 34	11.02.2021	Campylobacter coli	n.a.	4	16	2	2	0,5	<=0,5	CIP, ETP	2-fold
BfR-CA-19870	broiler, feces	BY 38	11.02.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	<=0,5	CIP, ETP	2-fold
BfR-CA-19875	broiler, feces	BY 47	23.02.2021	Campylobacter jejuni	n.a.	<=2	16	<=1	0,25	0,5	64	CIP, TET	2-fold
BfR-CA-19877	broiler, feces	BY 49	26.02.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	<=0,5	CIP, ETP	2-fold
BfR-CA-19878	broiler, feces	BY 50	26.02.2021	Campylobacter coli	n.a.	<=2	16	<=1	2	0,5	<=0,5	CIP, ETP	2-fold

BfR-CA-19879	broiler, feces	BY 51	26.02.2021	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19880	broiler, feces	BY 52	26.02.2021	Campylobacter jejuni	n.a.	<=2	<=0,12	<=1	<=0,12	0,5	<=0,5	sensitive	sensitive
BfR-CA-19881	broiler, feces	BY 53	02.03.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	1	>64	CIP, ETP, TET	3-fold
BfR-CA-19882	broiler, feces	BY 54	02.03.2021	Campylobacter coli	n.a.	4	8	<=1	1	1	>64	CIP, ETP, TET	3-fold
BfR-CA-19883	broiler, feces	BY 55	01.04.2021	Campylobacter jejuni	n.a.	<=2	16	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19884	broiler, feces	BY 57	01.04.2021	Campylobacter coli	n.a.	<=2	32	<=1	1	0,5	64	CIP, ETP, TET	3-fold
BfR-CA-19885	broiler, feces	BY 58	01.04.2021	Campylobacter jejuni	n.a.	<=2	16	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19886	broiler, feces	BY 59	01.04.2021	Campylobacter coli	n.a.	4	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19887	broiler, feces	BY 60	01.04.2021	Campylobacter coli	n.a.	4	8	<=1	0,5	0,5	64	CIP, TET	2-fold
BfR-CA-19888	broiler, feces	BY 61	01.04.2021	Campylobacter coli	n.a.	<=2	8	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19889	broiler, feces	BY 62	01.04.2021	Campylobacter jejuni	n.a.	<=2	<=0,12	<=1	<=0,12	0,5	<=0,5	sensitive	sensitive
BfR-CA-19890	broiler, feces	BY 63	01.04.2021	Campylobacter jejuni	n.a.	4	32	<=1	<=0,12	<=0,25	>64	CIP, TET	2-fold
BfR-CA-19891	broiler, feces	BY 64	01.04.2021	Campylobacter jejuni	n.a.	4	32	<=1	<=0,12	<=0,25	>64	CIP, TET	2-fold
BfR-CA-19892	broiler, feces	BY 65	01.04.2021	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	<=0,25	64	CIP, TET	2-fold
BfR-CA-19893	broiler, feces	BY 67	01.04.2021	Campylobacter jejuni	n.a.	<=2	32	<=1	<=0,12	<=0,25	>64	CIP, TET	2-fold
BfR-CA-19894	broiler, feces	BY 68	01.04.2021	Campylobacter coli	n.a.	4	16	<=1	2	0,5	<=0,5	CIP, ETP	2-fold
BfR-CA-19895	broiler, feces	BY 70	01.04.2021	Campylobacter jejuni	n.a.	<=2	32	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19896	broiler, feces	BY 71	01.04.2021	Campylobacter coli	n.a.	<=2	<=0,12	<=1	**0,5**	0,5	<=0,5	sensitive	sensitive
BfR-CA-19897	broiler, feces	BY 72	07.04.2021	Campylobacter coli	n.a.	4	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19898	broiler, feces	BY 73	07.04.2021	Campylobacter coli	n.a.	8	32	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19899	broiler, feces	BY 74	07.04.2021	Campylobacter coli	n.a.	<=2	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19900	broiler, feces	BY 75	07.04.2021	Campylobacter coli	n.a.	4	16	<=1	0,5	0,5	<=0,5	CIP	1-fold
BfR-CA-19901	broiler, feces	BY 76	07.04.2021	Campylobacter coli	n.a.	4	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19903	broiler, feces	BY 77	07.04.2021	Campylobacter coli	n.a.	4	32	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19904	broiler, feces	BY 78	07.04.2021	Campylobacter coli	n.a.	4	8	<=1	1	0,5	<=0,5	CIP, ETP	2-fold
BfR-CA-19905	broiler, feces	BY 79	07.04.2021	Campylobacter coli	n.a.	4	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19907	broiler, feces	BY 82	07.04.2021	Campylobacter coli	n.a.	4	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19908	broiler, feces	BY 83	07.04.2021	Campylobacter coli	n.a.	4	8	<=1	1	0,5	<=0,5	CIP, ETP	2-fold
BfR-CA-19909	broiler, feces	BY 84	07.04.2021	Campylobacter coli	n.a.	4	>32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19910	broiler, feces	BY 85	07.04.2021	Campylobacter coli	n.a.	4	8	<=1	1	0,5	<=0,5	CIP, ETP	2-fold
BfR-CA-19921	broiler, feces	BY 81	07.04.2021	Campylobacter coli	n.a.	<=2	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19923	broiler, feces	BY 87	07.04.2021	Campylobacter coli	n.a.	<=2	8	<=1	1	0,5	<=0,5	CIP, ETP	2-fold
BfR-CA-19924	broiler, feces	BY 88	07.04.2021	Campylobacter coli	n.a.	4	8	<=1	1	0,5	<=0,5	CIP, ETP	2-fold
BfR-CA-19925	broiler, feces	BY 89	07.04.2021	Campylobacter coli	n.a.	4	8	<=1	1	0,5	<=0,5	CIP, ETP	2-fold
BfR-CA-19926	broiler, feces	BY 90	07.04.2021	Campylobacter jejuni	n.a.	<=2	4	<=1	<=0,12	0,5	16	CIP, TET	2-fold
BfR-CA-19927	broiler, feces	BY 91	07.04.2021	Campylobacter coli	n.a.	4	>32	2	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19928	broiler, feces	BY 92	07.04.2021	Campylobacter coli	n.a.	4	32	<=1	<=0,12	0,5	>64	CIP, TET	2-fold
BfR-CA-19929	broiler, feces	BY 93	07.04.2021	Campylobacter coli	n.a.	4	8	<=1	1	0,5	<=0,5	CIP, ETP	2-fold
BfR-CA-19930	broiler, feces	BY 94	07.04.2021	Campylobacter coli	n.a.	4	>32	2	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19932	broiler, feces	BY 96	07.04.2021	Campylobacter jejuni	n.a.	<=2	4	<=1	<=0,12	0,5	16	CIP, TET	2-fold
BfR-CA-19933	broiler, feces	BY 97	07.04.2021	Campylobacter coli	n.a.	4	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19934	broiler, feces	BY 98	15.04.2021	Campylobacter coli	n.a.	<=2	32	<=1	1	1	>64	CIP, ETP, TET	3-fold
BfR-CA-19935	broiler, feces	BY 99	15.04.2021	Campylobacter coli	n.a.	<=2	8	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19936	broiler, feces	BY 100	15.04.2021	Campylobacter coli	n.a.	4	32	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19937	broiler, feces	BY 101	15.04.2021	Campylobacter coli	n.a.	4	32	4	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19938	broiler, feces	BY 102	15.04.2021	Campylobacter jejuni	n.a.	<=2	16	<=1	<=0,12	0,5	<=0,5	CIP	1-fold
BfR-CA-19939	broiler, feces	BY 103	15.04.2021	Campylobacter coli	n.a.	4	32	2	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19940	broiler, feces	BY 104	15.04.2021	Campylobacter coli	n.a.	4	16	2	1	1	>64	CIP, ETP, TET	3-fold
BfR-CA-19941	broiler, feces	BY 105	15.04.2021	Campylobacter coli	n.a.	<=2	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19942	broiler, feces	BY 106	15.04.2021	Campylobacter coli	n.a.	<=2	16	2	<=0,12	0,5	>64	CIP, TET	2-fold
BfR-CA-19943	broiler, feces	BY 107	15.04.2021	Campylobacter jejuni	n.a.	<=2	<=0,12	<=1	<=0,12	0,5	<=0,5	sensitive	sensitive
BfR-CA-19944	broiler, feces	BY 108	15.04.2021	Campylobacter coli	n.a.	<=2	4	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19945	broiler, feces	BY 109	15.04.2021	Campylobacter jejuni	n.a.	<=2	<=0,12	<=1	<=0,12	0,5	>64	TET	1-fold
BfR-CA-19946	broiler, feces	BY 110	15.04.2021	Campylobacter coli	n.a.	4	32	2	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19947	broiler, feces	BY 111	15.04.2021	Campylobacter jejuni	n.a.	<=2	8	<=1	<=0,12	0,5	>64	CIP, TET	2-fold
BfR-CA-19948	broiler, feces	BY 112	15.04.2021	Campylobacter coli	n.a.	4	32	2	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19949	broiler, feces	BY 113	15.04.2021	Campylobacter coli	n.a.	<=2	8	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19950	broiler, feces	BY 114	15.04.2021	Campylobacter coli	n.a.	4	32	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19953	broiler, feces	IndChi 2	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19954	broiler, feces	IndChi 3	16.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19955	broiler, feces	IndChi 4	17.06.2021	Campylobacter coli	n.a.	4	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19956	broiler, feces	IndChi 5	03.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19957	broiler, feces	IndChi 6	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19958	broiler, feces	IndChi 7	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19959	broiler, feces	IndChi 8	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19960	broiler, feces	IndChi 9	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19962	broiler, feces	IndChi 11	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19963	broiler, feces	IndChi 12	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19964	broiler, feces	IndChi 13	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19965	broiler, feces	IndChi 14	17.06.2021	Campylobacter jejuni	n.a.	4	16	<=1	0,25	0,5	>64	CIP, TET	2-fold
BfR-CA-19966	broiler, feces	IndChi 15	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19968	broiler, feces	IndChi 17	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19969	broiler, feces	IndChi 18	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	2	0,5	>64	CIP, ETP,TET	3-fold
BfR-CA-19970	broiler, feces	IndChi 19	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19971	broiler, feces	IndChi 20	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19972	broiler, feces	IndChi 21	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19973	broiler, feces	IndChi 22	17.06.2021	Campylobacter jejuni	n.a.	4	16	<=1	<=0,12	0,5	>64	CIP, TET	2-fold
BfR-CA-19974	broiler, feces	IndChi 23	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19975	broiler, feces	IndChi 24	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19976	broiler, feces	IndChi 25	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19977	broiler, feces	IndChi 26	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19978	broiler, feces	IndChi 27	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19979	broiler, feces	IndChi 28	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19980	broiler, feces	IndChi 29	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19981	broiler, feces	IndChi 30	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19982	broiler, feces	IndChi 31	17.06.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19983	broiler, feces	IndChi 32	09.07.2021	Campylobacter coli	n.a.	<=2	16	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19984	broiler, feces	IndChi 33	09.07.2021	Campylobacter coli	n.a.	<=2	16	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19985	broiler, feces	IndChi 34	09.07.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19986	broiler, feces	IndChi 35	09.07.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	64	CIP, ETP, TET	3-fold
BfR-CA-19987	broiler, feces	IndChi 36	09.07.2021	Campylobacter coli	n.a.	<=2	32	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19988	broiler, feces	IndChi 37	09.07.2021	Campylobacter coli	n.a.	<=2	16	<=1	0,5	0,5	>64	CIP, TET	2-fold
BfR-CA-19990	broiler, feces	IndChi 39	09.07.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19991	broiler, feces	IndChi 40	09.07.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19992	broiler, feces	IndChi 41	09.07.2021	Campylobacter coli	n.a.	4	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19993	broiler, feces	IndChi 42	09.07.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19994	broiler, feces	IndChi 43	09.07.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19997	broiler, feces	IndChi 46	09.07.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-19998	broiler, feces	IndChi 47	09.07.2021	Campylobacter jejuni	n.a.	<=2	8	<=1	0,25	0,5	<=0,5	CIP	1-fold
BfR-CA-19999	broiler, feces	IndChi 48	09.07.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-20000	broiler, feces	IndChi 49	09.07.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
BfR-CA-20001	broiler, feces	IndChi 50	09.07.2021	Campylobacter coli	n.a.	<=2	16	<=1	1	0,5	>64	CIP, ETP, TET	3-fold
n.a.	broiler, feces	BY 11	03.07.2020	non culturable - PCR C. coli	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	broiler, feces	BY 12	03.07.2020	non culturable - PCR mixed C. jejuni/C. coli	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	broiler, feces	BY 13	03.07.2020	non culturable - PCR mixed C. jejuni/C. coli	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.

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n.a.	broiler, feces	BY 16	03.07.2020	non culturable - PCR C. coli	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	broiler, feces	BY 17	03.07.2020	non culturable	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	broiler, feces	BY 19	03.07.2020	non culturable - PCR mixed C. jejuni/C. coli	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	broiler, feces	BY 21	17.07.2020	non culturable - PCR mixed C. jejuni/C. coli	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	broiler, feces	BY 22	17.07.2020	non culturable - PCR C. coli	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	broiler, feces	BY 23	17.07.2020	non culturable - PCR mixed C. jejuni/C. coli	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	broiler, feces	BY 24	17.07.2020	non culturable - PCR C. jejuni	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	broiler, feces	BY 26	17.07.2020	non culturable - PCR C. coli	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	broiler, feces	BY 56	01.04.2021	non culturable	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	broiler, feces	BY 69	01.04.2021	non culturable	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	human stool	H no cul Afkhazashvili	15.07.2020	non culturable - PCR C. jejuni	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	human stool	H29	25.12.2020	non culturable	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
n.a.	human stool	H no cu Kurtskhalia	16.06.2021	non culturable - PCR C. jejuni	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.

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TabS2_WGS_data_overview

strain No.	source	original No.	Isolation date	Species	NGS_Species	coverage depth	number contiqs	ST	CC	aspA	glnA	gltA	glyA	pgm	tkt	uncA	amr genecount	amr genecount aquired	amr genecount points	amr genes	mobile amr genecount	mobile amr genes	plasmids contigs	plasmids cumulativelength	plasmids circular	strain No.	Res profile
BfR-CA-19789	broiler, feces	BY 5	12.02.2020	Campylobacter coli	Campylobacter coli	74,5	54	1058	ST-828 complex	33	39	30	82	104	35	17	3	2	1	blaOXA-489;gyrA_T86I;tet(O)	0	None found	1	26044	0	BfR-CA-19789	CIP, TET
BfR-CA-19797	human stool	H8	06.07.2020	Campylobacter jejuni	Campylobacter jejuni	90,5	40	38	ST-48 complex	2	4	2	2	6	1	5	2	1	1	blaOXA-193;gyrA_T86I	0	None found	1	29179	0	BfR-CA-19797	CIP
BfR-CA-19798	human stool	H5	08.07.2020	Campylobacter jejuni	Campylobacter jejuni	76,0	45	11759	ST-574	7	84	2	10	11	3	3	4	2	2	50S_L22_A103V;blaOXA-193;gyrA_T86I;tet(O)	0	None found	0	0	0	BfR-CA-19798	CIP, TET
BfR-CA-19799	human stool	H9	13.07.2020	Campylobacter coli	Campylobacter coli	96,5	54	855	ST-828 complex	33	39	30	79	104	35	17	3	2	1	blaOXA-489;gyrA_T86I;tet(O)	0	None found	1	26043	0	BfR-CA-19799	CIP, ETP, TET
BfR-CA-19802	human stool	H12	20.08.2020	Campylobacter coli	Campylobacter coli	93,8	56	11762	ST-828 complex	33	39	30	82	104	47	731	3	2	1	blaOXA-594;gyrA_T86I;tet(O)	0	None found	1	40871	0	BfR-CA-19802	CIP, TET
BfR-CA-19804	human stool	H18	29.09.2020	Campylobacter coli	Campylobacter coli	64,2	70	855	ST-828 complex	33	39	30	79	104	35	17	4	2	2	50S_L22_A103V;blaOXA-193;gyrA_T86I;tet(O)	0	None found	9	43987	0	BfR-CA-19804	CIP, ETP, TET
BfR-CA-19805	human stool	H19	29.09.2020	Campylobacter jejuni	Campylobacter jejuni	80,1	31	356	ST-353 complex	14	17	5	2	11	3	6	1	0	1	gyrA_T86I	0	None found	0	0	0	BfR-CA-19805	CIP
BfR-CA-19806	human stool	H20	13.10.2020	Campylobacter jejuni	Campylobacter jejuni	67,9	33	356	ST-353 complex	14	17	5	2	11	3	6	1	0	1	gyrA_T86I	0	None found	0	0	0	BfR-CA-19806	CIP
BfR-CA-19807	human stool	H27	10.12.2020	Campylobacter coli	Campylobacter coli	94,6	29	854	ST-828 complex	33	38	30	82	104	43	17	3	2	1	aadE-Cc;gyrA_T86I;tet(O)	0	None found	1	3397	0	BfR-CA-19807	CIP, TET
BfR-CA-19808	human stool	H28	15.12.2020	Campylobacter coli	Campylobacter coli	53,9	38	8043	none	33	66	30	79	113	35	17	2	1	1	blaOXA-193;gyrA_T86I	0	None found	1	44061	0	BfR-CA-19808	CIP, ETP
BfR-CA-19812	human stool	H34	05.03.2021	Campylobacter jejuni	Campylobacter jejuni	67,2	135	531	none	2	71	5	62	11	67	6	3	2	1	blaOXA-452;gyrA_T86I;tet(O)	0	None found	2	5954	0	BfR-CA-19812	CIP, TET
BfR-CA-19817	human stool	H39	13.05.2021	Campylobacter jejuni	Campylobacter jejuni	53,1	28	1947	ST-22 complex	1	94	6	4	3	3	3	2	1	1	blaOXA-193;gyrA_T86I	0	None found	0	0	0	BfR-CA-19817	CIP
BfR-CA-19820	human stool	H13	20.08.2020	Campylobacter jejuni	Campylobacter jejuni	72,5	45	49	ST-49 complex	3	1	5	17	11	11	6	1	1	0	blaOXA-461	0	None found	2	73430	0	BfR-CA-19820	sensitiv
BfR-CA-19827	broiler, feces	BY 15	03.07.2020	Campylobacter coli	Campylobacter coli	57,5	40	825	ST-828 complex	33	39	30	82	113	47	17	0	0	0	0	0	None found	2	37212	0	BfR-CA-19827	sensitiv
BfR-CA-19828	broiler, feces	BY 18	03.07.2020	Campylobacter jejuni	Campylobacter jejuni	99,6	30	354	ST-354 complex	8	10	2	2	11	12	6	3	2	1	blaOXA-460;gyrA_T86I;tet(O)	0	None found	0	0	0	BfR-CA-19828	CIP, TET
BfR-CA-19831	broiler, feces	BY 33	11.02.2021	Campylobacter jejuni	Campylobacter jejuni	75,1	71	464	ST-464 complex	24	2	2	2	10	3	1	3	1	2	50S_L22_A103V;gyrA_T86I;tet(O)	0	None found	0	0	0	BfR-CA-19831	CIP, TET
BfR-CA-19833	broiler, feces	BY 37	11.02.2021	Campylobacter coli	Campylobacter coli	70,3	35	828	ST-828 complex	33	39	30	82	104	43	17	4	3	1	aadE-Cc;blaOXA-489;gyrA_T86I;tet(O)	0	None found	1	28684	1	BfR-CA-19833	CIP, TET
BfR-CA-19839	broiler, feces	BY 45	23.02.2021	Campylobacter jejuni	Campylobacter jejuni	66,7	19	1723	ST-354 complex	8	17	2	2	11	12	6	1	1	0	blaOXA-460	0	None found	0	0	0	BfR-CA-19839	sensitiv
BfR-CA-19845	human stool	H30	11.01.2021	Campylobacter jejuni	Campylobacter jejuni	50,6	55	11759	ST-574	7	84	2	10	11	3	3	4	2	2	50S_L22_A103V;blaOXA-193;gyrA_T86I;tet(O)	0	None found	0	0	0	BfR-CA-19845	CIP, TET
BfR-CA-19846	broiler, feces	BY 27	17.07.2020	Campylobacter jejuni	Campylobacter jejuni	80,6	56	305	ST-574 complex	9	53	2	10	11	3	3	4	2	2	50S_L22_A103V;blaOXA-193;gyrA_T86I;tet(O)	0	None found	0	0	0	BfR-CA-19846	CIP, TET
BfR-CA-19851	human stool	H41	08.06.2021	Campylobacter jejuni	Campylobacter jejuni	58,6	56	607	ST-607 complex	8	2	5	53	11	3	1	3	2	1	blaOXA-193;gyrA_T86I;tet(O)	0	None found	0	0	0	BfR-CA-19851	CIP, TET
BfR-CA-19853	human stool	H43	16.06.2021	Campylobacter jejuni	Campylobacter jejuni	102,9	33	658	ST-658 complex	2	4	2	4	19	3	6	2	2	0	blaOXA-193;tet(O)	0	None found	0	0	0	BfR-CA-19853	TET
BfR-CA-19854	human stool	H44	16.06.2021	Campylobacter coli	Campylobacter coli	93,3	49	902	ST-828 complex	33	39	30	79	104	43	17	3	2	1	blaOXA-489;gyrA_T86I;tet(O)	0	None found	1	26364	0	BfR-CA-19854	CIP, ETP, TET
BfR-CA-19857	human stool	H47	01.07.2021	Campylobacter coli	Campylobacter coli	97,6	52	902	ST-828 complex	33	39	30	79	104	43	17	4	3	1	aadE;blaOXA;gyrA_T86I;tet(O)	0	None found	0	0	0	BfR-CA-19857	CIP, TET
BfR-CA-19863	human stool	H53	30.07.2021	Campylobacter jejuni	Campylobacter jejuni	51,0	50	356	ST-353 complex	14	17	5	2	11	3	6	1	0	1	gyrA_T86I	0	None found	0	0	0	BfR-CA-19863	CIP
BfR-CA-19866	human stool	H56	23.09.2021	Campylobacter jejuni	Campylobacter jejuni	83,5	32	356	ST-353 complex	14	17	5	2	11	3	6	1	0	1	gyrA_T86I	0	None found	0	0	0	BfR-CA-19866	CIP
BfR-CA-19874	broiler, feces	BY 46	23.02.2021	Campylobacter coli	Campylobacter coli	102,3	38	902	ST-828 complex	33	39	30	79	104	43	17	2	0	2	50S_L22_A103V;gyrA_T86I	0	None found	0	0	0	BfR-CA-19874	CIP, ETP
BfR-CA-19876	broiler, feces	BY 48	26.02.2021	Campylobacter jejuni	Campylobacter jejuni	71,8	52	1723	ST-354 complex	8	17	2	2	11	12	6	3	2	1	blaOXA-460;gyrA_T86I;tet(O)	0	None found	0	0	0	BfR-CA-19876	CIP, TET
BfR-CA-19902	human stool	H29	25.12.2020	Campylobacter coli	Campylobacter coli	99,9	41	3990	ST-828 complex	33	66	30	79	104	43	17	3	2	1	blaOXA-489;gyrA_T86I;tet(O)	0	None found	0	0	0	BfR-CA-19902	CIP, ETP, TET
BfR-CA-19906	broiler, feces	BY 80	07.04.2021	Campylobacter coli	Campylobacter coli	68,4	55	828	ST-828 complex	33	39	30	82	104	43	17	2	1	1	blaOXA-193;gyrA_T86I	0	None found	0	0	0	BfR-CA-19906	CIP, ETP
BfR-CA-19911	broiler, feces	BY 66	01.04.2021	Campylobacter jejuni	Campylobacter jejuni	37,3	50	2801	ST-581 complex	7	112	5	62	11	3	6	3	2	1	blaOXA;gyrA_T86I;tet(O)	0	None found	1	1983	1	BfR-CA-19911	CIP, TET
BfR-CA-19922	broiler, feces	BY 86	07.04.2021	Campylobacter coli	Campylobacter coli	96,7	36	1058	ST-828 complex	33	39	30	82	104	35	17	3	2	1	blaOXA-489;gyrA_T86I;tet(O)	0	None found	1	26552	0	BfR-CA-19922	CIP, TET
BfR-CA-19931	broiler, feces	BY 95	07.04.2021	Campylobacter jejuni	Campylobacter jejuni	66,9	64	464	ST-464 complex	24	2	2	2	10	3	1	2	1	1	gyrA_T86I;tet(O)	0	None found	0	0	0	BfR-CA-19931	CIP, TET
BfR-CA-19951	broiler, feces	BY 115	15.04.2021	Campylobacter jejuni	Campylobacter jejuni	97,0	33	45	ST-45 complex	4	7	10	4	1	7	1	2	1	1	gyrA_T86I;tet(O)	0	None found	0	0	0	BfR-CA-19951	CIP, TET
BfR-CA-19952	broiler, feces	IndChi 1	03.06.2021	Campylobacter coli	Campylobacter coli	98,5	46	855	ST-828 complex	33	39	30	79	104	35	17	4	2	2	50S_L22_A103V;blaOXA-193;gyrA_T86I;tet(O)	0	None found	2	29158	1	BfR-CA-19952	CIP, ETP, TET
BfR-CA-19961	broiler, feces	IndChi 10	17.06.2021	Campylobacter coli	Campylobacter coli	62,4	39	855	ST-828 complex	33	39	30	79	104	35	17	4	2	2	50S_L22_A103V;blaOXA-193;gyrA_T86I;tet(O)	0	None found	2	29121	0	BfR-CA-19961	CIP, ETP, TET
BfR-CA-19967	broiler, feces	IndChi 16	17.06.2021	Campylobacter jejuni	Campylobacter jejuni	51,0	27	3628	ST-443 complex	7	17	2	337	23	3	12	4	2	2	50S_L22_A103V;blaOXA-193;gyrA_T86I;tet(O)	0	None found	0	0	0	BfR-CA-19967	CIP, TET
BfR-CA-19989	broiler, feces	IndChi 38	09.07.2021	Campylobacter coli	Campylobacter coli	95,9	39	855	ST-828 complex	33	39	30	79	104	35	17	4	2	2	50S_L22_A103V;blaOXA-193;gyrA_T86I;tet(O)	0	None found	2	29500	0	BfR-CA-19989	CIP, TET
BfR-CA-19995	broiler, feces	IndChi 44	09.07.2021	Campylobacter jejuni	Campylobacter jejuni	101,1	37	3628	ST-443 complex	7	17	2	337	23	3	12	4	2	2	50S_L22_A103V;blaOXA-193;gyrA_T86I;tet(O)	0	None found	0	0	0	BfR-CA-19995	CIP, TET
BfR-CA-19996	broiler, feces	IndChi 45	09.07.2021	Campylobacter coli	Campylobacter coli	74,5	47	855	ST-828 complex	33	39	30	79	104	35	17	4	2	2	50S_L22_A103V;blaOXA-193;gyrA_T86I;tet(O)	0	None found	2	29454	1	BfR-CA-19996	CIP, ETP, TET

TabS3_WGS_data_plasmids

strain No.	Contig	Accession	Identity	Query_length	Bitscore	Query_coverage	Details
BfR-CA-19789	contig00013	NZ_CP017874.1	98,272	12671	22177	96	Campylobacter coli strain WA333 plasmid pCCDM33S, complete sequence
BfR-CA-19797	contig00010	NZ_CP017231.1	99.532	7482	13623	46	Campylobacter jejuni strain FORC_046 plasmid pFORC46.2, complete sequence
BfR-CA-19799	contig00014	NZ_CP023547.1	98.494	13013	22940	90	Campylobacter coli strain CFSAN032805 plasmid pCFSAN032805_2, complete sequence
BfR-CA-19802	contig00011	NC_006134.1	98.882	20208	36056	49	Campylobacter coli plasmid pCC31, complete sequence
BfR-CA-19804	contig00014	NZ_CP017874.1	99.246	7031	12689	92	Campylobacter coli strain WA333 plasmid pCCDM33S, complete sequence
BfR-CA-19804	contig00015	NZ_CP017870.1	99.949	9711	17906	97	Campylobacter coli strain MG1116 plasmid pCCDM116S, complete sequence
BfR-CA-19804	contig00017	NZ_CP007187.1	94.148	1948	2896	72	Campylobacter coli RM1875 plasmid pRM1875_3.4kbp, complete sequence
BfR-CA-19804	contig00018	NC_022656.1	98.359	4145	7273	100	Campylobacter coli 15-537360 plasmid pCC42yr, complete sequence
BfR-CA-19804	contig00019	NZ_CP017870.1	95.296	4124	6540	99	Campylobacter coli strain MG1116 plasmid pCCDM116S, complete sequence
BfR-CA-19804	contig00020	NZ_CP017874.1	96.845	3708	6163	100	Campylobacter coli strain WA333 plasmid pCCDM33S, complete sequence
BfR-CA-19804	contig00021	NZ_CP017870.1	98.886	3592	6405	99	Campylobacter coli strain MG1116 plasmid pCCDM116S, complete sequence
BfR-CA-19804	contig00026	NZ_CP028188.1	99.596	1732	3160	100	Campylobacter coli strain CFSAN054106 plasmid pGMI16-001, complete sequence
BfR-CA-19804	contig00027	NZ_CP017870.1	99.934	1509	2782	100	Campylobacter coli strain MG1116 plasmid pCCDM116S, complete sequence
BfR-CA-19807	contig00013	NZ_CP007187.1	94.793	3092	4754	89	Campylobacter coli RM1875 plasmid pRM1875_3.4kbp, complete sequence
BfR-CA-19808	contig00011	NZ_CP017872.1	98.265	13893	24271	31	Campylobacter coli strain BP3183 plasmid pCCDM183, complete sequence
BfR-CA-19812	contig00018	NZ_CP014345.1	99.898	3918	7212	100	Campylobacter jejuni strain RM3194 plasmid, complete sequence
BfR-CA-19812	contig00031	NZ_CP017026.1	99.358	1713	3101	84	Campylobacter coli plasmid pCC14983A-1, complete sequence
BfR-CA-19820	contig00010	NZ_CP010074.1	99.023	16076	28795	64	Campylobacter jejuni subsp. jejuni strain 01-1512 plasmid pCj2, complete sequence
BfR-CA-19820	contig00011	NZ_CP028186.1	97.59	19296	33024	53	Campylobacter jejuni strain CFSAN054107 plasmid pGMI16-002, complete sequence
BfR-CA-19827	contig00017	NZ_CP007184.1	99.159	14393	25896	86	Campylobacter coli RM1875 plasmid pRM1875_35kb, complete sequence
BfR-CA-19827	contig00018	NZ_CP014746.1	95.905	6471	10414	70	Campylobacter jejuni strain OD267 plasmid pCJDM67 S, complete sequence
BfR-CA-19833	contig00011	NC_022656.1	98.591	11571	20461	40	Campylobacter coli 15-537360 plasmid pCC42yr, complete sequence
BfR-CA-19854	contig00013	NC_022656.1	98.191	14155	24705	89	Campylobacter coli 15-537360 plasmid pCC42yr, complete sequence
BfR-CA-19952	contig00011	NZ_CP023547.1	98.511	11686	20593	66	Campylobacter coli strain CFSAN032805 plasmid pCFSAN032805_2, complete sequence
BfR-CA-19952	contig00014	NZ_CP007187.1	94.583	3120	4774	90	Campylobacter coli RM1875 plasmid pRM1875_3.4kbp, complete sequence
BfR-CA-19961	contig00011	NZ_CP017874.1	97.526	11721	19989	87	Campylobacter coli strain WA333 plasmid pCCDM33S, complete sequence
BfR-CA-19961	contig00013	NZ_CP007187.1	94.558	3142	4802	91	Campylobacter coli RM1875 plasmid pRM1875_3.4kbp, complete sequence
BfR-CA-19989	contig00011	NZ_CP023547.1	98.967	10939	19571	62	Campylobacter coli strain CFSAN032805 plasmid pCFSAN032805_2, complete sequence
BfR-CA-19989	contig00013	NZ_CP007187.1	94.558	3142	4802	91	Campylobacter coli RM1875 plasmid pRM1875_3.4kbp, complete sequence
BfR-CA-19992	contig00011	NZ_CP017870.1	97.109	10825	18233	41	Campylobacter coli strain MG1116 plasmid pCCDM116S, complete sequence
BfR-CA-19996	contig00011	NZ_CP023547.1	98.967	10939	19571	63	Campylobacter coli strain CFSAN032805 plasmid pCFSAN032805_2, complete sequence
BfR-CA-19996	contig00013	NZ_CP007187.1	94.583	3120	4774	90	Campylobacter coli RM1875 plasmid pRM1875_3.4kbp, complete sequence

9.2.2 Publication 2: Multiplex Real-Time PCR for the Detection of Tetracycline, Ciprofloxacin, and Erythromycin Resistance Determinants from Human and Foodborne *Campylobacter jejuni* and *Campylobacter coli*

9 Appendix

Sample overview German isolates from food (FS_) and human origin (HS_). Vietnamese isolates from food (VE_					Phenotypic resistance determined by broth microdilution EUCAMP3 grey shading; resistant to antimicrobiol agen						Multiresistance level 1 2 3 ≥ 4
strain No. alias	Country of origin	isolation source	Campylobacter species	collection date	CHL MIC	ERY MIC	GEN MIC	CIP MIC	TET MIC	ETP MIC	Multiresistance
HS_1	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	0,5	4	<=0.5	<=0.12	1
HS_2	Germany	human stool sample	*C. jejuni*	2019	4	<=1	<=0.25	16	64	<=0.12	2
HS_3	Germany	human stool sample	*C. jejuni*	2019	<=2	4	<=0.25	<=0.12	<=0.5	<=0.12	0
HS_4	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	64	<=0.12	2
HS_5	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	>64	<=0.12	2
HS_6	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	<=0.5	<=0.12	1
HS_7	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	0,5	<=0.12	<=0.5	<=0.12	0
HS_8	Germany	human stool sample	*C. jejuni*	2020	<=2	<=1	<=0.25	8	32	<=0.12	2
HS_9	Germany	human stool sample	*C. jejuni*	2020	<=2	<=1	<=0.25	<=0.12	<=0.5	<=0.12	0
HS_10	Germany	human stool sample	*C. coli*	2020	16	8	0,5	>32	>64	2	3
HS_11	Germany	human stool sample	*C. jejuni*	2020	<=2	<=1	<=0.25	8	<=0.5	<=0.12	1
HS_12	Germany	human stool sample	*C. jejuni*	2020	<=2	<=1	<=0.25	4	32	<=0.12	2
HS_13	Germany	human stool sample	*C. jejuni*	2020	<=2	<=1	<=0.25	8	64	0,5	2
HS_14	Germany	human stool sample	*C. jejuni*	2020	<=2	<=1	<=0.25	8	64	<=0.12	2
HS_15	Germany	human stool sample	*C. jejuni*	2020	<=2	<=1	<=0.25	<=0.12	<=0.5	<=0.12	0
HS_16	Germany	human stool sample	*C. jejuni*	2020	<=2	<=1	<=0.25	16	<=0.5	<=0.12	1
HS_17	Germany	human stool sample	*C. jejuni*	2020	<=2	<=1	<=0.25	16	64	<=0.12	2
HS_18	Germany	human stool sample	*C. jejuni*	2020	<=2	<=1	<=0.25	8	8	<=0.12	2
HS_19	Germany	human stool sample	*C. coli*	2020	<=2	<=1	0,5	8	64	0,25	2
HS_20	Germany	human stool sample	*C. jejuni*	2020	<=2	<=1	<=0.25	<=0.12	<=0.5	<=0.12	0
HS_21	Germany	human stool sample	*C. coli*	2020	<=2	<=1	0,5	8	64	1	3
HS_22	Germany	human stool sample	*C. coli*	2020	<=2	512	1	8	<=0.5	<=0.12	2
HS_23	Germany	human stool sample	*C. jejuni*	2020	<=2	<=1	<=0.25	16	>64	>4	3
HS_24	Germany	human stool sample	*C. jejuni*	2020	4	<=1	<=0.25	16	>64	1	3
HS_25	Germany	human stool sample	*C. jejuni*	2021	<=2	<=1	0,5	16	8	<=0.12	2
HS_26	Germany	human stool sample	*C. jejuni*	2018	<=2	<=1	<=0.25	8	64	<=0.12	2
HS_27	Germany	human stool sample	*C. jejuni*	2018	<=2	<=1	<=0.25	8	<=0.5	<=0.12	1
HS_28	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	4	32	<=0.12	2
HS_29	Germany	human stool sample	*C. jejuni*	2019	<=2	2	<=0.25	32	>64	<=0.12	2
HS_30	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	4	<=0.12	2
HS_31	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	0,5	8	64	<=0.12	2
HS_32	Germany	human stool sample	*C. coli*	2019	<=2	<=1	<=0.25	8	32	0,5	2
HS_33	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	16	<=0.12	2
HS_34	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	2	<=0.12	2
HS_35	Germany	human stool sample	*C. coli*	2019	<=2	<=1	0,5	16	>64	1	3
HS_36	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	<=0.5	1	2
HS_37	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	0,5	8	64	<=0.12	2
HS_38	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	8	<=0.12	2
HS_39	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	16	64	<=0.12	2
HS_40	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	16	<=0.12	2
HS_41	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	16	<=0.12	2
HS_42	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	0,5	<=0.12	<=0.5	<=0.12	0
HS_43	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	0,5	<=0.12	<=0.5	<=0.12	0
HS_44	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	0.25	<=0.5	<=0.12	0
HS_45	Germany	human stool sample	*C. coli*	2019	<=2	2	1	8	<=0.5	<=0.12	1
HS_46	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	32	<=0.12	2
HS_47	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	<=0.5	<=0.12	1
HS_48	Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	>64	<=0.12	2

9 Appendix

Sample overview German isolates from food (FS_) and human origin (HS_). Vietnamese isolates from food (VE_					Phenotypic resistance determined by broth microdilution EUCAMP3 grey shading; resistant to antimicrobiol agen						Multiresistance level 1 2 3 ≥ 4
strain No.	alias	Country of origin	isolation source	Campylobacter species	collection date	CHL MIC	ERY MIC	GEN MIC	CIP MIC	TET MIC	ETP MIC	Multiresistance
HS_49		Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	16	<=0.12	2
HS_50		Germany	human stool sample	*C. jejuni*	2019	<=2	<=1	<=0.25	8	32	0,25	2
FS_51		Germany	retail, chicken breast	*C. jejuni*	2021	<=2	<=1	0,5	<=0.12	<=0.5	<=0.12	0
FS_52		Germany	retail, chicken breast	*C. jejuni*	2021	<=2	<=1	<=0.25	8	32	<=0.12	2
FS_53		Germany	retail, chicken breast	*C. jejuni*	2021	<=2	<=1	<=0.25	<=0.12	<=0.5	<=0.12	0
FS_54		Germany	retail, chicken breast	*C. jejuni*	2021	<=2	<=1	<=0.25	8	64	<=0.12	2
FS_55		Germany	retail, chicken breast	*C. coli*	2021	<=2	<=1	1	8	<=0.5	0,25	1
FS_56		Germany	retail, chicken meat	*C. jejuni*	2021	<=2	<=1	<=0.25	8	64	<=0.12	2
FS_57		Germany	retail, chicken leg	*C. jejuni*	2021	<=2	<=1	<=0.25	<=0.12	<=0.5	<=0.12	0
FS_58		Germany	retail, chicken breast	*C. jejuni*	2021	<=2	<=1	<=0.25	16	>64	<=0.12	2
FS_59		Germany	retail, chicken breast	*C. jejuni*	2021	<=2	<=1	<=0.25	4	<=0.5	<=0.12	1
FS_60		Germany	retail, chicken breast	*C. jejuni*	2021	<=2	<=1	0,5	<=0.12	<=0.5	<=0.12	0
FS_61		Germany	retail, chicken breast	*C. jejuni*	2021	<=2	<=1	<=0.25	<=0.12	<=0.5	<=0.12	0
FS_62		Germany	retail, chicken breast	*C. jejuni*	2021	<=2	<=1	<=0.25	4	8	<=0.12	2
FS_63		Germany	retail, chicken meat	*C. jejuni*	2019	<=2	<=1	<=0.25	<=0.12	<=0.5	<=0.12	0
FS_64		Germany	retail, chicken meat	*C. jejuni*	2019	<=2	<=1	0,5	16	>64	<=0.12	2
FS_65		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	<=0.25	16	>64	<=0.12	2
FS_66		Germany	retail, chicken breast	*C. coli*	2019	<=2	<=1	0,5	16	>64	0,5	2
FS_67		Germany	retail, chicken breast	*C. coli*	2019	<=2	<=1	0,5	<=0.12	32	<=0.12	1
FS_68		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	<=0.25	8	64	<=0.12	2
FS_69		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	<=0.25	16	<=0.5	<=0.12	1
FS_70		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	<=0.25	<=0.12	<=0.5	<=0.12	0
FS_71		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	<=0.25	8	8	<=0.12	2
FS_72		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	0,5	8	<=0.5	0,25	1
FS_73		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	<=0.25	8	<=0.5	<=0.12	1
FS_74		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	<=0.25	8	>64	<=0.12	2
FS_75		Germany	broiler, neck skin	*C. jejuni*	2019	<=2	<=1	<=0.25	<=0.12	<=0.5	<=0.12	0
FS_76		Germany	retail, chicken breast	*C. coli*	2019	<=2	<=1	0,5	<=0.12	64	1	2
FS_77		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	<=0.25	4	<=0.5	<=0.12	1
FS_78		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	<=0.25	4	16	<=0.12	2
FS_79		Germany	retail, chicken breast	*C. coli*	2019	<=2	<=1	0,5	8	<=0.5	<=0.12	1
FS_80		Germany	retail, chicken leg	*C. jejuni*	2019	<=2	<=1	<=0.25	<=0.12	<=0.5	<=0.12	0
FS_81		Germany	broiler, neck skin	*C. jejuni*	2019	<=2	<=1	0,5	0,25	32	<=0.12	1
FS_82		Germany	Chicken eggs	*C. coli*	2020	4	4	0,5	0,25	<=0.5	2	1
FS_83		Germany	broiler, neck skin	*C. jejuni*	2019	<=2	<=1	0,5	<=0.12	<=0.5	<=0.12	0
FS_84		Germany	broiler, neck skin	*C. coli*	2019	4	2	0,5	16	>64	0,5	2
FS_85		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	<=0.25	8	<=0.5	<=0.12	1
FS_86		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	<=0.25	8	<=0.5	<=0.12	1
FS_87		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	<=0.25	16	64	<=0.12	2
FS_88		Germany	retail, chicken breast	*C. jejuni*	2019	<=2	<=1	0,5	16	<=0.5	<=0.12	1
FS_89		Germany	retail, chicken breast	*C. jejuni*	2020	<=2	<=1	<=0.25	8	8	<=0.12	2
FS_90		Germany	broiler, neck skin	*C. coli*	2019	<=2	<=1	0,5	<=0.12	64	0,5	1
FS_91		Germany	Unknown	*C. jejuni*	2020	4	<=1	<=0.25	16	>64	0,5	2
FS_92		Germany	turkey, neck skin	*C. coli*	2020	<=2	<=1	1	<=0.12	>64	1	2
FS_93		Germany	turkey, neck skin	*C. coli*	2020	<=2	<=1	<=0.25	<=0.12	<=0.5	0,25	0
FS_94		Germany	broiler, neck skin	*C. coli*	2020	4	2	0,5	0,25	<=0.5	0,25	0
FS_95		Germany	broiler, neck skin	*C. coli*	2020	<=2	<=1	0,5	8	>64	4	3

9 Appendix

Sample overview German isolates from food (FS_) and human origin (HS_). Vietnamese isolates from food (VE_						Phenotypic resistance determined by broth microdilution EUCAMP3 grey shading: resistant to antimicrobiol agen						Multiresistance level 1 2 3 ≥ 4
strain No.	alias	Country of origin	isolation source	Campylobacter species	collection date	CHL MIC	ERY MIC	GEN MIC	CIP MIC	TET MIC	ETP MIC	Multiresistance
FS_96		Germany	broiler, neck skin	*C. jejuni*	2020	<=2	<=1	<=0.25	<=0.12	<=0.5	0,25	0
FS_97		Germany	broiler, neck skin	*C. coli*	2020	<=2	<=1	0,5	<=0.12	<=0.5	0,5	0
FS_98		Germany	retail, chicken breast	*C. coli*	2020	<=2	<=1	0,5	8	32	2	3
FS_99		Germany	retail, chicken breast	*C. jejuni*	2020	<=2	<=1	<=0.25	8	64	<=0.12	2
FS_100		Germany	Chicken eggs	*C. coli*	2020	<=2	<=1	<=0.25	16	<=0.5	4	2
HS_101		Germany	human stool sample, external lab	*C. coli*	2022	<=2	<=1	1	8	64	0,25	2
HS_102		Germany	human stool sample, external lab	*C. coli*	2022	4	<=1	0,5	8	64	2	3
HS_103		Germany	human stool sample, external lab	*C. coli*	2022	<=2	512	0,5	8	>64	1	4
HS_104		Germany	human stool sample, external lab	*C. coli*	2022	<=2	<=1	0,5	8	<=0.5	1	2
HS_105		Germany	human stool sample, external lab	*C. coli*	2022	4	<=1	0,5	16	1	2	2
HS_106		Germany	human stool sample, external lab	*C. coli*	2022	4	<=1	<=0.25	0,25	<=0.5	0,5	0
HS_107		Germany	human stool sample, external lab	*C. coli*	2022	4	<=1	1	16	64	0,25	2
HS_108		Germany	human stool sample, external lab	*C. coli*	2022	<=2	<=1	0,5	8	64	0,5	2
HS_109		Germany	human stool sample, external lab	*C. coli*	2022	<=2	<=1	0,5	0,25	<=0.5	0,5	0
HS_110		Germany	human stool sample, external lab	*C. coli*	2022	<=2	<=1	1	8	64	0,5	2
FS_111	BfR-CA-19312	Germany	broiler, skin	*C. coli*	2020	<=2	<=1	0,5	8	64	0,5	2
FS_112	BfR-CA-19320	Germany	retail, chicken breast	*C. jejuni*	2020	<=2	<=1	<=0.25	4	<=0.5	<=0.12	1
FS_113	BfR-CA-20317	Germany	retail, chicken breast	*C. jejuni*	2021	8	<=1	<=0.25	<=0.12	1	1	1
FS_114	BfR-CA-20598	Germany	retail, chicken breast	*C. jejuni*	2022	<=2	<=1	<=0.25	16	64	2	3
FS_115	BfR-CA-20788	Germany	retail, chicken meat	*C. coli*	2022	<=2	<=1	0,5	16	64	2	3
FS_116	BfR-CA-20832	Germany	broiler, cecum	*C. coli*	2022	<=2	<=1	0,5	0,25	<=0.5	1	1
FS_117	BfR-CA-20996	Germany	retail, chicken meat	*C. jejuni*	2022	<=2	<=1	<=0.25	8	<=0.5	<=0.12	1
FS_118	BfR-CA-21003	Germany	retail, chicken meat	*C. coli*	2022	8	8	1	<=0.12	>64	0,5	1
FS_119	BfR-CA-21076	Germany	retail, chicken breast	*C. coli*	2022	<=2	512	1	8	<=0.5	<=0.12	2
FS_120	BfR-CA-21077	Germany	retail, chicken breast	*C. jejuni*	2022	<=2	<=1	<=0.25	8	<=0.5	<=0.12	1
HS_121		Germany	human stool sample, external lab	*C. coli*	2022	4	<=1	1	16	<=0.5	0,5	1
HS_122		Germany	human stool sample, external lab	*C. jejuni*	2022	<=2	<=1	<=0.25	32	>64	<=0.12	2
HS_123		Germany	human stool sample, external lab	*C. coli*	2023	<=2	<=1	0,5	<=0.12	32	0,5	1
HS_124		Germany	human stool sample, external lab	*C. coli*	2023	<=2	<=1	<=0.25	4	16	0,5	2
HS_125		Germany	human stool sample, external lab	*C. coli*	2023	4	<=1	0,5	32	>64	4	3
HS_126		Germany	human stool sample, external lab	*C. coli*	2023	4	<=1	1	<=0.12	<=0.5	1	1
HS_127		Germany	human stool sample, external lab	*C. coli*	2023	4	2	0,5	16	>64	0,25	2
HS_128		Germany	human stool sample, external lab	*C. coli*	2023	<=2	<=1	<=0.25	<=0.12	<=0.5	0,5	0
FS_129	BfR-CA-19086	Germany	broiler, meat	*C. jejuni*	2020	<=2	<=1	0.5	8	32	2	3
VE_01	BfR-CA-15062	Vietnam	broiler, feces	*C. coli*	2017	>64	>512	>16	32	>64	1	≥ 4
VE_02	BfR-CA-15077	Vietnam	broiler, feces	*C. coli*	2017	64	>512	>16	32	>64	2	≥ 4
VE_03	BfR-CA-15986	Vietnam	broiler, feces	*C. coli*	2016	4	>512	>16	32	>64	4	≥ 4
VE_04	BfR-CA-15987	Vietnam	broiler, feces	*C. coli*	2016	8	>512	1	32	>64	4	4
VE_05	BfR-CA-15989	Vietnam	broiler, feces	*C. coli*	2016	>64	512	>16	32	>64	2	≥ 4
VE_06	BfR-CA-15990	Vietnam	broiler, feces	*C. coli*	2016	>64	>512	>16	>32	>64	>4	≥ 4
VE_07	BfR-CA-15991	Vietnam	broiler, feces	*C. coli*	2016	>64	>512	>16	>32	>64	>4	≥ 4
VE_08	BfR-CA-15994	Vietnam	broiler, feces	*C. coli*	2016	64	512	>16	>32	>64	4	≥ 4
VE_09	BfR-CA-16036	Vietnam	broiler, feces	*C. coli*	2017	4	>512	>16	>32	>64	1	≥ 4
VE_10	BfR-CA-16046	Vietnam	broiler, feces	*C. coli*	2017	64	>512	>16	16	>64	>4	≥ 4
VE_11	BfR-CA-16057	Vietnam	broiler, feces	*C. coli*	2017	>64	>512	>16	16	>64	>4	≥ 4
VE_12	BfR-CA-16059	Vietnam	broiler, feces	*C. coli*	2017	>64	>512	>16	16	>64	>4	≥ 4
VE_13	BfR-CA-16081	Vietnam	broiler, feces	*C. jejuni*	2017	>64	2	0.5	>32	>64	4	4
VE_14	BfR-CA-16092	Vietnam	broiler, feces	*C. jejuni*	2017	>64	>512	>16	>32	>64	2	≥ 4
VE_15	BfR-CA-16107	Vietnam	broiler, feces	*C. coli*	2017	16	512	>16	>32	>64	2	≥ 4
VE_16	BfR-CA-16196	Vietnam	broiler, feces	*C. coli*	2017	>64	>512	>16	16	>64	4	≥ 4
VE_17	BfR-CA-16261	Vietnam	broiler, feces	*C. coli*	2017	>64	256	>16	>32	>64	4	≥ 4
VE_18	BfR-CA-18689	Vietnam	broiler, feces	*C. jejuni*	2017	>64	<=1	>16	>32	>64	0.5	4
VE_19	BfR-CA-19033	Vietnam	broiler, meat	*C. coli*	2018	8	256	>16	>32	>64	2	≥ 4
VE_20	BfR-CA-19119	Vietnam	broiler, meat	*C. coli*	2018	8	>512	>16	>32	>64	1	≥ 4
VE_21	BfR-CA-16298	Vietnam	broiler, feces	*C. coli*	2017	8	512	0.5	16	>64	2	4
DSM 4688			reference strain	*C. jejuni*		<=2	<=1	0,5	<=0.12	<=0.5	<=0.12	
2012-70-443-2			reference strain	*C. coli*		<=2	<=1	0,5	<=0.12	<=0.5	<=0.12	

9 Appendix

Primer and probe binding sites (based on Aquamis)

S: sensitivity; R: resistance

grey shading: phenotypically resistant isolate

(1*): imperfect binding site with pm due to additional mutation A>G

Commonly, 2 binding sites for 2 primers (forward and reverse) and 1 binding site for the probe were identified

In some cases, more binding sites are observed for *tet* (O) and *23S rRNA* , which indicate the presence of 2 or 3 copies of a gene: 4 or 6 binding sites for primers and 2 or 3 binding sites for the probe

degenerated nucleotide Y (C/T) in *gyrA_Cc* : C for wt1 and pm1 ; T for wt2 and pm2

		tetracycline			ciprofloxacin *C. coli*						ciprofloxacin *C. jejuni*			erythromycin					
strain No.	***Campylobacter* species**	**TET R/S**	**tet(O) primers**	**tet(O) wt**	**CIP R/S**	**gyrA_Cc**	**gyrA_Cc_wt1**	**gyrA_Cc_wt2**	**gyrA_Cc_pm1**	**gyrA_Cc_pm2**	**gyrA_Cj**	**gyrA_Cj_wt**	**gyrA_Cj_pm**	**ERY R/S**	**23S**	**23S_wt**	**23S_pm**	**erm(B) primers**	**erm(B) wt**
HS_1	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_2	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_3	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
HS_4	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_5	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_6	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_7	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
HS_8	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_9	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
HS_10	*C. coli*	1	4	2	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_11	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_12	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_13	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_14	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_15	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
HS_16	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_17	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_18	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_19	*C. coli*	1	4	2	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_20	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
HS_21	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_22	*C. coli*	0	0	0	1	2	0	0	1	0	0	0	0	1	2	0	1	0	0
HS_23	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_24	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_25	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_26	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_27	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_28	*C. jejuni*	1	4	2	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_29	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_30	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_31	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_32	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_33	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_34	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_35	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_36	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_37	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_38	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_39	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_40	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_41	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0

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degenerated nucleotide Y (C/T) in *gyrA_Cc* : C for wt1 and pm1 ; T for wt2 and pm2

		tetracycline			ciprofloxacin *C. coli*						ciprofloxacin *C. jejuni*			erythromycin					
strain No.	***Campylobacter* species**	**TET R/S**	**tet(O) primers**	**tet(O) wt**	**CIP R/S**	**gyrA_Cc**	**gyrA_Cc_wt1**	**gyrA_Cc_wt2**	**gyrA_Cc_pm1**	**gyrA_Cc_pm2**	**gyrA_Cj**	**gyrA_Cj_wt**	**gyrA_Cj_pm**	**ERY R/S**	**23S**	**23S_wt**	**23S_pm**	**erm(B) primers**	**erm(B) wt**
HS_42	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
HS_43	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
HS_44	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
HS_45	*C. coli*	0	0	0	1	2	0	0	0	1	0	0	0	0	2	1	0	0	0
HS_46	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_47	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_48	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_49	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_50	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_51	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
FS_52	*C. jejuni*	1	4	2	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_53	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
FS_54	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_55	*C. coli*	0	0	0	1	2	0	0	1	0	0	0	0	0	4	2	0	0	0
FS_56	*C. jejuni*	1	4	2	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_57	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
FS_58	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_59	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_60	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
FS_61	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
FS_62	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_63	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
FS_64	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_65	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_66	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
FS_67	*C. coli*	1	2	1	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
FS_68	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_69	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	6	3	0	0	0
FS_70	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
FS_71	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_72	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	6	3	0	0	0
FS_73	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_74	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_75	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
FS_76	*C. coli*	1	2	1	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
FS_77	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_78	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_79	*C. coli*	0	0	0	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
FS_80	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
FS_81	*C. jejuni*	1	2	1	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0

Primer and probe binding sites (based on Aquamis)

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degenerated nucleotide Y (C/T) in *gyrA_Cc* : C for wt1 and pm1 ; T for wt2 and pm2

		tetracycline			ciprofloxacin *C. coli*						ciprofloxacin *C. jejuni*			erythromycin					
strain No.	***Campylobacter* species**	**TET R/S**	**tet(O) primers**	**tet(O) wt**	**CIP R/S**	**gyrA_Cc**	**gyrA_Cc_wt1**	**gyrA_Cc_wt2**	**gyrA_Cc_pm1**	**gyrA_Cc_pm2**	**gyrA_Cj**	**gyrA_Cj_wt**	**gyrA_Cj_pm**	**ERY R/S**	**23S**	**23S_wt**	**23S_pm**	**erm(B) primers**	**erm(B) wt**
FS_82	*C. coli*	0	0	0	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
FS_83	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
FS_84	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
FS_85	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_86	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_87	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_88	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_89	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_90	*C. coli*	1	2	1	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
FS_91	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_92	*C. coli*	1	2	1	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
FS_93	*C. coli*	0	0	0	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
FS_94	*C. coli*	0	0	0	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
FS_95	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
FS_96	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
FS_97	*C. coli*	0	0	0	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
FS_98	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
FS_99	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_100	*C. coli*	0	0	0	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_101	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_102	*C. coli*	1	4	2	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_103	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	1	2	0	1	0	0
HS_104	*C. coli*	0	0	0	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_105	*C. coli*	0	0	0	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_106	*C. coli*	0	0	0	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
HS_107	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_108	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_109	*C. coli*	0	0	0	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
HS_110	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	4	2	0	0	0
FS_111	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
FS_112	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	4	2	0	0	0
FS_113	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
FS_114	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
FS_115	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
FS_116	*C. coli*	0	0	0	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
FS_117	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	4	2	0	0	0
FS_118	*C. coli*	1	2	1	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
FS_119	*C. coli*	0	0	0	1	2	0	0	1	0	0	0	0	1	2	0	1	0	0
FS_120	*C. jejuni*	0	0	0	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_121	*C. coli*	0	0	0	1	2	0	0	1	0	0	0	0	0	4	2	0	0	0
HS_122	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
HS_123	*C. coli*	1	2	1	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
HS_124	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_125	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0

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strain No.	***Campylobacter* species**	**TET R/S**	**tet(O) primers**	**tet(O) wt**	**CIP R/S**	**gyrA_Cc**	**gyrA_Cc_wt1**	**gyrA_Cc_wt2**	**gyrA_Cc_pm1**	**gyrA_Cc_pm2**	**gyrA_Cj**	**gyrA_Cj_wt**	**gyrA_Cj_pm**	**ERY R/S**	**23S**	**23S_wt**	**23S_pm**	**erm(B) primers**	**erm(B) wt**
HS_126	*C. coli*	0	0	0	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
HS_127	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	0	2	1	0	0	0
HS_128	*C. coli*	0	0	0	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0
FS_129	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	(1*) +A>G	0	2	1	0	0	0

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degenerated nucleotide Y (C/T) in *gyrA_Cc* : C for wt1 and pm1 ; T for wt2 and pm2

		tetracycline			ciprofloxacin *C. coli*						ciprofloxacin *C. jejuni*			erythromycin					
strain No.	***Campylobacter* species**	**TET R/S**	**tet(O) primers**	**tet(O) wt**	**CIP R/S**	**gyrA_Cc**	**gyrA_Cc_wt1**	**gyrA_Cc_wt2**	**gyrA_Cc_pm1**	**gyrA_Cc_pm2**	**gyrA_Cj**	**gyrA_Cj_wt**	**gyrA_Cj_pm**	**ERY R/S**	**23S**	**23S_wt**	**23S_pm**	**erm(B) primers**	**erm(B) wt**
VE_01	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	1	2	1	0	2	1
VE_02	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	1	2	0	1	0	0
VE_03	*C. coli*	1	3	1	1	2	0	0	1	0	0	0	0	1	2	0	1	0	0
VE_04	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	1	2	1	0	2	1
VE_05	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	1	2	1	0	2	1
VE_06	*C. coli*	1	4	1	1	2	0	0	1	0	0	0	0	1	2	0	1	0	0
VE_07	*C. coli*	1	3	1	1	2	0	0	1	0	0	0	0	1	2	0	1	0	0
VE_08	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	1	2	1	0	2	1
VE_09	*C. coli*	1	4	1	1	2	0	0	1	0	0	0	0	1	2	0	1	0	0
VE_10	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	1	2	1	0	2	1
VE_11	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	1	2	0	1	0	0
VE_12	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	1	2	0	1	0	0
VE_13	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
VE_14	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	1	2	0	1	0	0
VE_15	*C. coli*	1	3	1	1	2	0	0	1	0	0	0	0	1	2	1	0	2	1
VE_16	*C. coli*	1	2	1	1	2	0	0	1	0	0	0	0	1	2	0	1	0	0
VE_17	*C. coli*	1	3	1	1	2	0	0	1	0	0	0	0	1	2	1	0	2	1
VE_18	*C. jejuni*	1	2	1	1	0	0	0	0	0	2	0	1	0	2	1	0	0	0
VE_19	*C. coli*	1	3	1	1	2	0	0	1	0	0	0	0	1	2	1	0	2	1
VE_20	*C. coli*	1	3	1	1	2	0	0	1	0	0	0	0	1	2	1	0	2	1
VE_21	*C. coli*	1	2	1	1	2	0	0	(1*) +A>G	0	0	0	0	1	2	1	0	2	1
DSM 4688	*C. jejuni*	0	0	0	0	0	0	0	0	0	2	1	0	0	2	1	0	0	0
2012-70-443-2	*C. coli*	0	0	0	0	2	1	0	0	0	0	0	0	0	2	1	0	0	0

Pentaplex real-time PCR assay:
Screening of *tet* (O), GyrA_T86I, *erm* (B), *23S rRNA* _A2075G, IAC

real-time PCR-instrument	AriaMx
detection system	FAM, ROX, HEX, Cy5, ATTO425
mastermix	QuantiNova, Qiagen

Components	Concentration of working solutions	Final concentration in PCR assay	Volume in µL for 1 sample
QuantiNova Multiplex	4x	1x	6,250
PCR-grade water		-	2,750
tet(O)-fw	20 µM	150 nM	0,188
tet(O)-re	20 µM	150 nM	0,188
tet(O)-probe **(FAM)**	10 µM	100 nM	0,250
gyrA_Cj_fw	20 µM	400 nM	0,500
gyrA_Cj_re	20 µM	400 nM	0,500
gyrA_Cj_wt	20 µM	600 nM	0,750
gyrA_Cj_pm **(ROX)**	10 µM	200 nM	0,500
gyrA_Cc_fw	20 µM	400 nM	0,500
gyrA_Cc_re	20 µM	400 nM	0,500
gyrA_Cc_wt	20 µM	600 nM	0,750
gyrA_Cc_pm **(ROX)**	10 µM	200 nM	0,500
erm(B)_fw	20 µM	400 nM	0,500
erm(B)_re	20 µM	400 nM	0,500
erm(B)-probe **(Cy5)**	10 µM	200 nM	0,500
23S_A2075G_fw	20 µM	400 nM	0,500
23S_A2075G_re	20 µM	400 nM	0,500
23S_A2075G_wt	20 µM	600 nM	0,750
23S_A2075G_pm **(HEX)**	10 µM	200 nM	0,500
IPC-ntb2-fw	20 µM	300 nM	0,375
IPC-ntb2-re	20 µM	300 nM	0,375
IPC-ntb2-probe **(ATTO425)**	10 µM	150 nM	0,375
IPC-ntb2 plasmid, 50 copies/µL	50 copies/µL	50 copies	1,000
Total volume of mastermix		**-**	**20,000**
Sample DNA, Extraction control, NTC		-	5
Total volume of one reaction		-	25

Thermal profile

Phase		Time	Temperature	Cyles
Initial denaturation		2 min	95 °C	1 ×
Amplification	denaturation	10 sec	95 °C	40 ×
	annealing	20 sec	**60 °C**	
	elongation	20 sec	72 °C	

Pentaplex real-time PCR assay:
Screening of *tet* (O), GyrA_T86I, *erm* (B), *23S rRNA* _A2075G, IAC

real-time PCR-instrument	Quantstudio5, CFX96 Touch System
detection system	FAM, ROX, HEX, Cy5, Cy5.5
mastermix	QuantiNova, Qiagen

Components	Concentration of working solutions	Final concentration in PCR assay	Volume in µL for 1 sample
QuantiNova Multiplex	4x	1x	6,250
PCR-grade water		-	2,750
tet(O)-fw	20 µM	150 nM	0,188
tet(O)-re	20 µM	150 nM	0,188
tet(O)-probe **(FAM)**	10 µM	100 nM	0,250
gyrA_Cj_fw	20 µM	400 nM	0,500
gyrA_Cj_re	20 µM	400 nM	0,500
gyrA_Cj_wt	20 µM	600 nM	0,750
gyrA_Cj_pm **(ROX)**	10 µM	200 nM	0,500
gyrA_Cc_fw	20 µM	400 nM	0,500
gyrA_Cc_re	20 µM	400 nM	0,500
gyrA_Cc_wt	20 µM	600 nM	0,750
gyrA_Cc_pm **(ROX)**	10 µM	200 nM	0,500
erm(B)_fw	20 µM	400 nM	0,500
erm(B)_re	20 µM	400 nM	0,500
erm(B)-probe **(Cy5)**	10 µM	200 nM	0,500
23S_A2075G_fw	20 µM	400 nM	0,500
23S_A2075G_re	20 µM	400 nM	0,500
23S_A2075G_wt	20 µM	600 nM	0,750
23S_A2075G_pm **(HEX)**	10 µM	200 nM	0,500
IPC-ntb2-fw	20 µM	300 nM	0,375
IPC-ntb2-re	20 µM	300 nM	0,375
IPC-ntb2-probe **(Cy5.5)**	10 µM	150 nM	0,375
IPC-ntb2 plasmid, 50 copies/µL	50 copies/µL	50 copies	1,000
Total volume of mastermix		**-**	**20,000**
Sample DNA, Extraction control, NTC		-	5
Total volume of one reaction		-	25

Thermal profile

Phase		Time	Temperature	Cyles
Initial denaturation		2 min	95 °C	1 ×
Amplification	denaturation	10 sec	95 °C	40 ×
	annealing	20 sec	**60 °C**	
	elongation	20 sec	72 °C	

Triplex real-time PCR assay:
Screening of *tet* (O), GyrA_T86I, IAC

real-time PCR-instrument	AriaMx, Quantstudio5, CFX96 Touch System
detection system	FAM, ROX, HEX
mastermix	QuantiNova, Qiagen

Components	Concentration of working solutions	Final concentration in PCR assay	Volume in µL for 1 sample
QuantiNova Multiplex	4x	1x	6,250
PCR-grade water		-	6,500
tet(O)-fw	20 µM	150 nM	0,188
tet(O)-re	20 µM	150 nM	0,188
tet(O)-probe **(FAM)**	10 µM	100 nM	0,250
gyrA_Cj_fw	20 µM	400 nM	0,500
gyrA_Cj_re	20 µM	400 nM	0,500
gyrA_Cj_wt	20 µM	600 nM	0,750
gyrA_Cj_pm **(ROX)**	10 µM	200 nM	0,500
gyrA_Cc_fw	20 µM	400 nM	0,500
gyrA_Cc_re	20 µM	400 nM	0,500
gyrA_Cc_wt	20 µM	600 nM	0,750
gyrA_Cc_pm **(ROX)**	10 µM	200 nM	0,500
IPC-ntb2-fw	20 µM	300 nM	0,375
IPC-ntb2-re	20 µM	300 nM	0,375
IPC-ntb2-probe **(HEX)**	10 µM	150 nM	0,375
IPC-ntb2 plasmid, 50 copies/µL	50 copies/µL	50 copies	1,000
Total volume of mastermix		**-**	**20,000**
Sample DNA, Extraction control, NTC		-	5
Total volume of one reaction		-	25

Thermal profile

Phase		Time	Temperature	Cyles
Initial denaturation		2 min	95 °C	1 ×
Amplification	denaturation	10 sec	95 °C	40 ×
	annealing	20 sec	**60 °C**	
	elongation	20 sec	72 °C	

Duplex real-time PCR assay:
Screening of *erm* (B), *23S rRNA* _A2075G

real-time PCR-instrument	AriaMx, Quantstudio5, CFX96 Touch System
detection system	FAM, HEX
mastermix	QuantiNova, Qiagen

Components	Concentration of working solutions	Final concentration in PCR assay	Volume in µL for 1 sample
QuantiNova Multiplex	4x	1x	6,250
PCR-grade water		-	9,000
erm(B)_fw	20 µM	400 nM	0,500
erm(B)_re	20 µM	400 nM	0,500
erm(B)-probe **(FAM)**	10 µM	200 nM	0,500
23S_A2075G_fw	20 µM	400 nM	0,500
23S_A2075G_re	20 µM	400 nM	0,500
23S_A2075G_wt	20 µM	600 nM	0,750
23S_A2075G_pm **(HEX)**	10 µM	200 nM	0,500
Total volume of mastermix		**-**	**20,000**
Sample DNA, Extraction control, NTC		-	5
Total volume of one reaction		-	25

Thermal profile

Phase		Time	Temperature	Cyles
Initial denaturation		2 min	95 °C	1 ×
Amplification	denaturation	10 sec	95 °C	40 ×
	annealing	20 sec	**60 °C**	
	elongation	20 sec	72 °C	

QuantiNova and AriaMx

VE_01, *C. coli*

Target	Efficiency	RSq	Slope	Intercept
tet (O)	103.06	0.997	-3.25	35.8
GyrA_T86I	98.40	0.994	-3.36	36.1
erm (B)	109.70	0.991	-3.11	36.7

VE-14 *C. jejuni*

Target	Efficiency	RSq	Slope	Intercept
tet (O)	105.30	0.999	-3.20	34.5
GyrA_T86I	91.22	0.997	-3.55	36.9
23S rRNA _A2075G	97.95	0.999	-3.37	35.2

HiDi polymerase and AriaMx

VE_01, *C. coli*

Target	Efficiency	RSq	Slope	Intercept
tet (O)	87.33	0.988	-3.67	38.0
GyrA_T86I	95.00	0.982	-3.45	37.3
erm (B)	104.27	0.987	-3.22	36.6

VE-14 *C. jejuni*

Target	Efficiency	RSq	Slope	Intercept
tet (O)	89.72	0.993	-3.60	36.2
gyrA _T86I	81.29	0.986	-3.87	37.3
23S rRNA _A2075G	93.56	0.991	-3.49	37.0

QuantiNova and Quantstudio5

VE_01, *C. coli*

Target	Efficiency	RSq	Slope	Intercept
tet (O)	96.77	0.998	-3.40	35.2
GyrA_T86I	93.66	0.996	-3.48	36.4
erm (B)	99.66	0.998	-3.33	36.8

VE-14 *C. jejuni*

Target	Efficiency	RSq	Slope	Intercept
tet (O)	105.11	0.994	-3.21	33.7
GyrA_T86I	93.76	0.997	-3.48	36.5
23S rRNA _A2075G	99.20	0.997	-3.34	35.1

HiDi polymerase and Quantstudio5

VE_01, *C. coli*

Target	Efficiency	RSq	Slope	Intercept
tet (O)	91.40	0.992	-3.55	35.4
GyrA_T86I	88.35	0.996	-3.64	37.4
erm (B)	89.70	0.997	-3.60	35.7

VE-14 *C. jejuni*

Target	Efficiency	RSq	Slope	Intercept
tet (O)	93.24	0.988	-3.50	33.8
GyrA_T86I	81.10	0.996	-3.88	37.8
23S rRNA _A2075G	92.42	0.995	-3.52	34.0

QuantiNova and CFX96 Touch System

VE_01, *C. coli*

Target	Efficiency	RSq	Slope	Intercept
tet (O)	95.14	0.994	-3.44	37.3
GyrA_T86I	94.62	0.994	-3.46	37.7
erm (B)	101.32	0.994	-3.29	37.5

VE-14 *C. jejuni*

Target	Efficiency	RSq	Slope	Intercept
tet (O)	100.07	0.997	-3.32	36.1
GyrA_T86I	89.78	0.994	-3.59	37.2
23S rRNA _A2075G	94.93	0.996	-3.45	36.9

HiDi polymerase and CFX96 Touch System

VE_01, *C. coli*

Target	Efficiency	RSq	Slope	Intercept
tet (O)	86.00	0.988	-3.71	36.3
GyrA_T86I	89.43	0.992	-3.6	36.2
erm (B)	93.42	0.995	-3.49	36.2

VE-14 *C. jejuni*

Target	Efficiency	RSq	Slope	Intercept
tet (O)	87.15	0.987	-3.67	34.8
GyrA_T86I	82.98	0.982	-3.81	38.7
23S rRNA _A2075G	94.03	0.998	-3.47	34.5

9.2.3 Publication 3: Identification of knowledge gaps in whole-genome sequence analysis of multi-resistant thermotolerant *Campylobacter* spp.

Supplementary Figures

Identification of knowledge gaps in whole-genome sequence analysis of multi-resistant thermotolerant *Campylobacter* spp.

Michael Zarske, Huong Quynh Luu, Carlus Deneke, Marie-Theres Knüver, Maja Thieck, Ha Thi Thu Hoang, Nancy Bretschneider, Ngoc Thi Pham, Ingrid Huber, Kerstin Stingl

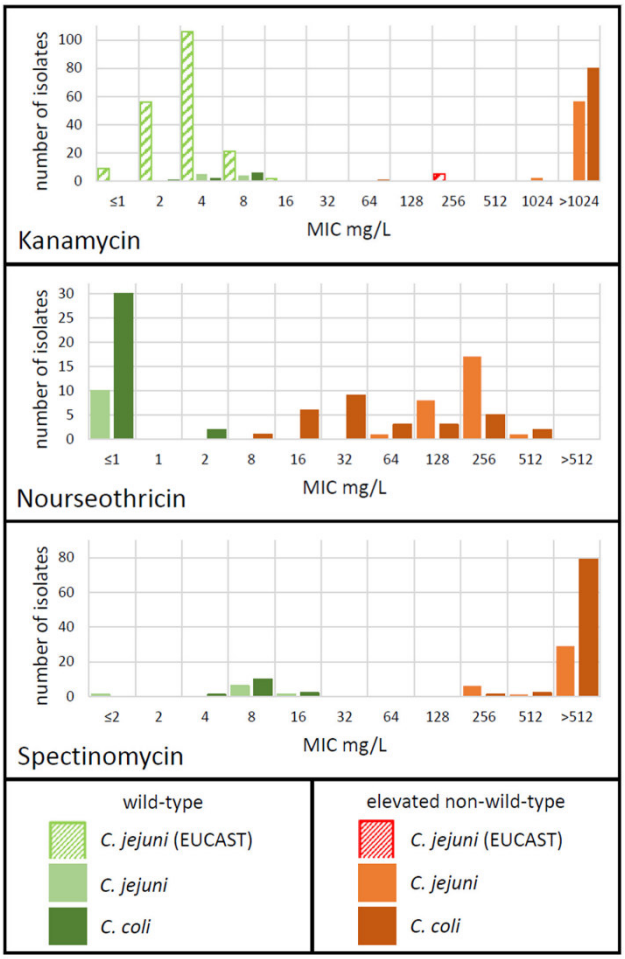

Figure S1. Distributions of MIC values of *Campylobacter* spp. isolates for antimicrobials lacking an epidemiological cutoff (ECOFF) value. Isolates were categorized into wild-type (green) and elevated non-wild-type (red) based on their MICs. Hatched bars, data from EUCAST (last accession on 11/16/2023); filled bars, results of this study.

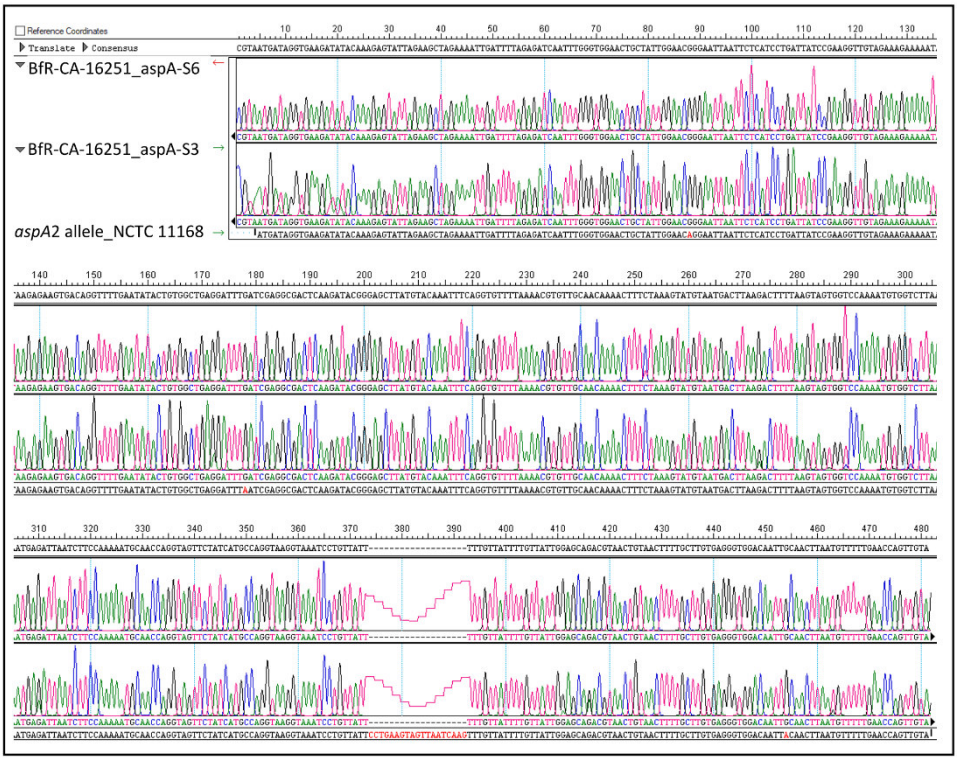

Figure S2. Sanger sequencing traces confirmed a deletion of 19 bp in *aspA* of BfR-CA-16251. A PCR fragment of *aspA*, amplified with primers aspA-A9/-A10 from BfR-CA-16251, was subjected to Sanger sequencing using primers aspA-S3 and aspA-S6. The obtained sequences were aligned to the MLST allele 2 of *aspA*, as present in *C. jejuni* NCTC 11168 (NC_002163.1), utilizing Lasergene SeqMan Pro (Lasergene 17, DNASTAR Inc., Madison, WI, USA). The deletion of 19 bases (highlighted in red) within *aspA* in BfR-CA-16251, also observed upon assembly of short-read NGS data, was confirmed. The ruler annotates the base positions in the *aspA* fragment, defined as an allele for MLST at PubMLST (45).

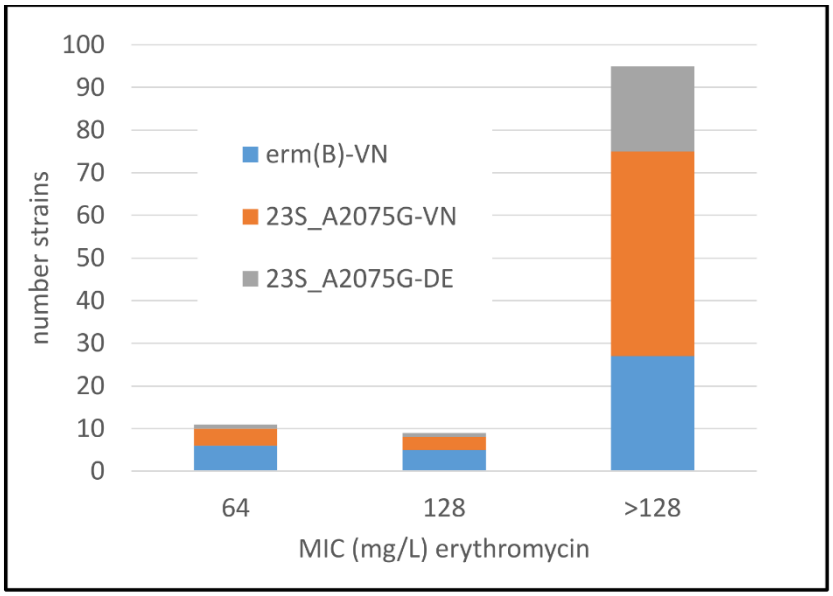

Figure S3. Minimum inhibitory concentration of erythromycin is similarly distributed among *erm*(B) and 23S_A2075G carrying *Campylobacter* isolates. The obtained results demonstrate that MIC values of erythromycin cannot differentiate between the presence of *erm*(B) and 23S_A2075G.

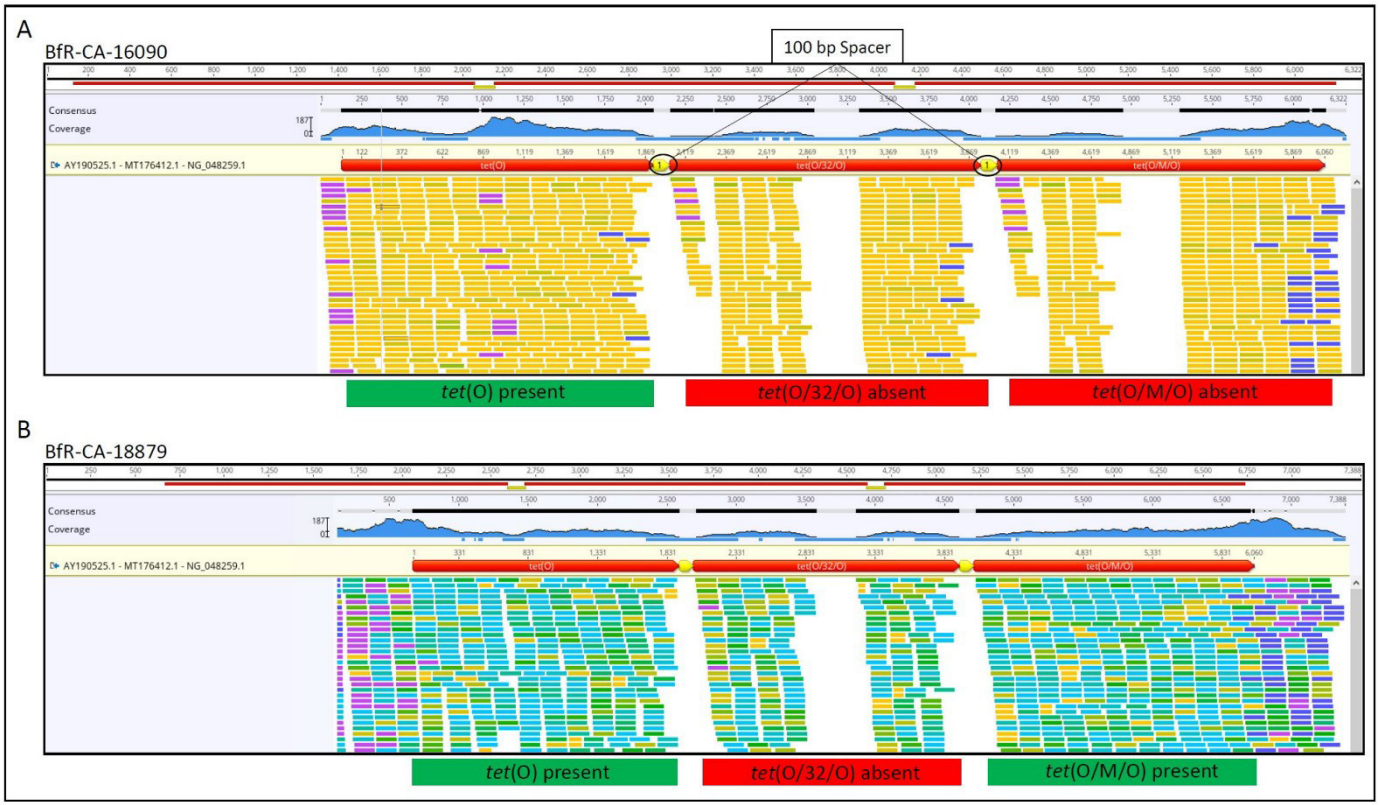

Figure S4. Identification of multiple copies of *tet*(O) variant genes using Geneious Prime. An artificial template of three reference genes, *tet*(O) (Acc. AY190525.1), *tet*(O/32/O) (Acc. MT176412.1) and *tet*(O/M/O) (Acc. NG_048259.1), separated by 100 bp spacers (highlighted in yellow) was created for mapping of trimmed raw reads from isolates showing tetracycline resistance but displaying absence or only partial *tet*(O) genes according to AMRFinderPlus. Two examples of strains carrying multiple *tet*(O) variants are shown. **A.** Read mapping of BfR-CA-16090 to the template indicated full-length presence of *tet*(O). **B.** Mapping reads of BfR-CA-18879 revealed presence of both *tet*(O) and *tet*(O/M/O) genes.

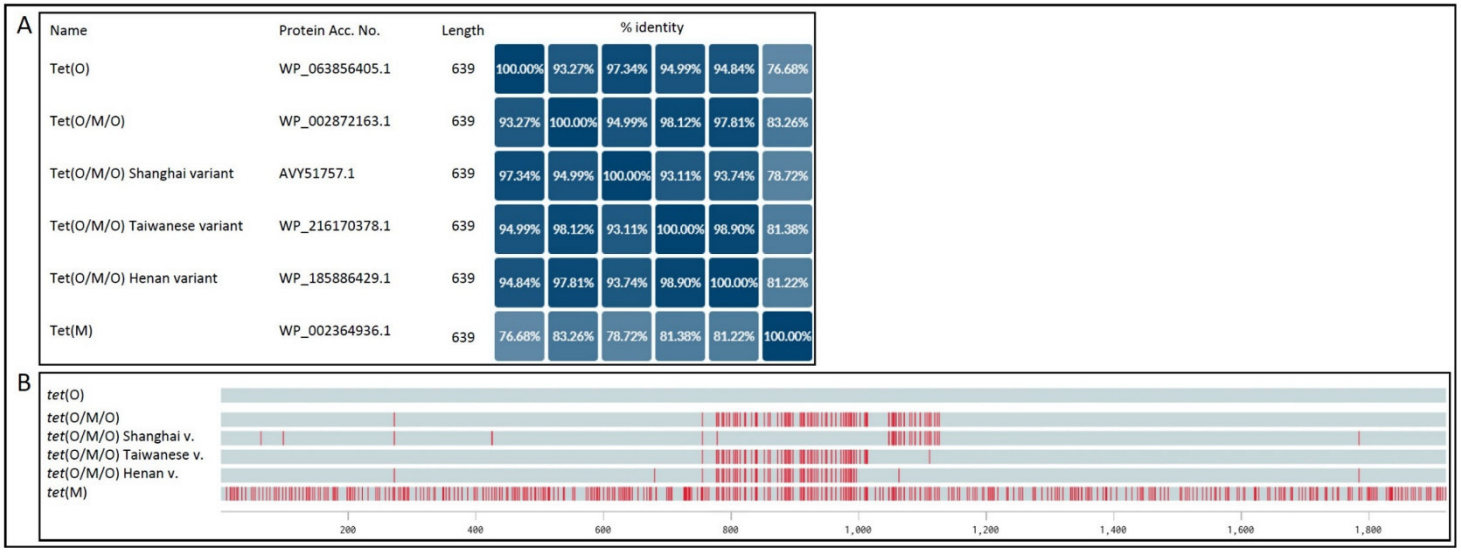

Figure S5. Visualization of different *tet*(O/M/O) variants found in Vietnamese *Campylobacter* spp.. **A** percent of amino acid identity shared among the reference sequences. NCBI Protein Acc. No. and respective lengths are illustrated. Percent identity matrix generated with UniProt Align tool (56). **B** Nucleotide Alignment highlighting the areas of *tet*(M) introgression into *tet*(O) among the different *tet*(O/M/O) variants found in Vietnamese isolates. NCBI Nucleotide Accession of genes shown are presented in Table S3. Alignment generated with Benchling's DNA sequence alignment tool (110).

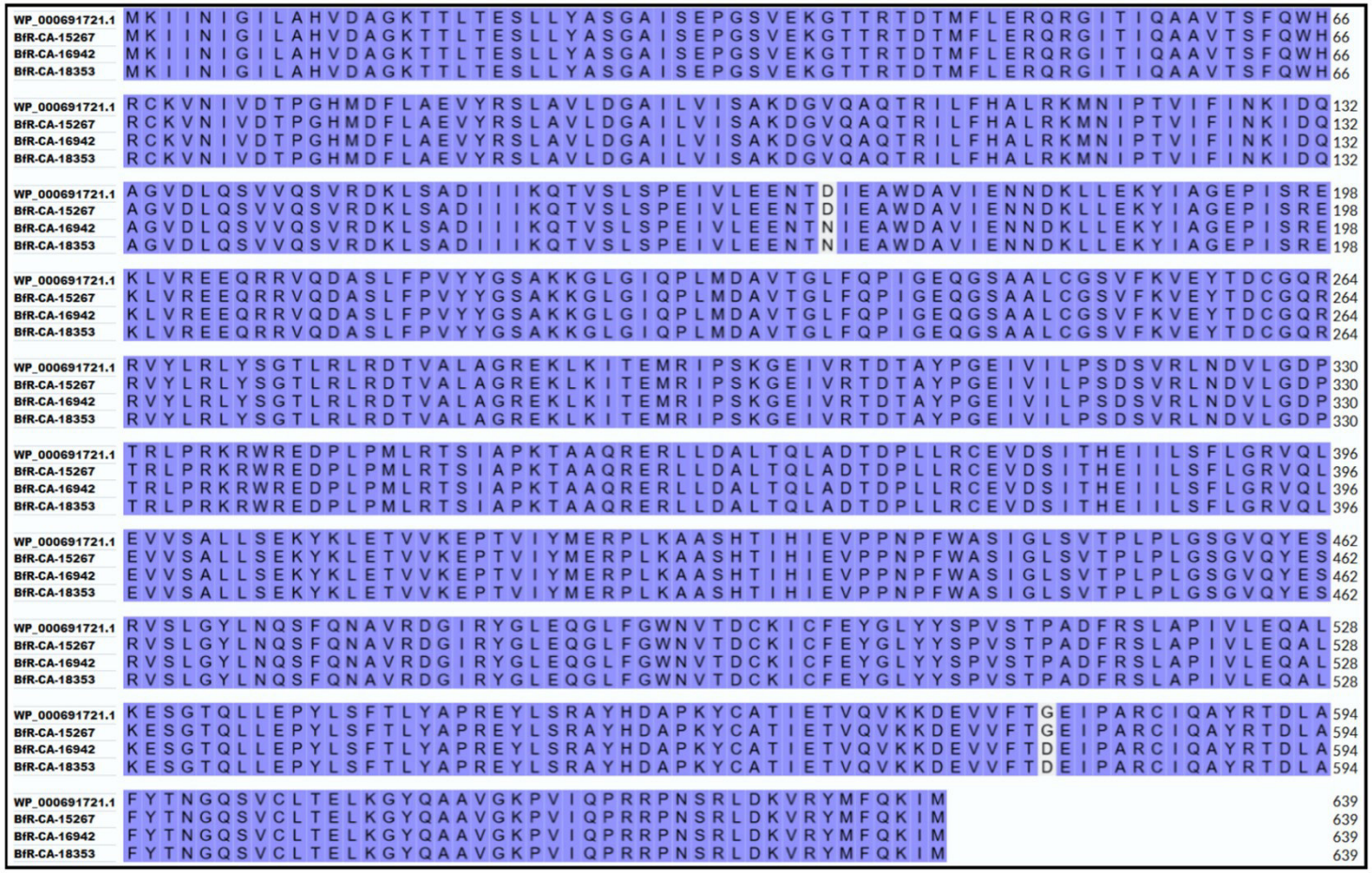

Figure S6. Protein Alignment of reference Tet(W) (WP_000691721.1) and translated gene assemblies of the three isolates harboring *tet*(W). The tetracycline sensitive isolates, BfR-CA-16942 and BfR-CA-18353, showed two amino acid substitutions (D171N and G579D) in Tet(W), while Tet(W) of the tetracycline resistant BfR-CA-15267 was 100 % identical to the reference protein. Protein alignment was created with Uniprot Align tool (56).

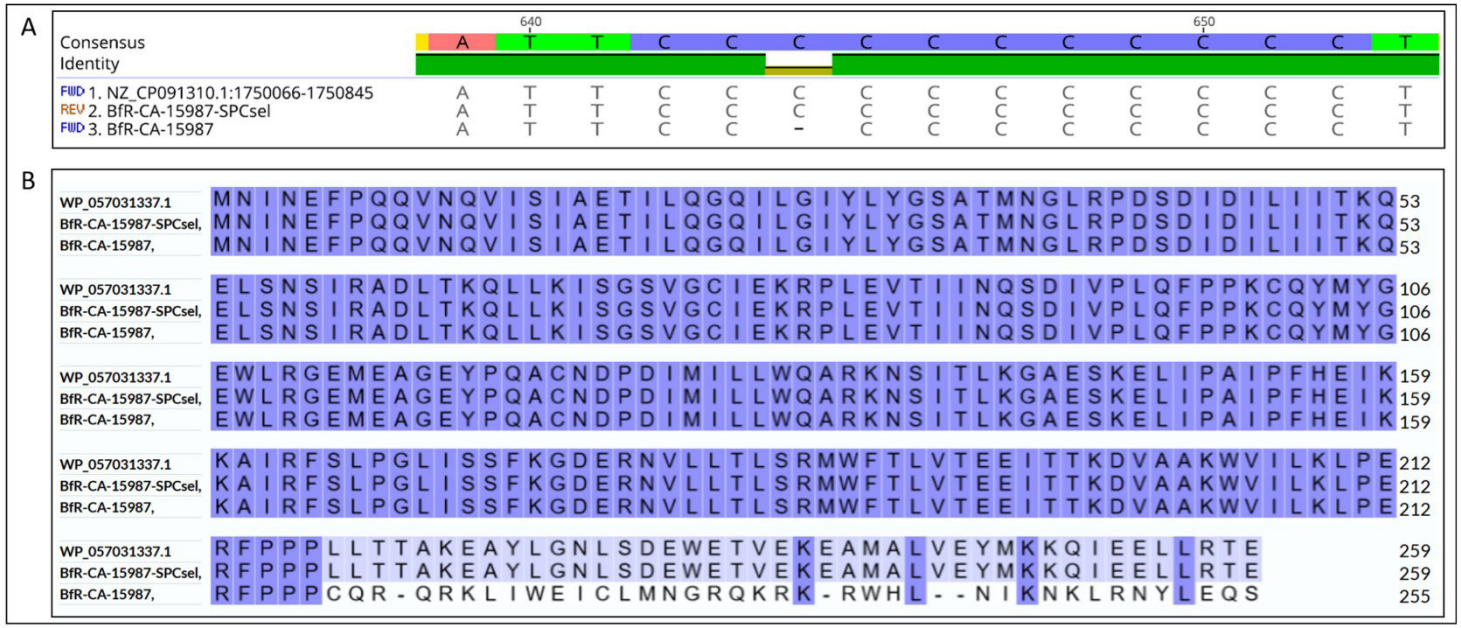

Figure S7. *aad9* is a phase-variable gene frequently inactivated by frame-shifting. **A,** Gene alignment of the poly-C tract in reference gene *aad9* (NZ_CP091310.1) with the corresponding region in BfR-CA-15987 and the spectinomycin re-selected BfR-CA-15987-SPCsel; **B,** Protein alignment of reference Aad9 (WP_057031337.1) with translated *aad9* gene assemblies obtained from BfR-CA-15987 before and after re-selection (BfR-CA-15987-SPCsel) on spectinomycin. Re-selection induced insertion of 1 cytosine into the poly-C tract (leading to 11 cytosines) (**A**), resulting in the restoration of full-length protein (**B**). Nucleotide and protein alignments were created with Geneious Prime software (**A**) and the Uniprot Align tool (56) (**B**), respectively.

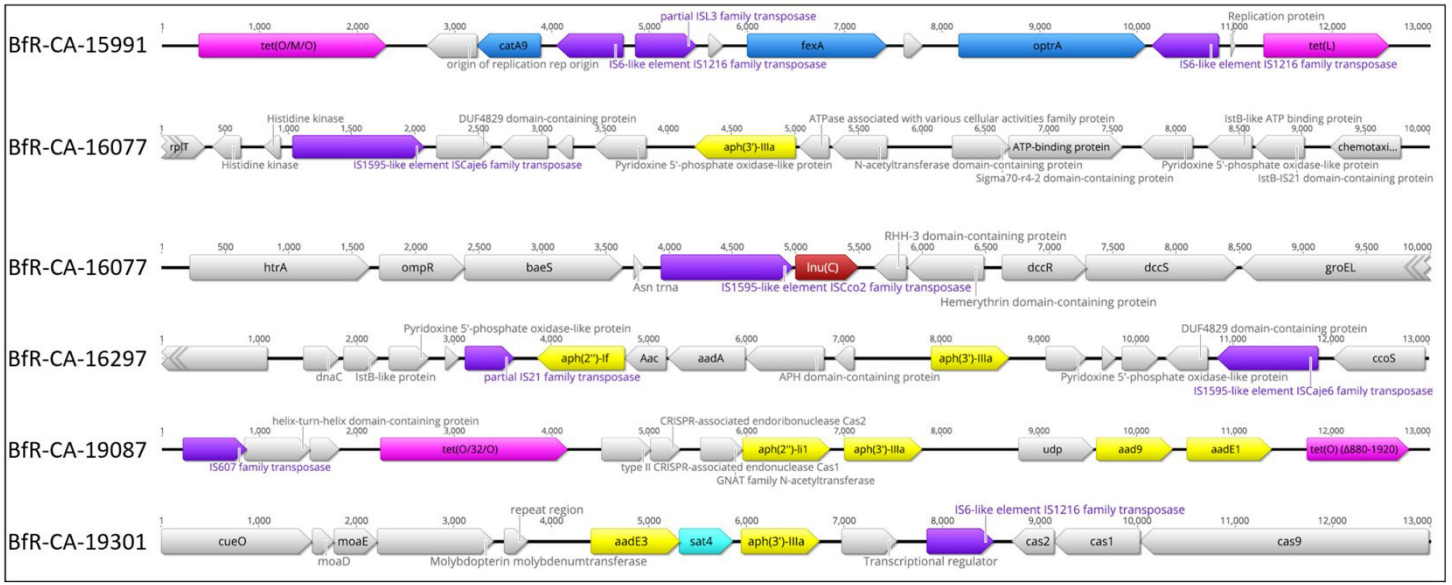

Figure S8. AMR genes in proximity to transposase genes not depicted in Figure 5 but part of Table 4. Transposase genes are marked in purple. AMR genes from different antimicrobial classes are depicted in different colors; blue, phenicol resistance genes (*catA, fexA, optrA*), red, *lnu*(C) genes; light purple, *tet* genes; yellow, aminoglycoside resistance genes; Grey arrows, non-AMR related genes.

9 Appendix

Supplementary Tables

Identification of knowledge gaps in whole-genome sequence analysis of multi-resistant thermotolerant *Campylobacter* spp.

Michael Zarske, Huong Quynh Luu, Carlus Deneke, Marie-Theres Knüver, Maja Thieck, Ha Thi Thu Hoang, Nancy Bretschneider, Ngoc Thi Pham, Ingrid Huber, Kerstin Sting

Legends:

Table S1	**Sample overview, including geno- and phenotype of AMR and WGS data overview;** All samples were sequenced by Illumina short-read technology
blue shading	Samples additionally sequenced by Oxford Nanopore Technology
green shading	phenotypical sensitive
red shading	phenotypical resistant
red	Genes not found
~~crossed out~~	Genes that were falsely annotated
bold	Genes only partially found, but manually confirmed as full-length
bold + blue	aad9 falsely annotated as truncated due to frame-shifting in the poly-C tract
tet(O)x	Additional full-length or partial allelic variants of tet(O) genes identified through read mapping using Geneious Prime Software
yellow shading	new allele variants and ST-Types

Table S2	**Proof of principle comparison of AMR gene detection based on SKESA or Shovill genome assemblies**
	The coverage of the gene is expressed as a percentage of the full-length translated protein sequence
red	Genes not found
bold	Genes only partially found, but manually confirmed as full-length
red shading	differences in AMR detection based on SKESA vs. Shovill

Table S3	**Reference sequences, showing the closest related NBCI RefSeq entries for the antimicrobial resistance genes found within this study**

Table S4	**Statistical analysis of phenotypic resistance among *C. jejuni* and *C. coli* in Vietnam and Germany**
	Odds ratio (OR) with 95 % confidence interval (CI) were calculated
bold	Odds ratios with p-values of less than 0.05

Table S5	**Ridom Seqsphere+ distance matrix, highlighting the phylogenetic diversity based on cgMLST**
green shading	isolate pairs with ≤ 10 allele distance
orange shading	isolate pairs with 11-100 allele distance
no shading	isolates with >100 allele distance

9 Appendix

Sample overview Samples highlighted in blue were additionally sequenced with Oxford Nanopore Technology								**phenotypic resistance determined by broth microdilution with EUCAMP2 and custom plate formats** green shading, sensitive; red shading, resistant														
BioProject No.	**BioSample-No.**	**isolate No.**	**Country of origin**	**isolation source**	**Alias**	**collection date**	**Species**	**CIP**	**NAL**	**ERY**	**TET**	**GEN**	**STR**	**AMP**	**KAN**	**NTC (STC)**	**CHL**	**FLO**	**SPC**	**LCM**	**Res profile [EUCAMP2]**	**Res type [EUCAMP2]**
PRJNA872862	SAMN34728690	BfR-CA-11843	Germany	broiler, meat		04.12.2013	Campylobacter coli	>4	64	4	32	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728691	BfR-CA-11858	Germany	broiler, meat		14.01.2014	Campylobacter coli	8	64	128	32	0,5	0,5								CIP, ERY, NAL, TET	3-fold
PRJNA872862	SAMN34728692	BfR-CA-11892	Germany	broiler, meat		14.01.2014	Campylobacter coli	16	64	<=1	32	0,5	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728693	BfR-CA-11893	Germany	broiler, cecum		03.02.2014	Campylobacter coli	0,25	4	2	<=0,5	0,5	1	8	8	2	4				sensitive	sensitive
PRJNA872862	SAMN34728694	BfR-CA-11930	Germany	broiler, meat		04.03.2014	Campylobacter coli	<=0,12	8	<=1	>64	1	2								TET	1-fold
PRJNA872862	SAMN34728695	BfR-CA-12208	Germany	broiler, meat		13.06.2014	Campylobacter coli	16	64	<=1	64	0,25	2	512	>1024	256					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728696	BfR-CA-12658	Germany	broiler, meat		03.07.2014	Campylobacter coli	>16	32	>128	32	<=0,12	1								CIP, ERY, NAL, TET	3-fold
PRJNA872862	SAMN34728697	BfR-CA-12887	Germany	broiler, cecum		09.10.2014	Campylobacter coli	16	64	<=1	<=0,5	0,5	1								CIP, NAL	1-fold
PRJNA872862	SAMN34728698	BfR-CA-12897	Germany	broiler, liver		16.10.2014	Campylobacter coli	8	64	<=1	64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728699	BfR-CA-12906	Germany	broiler, liver		06.10.2014	Campylobacter coli	>16	64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728700	BfR-CA-12973	Germany	broiler, feces		20.10.2014	Campylobacter coli	<=0,12	4	<=1	64	0,5	2								TET	1-fold
PRJNA872862	SAMN34728701	BfR-CA-13310	Germany	broiler, meat		17.06.2015	Campylobacter coli	16	>64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA872862	SAMN34728702	BfR-CA-13470	Germany	broiler, meat		16.09.2015	Campylobacter coli	8	64	2	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728703	BfR-CA-13526	Germany	broiler, meat		16.09.2015	Campylobacter coli	16	64	>128	>64	0,5	>16								CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34728704	BfR-CA-13528	Germany	broiler, meat		24.09.2015	Campylobacter coli	>16	64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728705	BfR-CA-13537	Germany	broiler, heart		06.10.2015	Campylobacter coli	16	64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577889	BfR-CA-13895	Germany	broiler, egg		24.02.2016	Campylobacter coli	0,5	4	2	<=0,5	0,25	1								sensitive	sensitive
PRJNA648048	SAMN15617887	BfR-CA-13918	Germany	broiler, meat		17.02.2016	Campylobacter jejuni	<=0,12	8	<=1	<=0,5	0,5	1								sensitive	sensitive
PRJNA595957	SAMN13577890	BfR-CA-13919	Germany	turkey, cecum		07.03.2016	Campylobacter coli	>16	32	<=1	<=0,5	0,25	1								CIP, NAL	1-fold
PRJNA648048	SAMN15617888	BfR-CA-13937	Germany	broiler, meat		07.03.2016	Campylobacter jejuni	>16	>64	2	<=0,5	0,5	1								CIP, NAL	1-fold
PRJNA872862	SAMN34728706	BfR-CA-13938	Germany	turkey, cecum		14.03.2016	Campylobacter coli	8	32	<=1	<=0,5	0,5	1		>1024	<=1			8		CIP, NAL	1-fold
PRJNA648048	SAMN15617889	BfR-CA-13939	Germany	broiler, meat		14.03.2016	Campylobacter jejuni	16	32	<=1	16	0,25	0,5								CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577891	BfR-CA-13953	Germany	turkey, cecum		07.03.2016	Campylobacter coli	>16	>64	<=1	>64	0,5	1	>512	>1024	32					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728707	BfR-CA-13971	Germany	turkey, cecum		21.03.2016	Campylobacter coli	8	16	>128	32	0,25	1								CIP, ERY, TET	3-fold
PRJNA872862	SAMN34728708	BfR-CA-13985	Germany	turkey, cecum		21.03.2016	Campylobacter jejuni	16	64	<=1	64	0,5	>16	>512	>1024	128					CIP, NAL, STR, TET	3-fold
PRJNA648048	SAMN15617890	BfR-CA-14088	Germany	broiler, meat		27.04.2016	Campylobacter jejuni	16	32	<=1	<=0,5	0,5	4								CIP, NAL	1-fold
PRJNA648048	SAMN15617891	BfR-CA-14109	Germany	broiler, meat		03.02.2016	Campylobacter jejuni	0,25	4	<=1	<=0,5	0,5	2								sensitive	sensitive
PRJNA648048	SAMN15617892	BfR-CA-14180	Germany	broiler, meat		31.05.2016	Campylobacter jejuni	16	64	<=1	32	0,5	1								CIP, NAL, TET	2-fold
PRJNA648048	SAMN15617893	BfR-CA-14181	Germany	broiler, meat		31.05.2016	Campylobacter jejuni	16	64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA872862	SAMN34728709	BfR-CA-14216	Germany	turkey, cecum		07.06.2016	Campylobacter coli	>16	32	4	32	0,5	2								CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577892	BfR-CA-14226	Germany	turkey, cecum		14.06.2016	Campylobacter coli	>16	32	2	64	1	8								CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728710	BfR-CA-14373	Germany	broiler, cecum		26.07.2016	Campylobacter jejuni	8	>64	<=1	>64	0,5	0,5								CIP, NAL, TET	2-fold
PRJNA562653	SAMN12647218	BfR-CA-14430	Germany	broiler, meat		10.08.2016	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577893	BfR-CA-14582	Germany	broiler, meat		05.09.2016	Campylobacter coli	>16	64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA872862	SAMN34728711	BfR-CA-14583	Germany	broiler, meat		14.09.2016	Campylobacter coli	16	32	<=1	32	0,25	0,5								CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577894	BfR-CA-14610	Germany	turkey, cecum		25.04.2016	Campylobacter coli	4	32	<=1	<=0,5	0,5	1								CIP, NAL	1-fold
PRJNA595957	SAMN13577895	BfR-CA-14731	Germany	turkey, meat		06.10.2016	Campylobacter coli	0,5	4	<=1	<=0,5	0,5	1								sensitive	sensitive
PRJNA872862	SAMN34728712	BfR-CA-14781	Germany	broiler, cecum		24.10.2016	Campylobacter jejuni	16	64	<=1	64	0,5	1								CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577896	BfR-CA-14810	Germany	broiler, egg		25.10.2016	Campylobacter coli	0,25	4	<=1	<=0,5	0,5	16		>1024	512			4		STR	1-fold
PRJNA872862	SAMN34728713	BfR-CA-14815	Germany	broiler, cecum		24.10.2016	Campylobacter coli	16	64	<=1	64	1	2								CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577897	BfR-CA-14825	Germany	turkey, cecum		07.11.2016	Campylobacter coli	8	32	<=1	<=0,5	<=0,12	0,5								CIP, NAL	1-fold
PRJNA595957	SAMN13577898	BfR-CA-14833	Germany	broiler, egg		08.11.2016	Campylobacter coli	0,5	8	2	<=0,5	0,25	1								sensitive	sensitive
PRJNA872862	SAMN34728714	BfR-CA-14857	Germany	broiler, skin		07.11.2016	Campylobacter jejuni	>16	<=1	<=1	64	0,5	1	>512	8	<=1	<=2	2	8	4	CIP, TET	2-fold
PRJNA872862	SAMN34728715	BfR-CA-14872	Germany	broiler, cecum		31.10.2016	Campylobacter jejuni	>16	<=1	<=1	<=0,5	0,25	1								CIP	1-fold

PRJNA648048	SAMN15617904	BfR-CA-14940	Germany	broiler, meat		20.04.2016	Campylobacter jejuni	0,25	4	<=1	<=0,5	1	2	16	4	<=1					sensitive	sensitive
PRJNA595957	SAMN13577899	BfR-CA-14943	Germany	turkey, cecum		12.12.2016	Campylobacter coli	>16	32	<=1	<=0,5	0,5	1								CIP, NAL	1-fold
PRJNA872862	SAMN34728716	BfR-CA-14958	Germany	goose, meat		16.12.2016	Campylobacter coli	8	64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577900	BfR-CA-14973	Germany	broiler, egg		07.12.2016	Campylobacter coli	8	32	<=1	<=0,5	0,5	>16		>1024	256			8		CIP, NAL, STR	2-fold
PRJNA872862	SAMN34728717	BfR-CA-14974	Germany	broiler, egg		13.12.2016	Campylobacter coli	16	64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA595957	SAMN13577901	BfR-CA-15005	Germany	turkey, skin		06.10.2016	Campylobacter coli	16	64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA872862	SAMN34728718	BfR-CA-15035	Germany	broiler, egg		15.03.2017	Campylobacter jejuni	<=0,12	4	<=1	<=0,5	0,5	1								sensitive	sensitive
PRJNA872862	SAMN34728719	BfR-CA-15062	Vietnam	broiler, feces	CG53-H1	10.04.2017	Campylobacter coli	>16	>64	>128	>64	>16	>16	>512	>1024	<=1	128	4	>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728720	BfR-CA-15077	Vietnam	broiler, feces	CG23-H16	10.04.2017	Campylobacter coli	>16	64	>128	>64	>16	1	512	>1024	<=1	64	2	>512	>128	CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34728721	BfR-CA-15078	Vietnam	broiler, feces	CG38-H17	10.04.2017	Campylobacter jejuni	>16	64	128	64	>16	0,5				64		256		CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34728722	BfR-CA-15080	Vietnam	broiler, feces	CG29-H19	10.04.2017	Campylobacter jejuni	>16	>64	2	>64	0,5	1	8	4	<=1	<=2	4	8	16	CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577902	BfR-CA-15124	Germany	broiler, meat		09.05.2017	Campylobacter coli	8	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728723	BfR-CA-15245	Germany	broiler, egg		08.08.2017	Campylobacter jejuni	<=0,12	4	<=1	<=0,5	0,5	1								sensitive	sensitive
PRJNA872862	SAMN34728724	BfR-CA-15246	Germany	broiler, egg		08.08.2017	Campylobacter jejuni	16	>64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA595957	SAMN13577903	BfR-CA-15267	Germany	broiler, egg		18.08.2017	Campylobacter coli	0,5	8	<=1	>64	0,25	1	>512	<=2	<=1	<=2	2	8	8	TET	1-fold
PRJNA595957	SAMN13577904	BfR-CA-15268	Germany	broiler, meat		24.08.2017	Campylobacter coli	>16	64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA595957	SAMN13577905	BfR-CA-15281	Germany	turkey, meat		28.08.2017	Campylobacter coli	16	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728725	BfR-CA-15282	Germany	turkey, meat		28.08.2017	Campylobacter jejuni	<=0,12	4	<=1	64	0,5	2								TET	1-fold
PRJNA595957	SAMN13577906	BfR-CA-15286	Germany	broiler, meat		06.09.2017	Campylobacter coli	8	>64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA595957	SAMN13577907	BfR-CA-15287	Germany	broiler, meat		05.09.2017	Campylobacter coli	8	>64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA872862	SAMN34728726	BfR-CA-15324	Germany	broiler, egg		15.09.2017	Campylobacter jejuni	8	64	<=1	<=0,5	0,25	1								CIP, NAL	1-fold
PRJNA595957	SAMN13577909	BfR-CA-15396	Germany	broiler, meat		14.11.2017	Campylobacter coli	>16	>64	<=1	>64	0,5	1	>512	>1024	32					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728727	BfR-CA-15403	Germany	broiler, meat		06.11.2017	Campylobacter coli	16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577910	BfR-CA-15426	Germany	broiler, meat		09.11.2017	Campylobacter coli	16	64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA595957	SAMN13577911	BfR-CA-15489	Germany	turkey, cecum		14.02.2018	Campylobacter coli	>16	64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728728	BfR-CA-15500	Germany	broiler, egg		16.02.2018	Campylobacter jejuni	<=0,12	2	<=1	32	0,5	1								TET	1-fold
PRJNA872862	SAMN34728729	BfR-CA-15532	Germany	duck, meat		06.03.2018	Campylobacter jejuni	16	>64	<=1	16	0,5	1								CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577912	BfR-CA-15533	Germany	duck, meat		06.03.2018	Campylobacter coli	8	64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728730	BfR-CA-15629	Germany	duck, meat		12.03.2018	Campylobacter coli	>16	>64	4	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577913	BfR-CA-15630	Germany	turkey, meat		17.04.2018	Campylobacter coli	>16	>64	2	>64	0,5	1	>512	>1024	32					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728731	BfR-CA-15687	Germany	turkey, cecum		10.04.2018	Campylobacter coli	>16	64	2	>64	>16	4								CIP, GEN, NAL, TET	3-fold
PRJNA595957	SAMN13577914	BfR-CA-15892	Germany	turkey, cecum		15.05.2018	Campylobacter coli	>16	>64	<=1	>64	0,5	1	>512	>1024	16					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728732	BfR-CA-15913	Germany	broiler, cecum		05.06.2018	Campylobacter coli	8	64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728733	BfR-CA-15969	Germany	turkey, meat		03.07.2018	Campylobacter coli	16	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728734	BfR-CA-15978	Germany	turkey, cecum		04.07.2018	Campylobacter coli	8	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728735	BfR-CA-15985	Vietnam	broiler, feces	CG60	24.11.2016	Campylobacter jejuni	>16	>64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728736	BfR-CA-15986	Vietnam	broiler, feces	CG59	24.11.2016	Campylobacter coli	>16	>64	>128	>64	>16	>16	256	>1024	<=1	4	2	8	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728737	BfR-CA-15987	Vietnam	broiler, feces	CG61	24.11.2016	Campylobacter coli	>16	>64	>128	>64	0,5	16	>512	8	<=1	8	4	>512	>128	CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34728738	BfR-CA-15988	Vietnam	broiler, feces	CG65	24.11.2016	Campylobacter coli	>16	>64	4	>64	0,5	>16				8		>512		CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728739	BfR-CA-15989	Vietnam	broiler, feces	CG77	25.12.2016	Campylobacter coli	>16	>64	>128	>64	>16	>16	>512	>1024	<=1	128	>16	>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728740	BfR-CA-15990	Vietnam	broiler, feces	CG78	25.12.2016	Campylobacter coli	>16	>64	>128	>64	>16	>16	>512	>1024	<=1	>128	>16	>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728741	BfR-CA-15991	Vietnam	broiler, feces	CG85	25.12.2016	Campylobacter coli	>16	>64	>128	>64	>16	>16	>512	>1024	<=1	128	>16	16	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728742	BfR-CA-15992	Vietnam	broiler, feces	CG86	25.12.2016	Campylobacter coli	>16	64	2	>64	>16	>16	256	>1024		64				CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728743	BfR-CA-15993	Vietnam	broiler, feces	CG87	25.12.2016	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728744	BfR-CA-15994	Vietnam	broiler, feces	CG55	24.11.2016	Campylobacter coli	>16	64	128	>64	>16	>16	512	>1024	<=1	128	4	>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728745	BfR-CA-15995	Vietnam	broiler, feces	CG57	24.11.2016	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728746	BfR-CA-15996	Vietnam	broiler, feces	CG62	24.11.2016	Campylobacter jejuni	>16	>64	<=1	>64	>16	>16	512	>1024		128		>512		CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728747	BfR-CA-15997	Vietnam	broiler, feces	CG63	24.11.2016	Campylobacter jejuni	<=0,12	8	<=1	64	0,25	1								TET	1-fold
PRJNA872862	SAMN34728748	BfR-CA-15998	Vietnam	broiler, feces	CG64	24.11.2016	Campylobacter jejuni	>16	>64	<=1	>64	0,5	>16								CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728749	BfR-CA-15999	Vietnam	broiler, feces	CG67	24.11.2016	Campylobacter jejuni	>16	>64	>128	>64	0,25	1								CIP, ERY, NAL, TET	3-fold
PRJNA872862	SAMN34728750	BfR-CA-16000	Vietnam	broiler, feces	CG68	24.11.2016	Campylobacter jejuni	>16	>64	<=1	>64	0,25	1	32			4			4	CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728751	BfR-CA-16001	Vietnam	broiler, feces	CG69	24.11.2016	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1	256	8		8			4	CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728752	BfR-CA-16002	Vietnam	broiler, feces	CG71	24.11.2016	Campylobacter jejuni	16	>64	<=1	64	0,25	1	64	4		<=2			4	CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728753	BfR-CA-16003	Vietnam	broiler, feces	CG72	24.11.2016	Campylobacter jejuni	>16	>64	2	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728754	BfR-CA-16004	Vietnam	broiler, feces	CG73	24.11.2016	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold

PRJNA872862	SAMN34728755	BfR-CA-16006	Vietnam	broiler, feces	CG75	25.12.2016	Campylobacter coli	16	64	>128	>64	>16	>16	512	>1024		64		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728756	BfR-CA-16007	Vietnam	broiler, feces	CG76	25.12.2016	Campylobacter jejuni	>16	>64	<=1	>64	>16	1	512	>1024		64		>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728757	BfR-CA-16008	Vietnam	broiler, feces	CG79	25.12.2016	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728758	BfR-CA-16010	Vietnam	broiler, feces	CG81	25.12.2016	Campylobacter coli	>16	>64	4	>64	0,5	16			<=1			>512		CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728759	BfR-CA-16011	Vietnam	broiler, feces	CG82	25.12.2016	Campylobacter jejuni	0,5	16	<=1	>64	0,5	1								TET	1-fold
PRJNA872862	SAMN34728760	BfR-CA-16012	Vietnam	broiler, feces	CG83	25.12.2016	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728761	BfR-CA-16013	Vietnam	broiler, feces	CG84	25.12.2016	Campylobacter jejuni	>16	>64	2	>64	>16	>16				128		>512		CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728762	BfR-CA-16014	Vietnam	broiler, feces	CG88	25.12.2016	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728763	BfR-CA-16015	Vietnam	broiler, feces	CG89	25.12.2016	Campylobacter jejuni	>16	>64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728764	BfR-CA-16016	Vietnam	broiler, feces	CG90	25.12.2016	Campylobacter coli	>16	64	128	>64	>16	>16	512	>1024		128		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728765	BfR-CA-16021	Vietnam	broiler, feces	CG95	25.12.2016	Campylobacter jejuni	>16	>64	<=1	>64	>16	1	>512	>1024		128		>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728766	BfR-CA-16022	Vietnam	broiler, feces	CG99	12.01.2017	Campylobacter jejuni	8	64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728767	BfR-CA-16023	Vietnam	broiler, feces	CG101	12.01.2017	Campylobacter coli	16	64	4	>64	>16	>16	256	>1024		16		>512		CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728768	BfR-CA-16024	Vietnam	broiler, feces	CG102	12.01.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	2		>1024	<=1					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728769	BfR-CA-16026	Vietnam	broiler, feces	CG107	12.01.2017	Campylobacter jejuni	8	64	2	64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728770	BfR-CA-16027	Vietnam	broiler, feces	CG108	12.01.2017	Campylobacter coli	16	64	>128	>64	>16	>16	>512	>1024		128		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728771	BfR-CA-16028	Vietnam	broiler, feces	CG109	12.01.2017	Campylobacter coli	>16	64	2	>64	>16	>16		>1024		4		>512		CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728772	BfR-CA-16029	Vietnam	broiler, feces	CG111	12.01.2017	Campylobacter jejuni	>16	>64	<=1	>64	>16	2	512	>1024		128		>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728773	BfR-CA-16030	Vietnam	broiler, feces	CG112	12.01.2017	Campylobacter jejuni	>16	>64	<=1	>64	>16	1	>512	>1024		64		>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728774	BfR-CA-16031	Vietnam	broiler, feces	CG113	12.01.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728775	BfR-CA-16032	Vietnam	broiler, feces	CG114	12.01.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728776	BfR-CA-16033	Vietnam	broiler, feces	CG115	12.01.2017	Campylobacter jejuni	>16	>64	<=1	>64	>16	2				128		>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728777	BfR-CA-16034	Vietnam	broiler, feces	CG116	12.01.2017	Campylobacter jejuni	>16	>64	<=1	>64	>16	1				128		>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728778	BfR-CA-16035	Vietnam	broiler, feces	CG117	12.01.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728779	BfR-CA-16036	Vietnam	broiler, feces	CG119	12.01.2017	Campylobacter coli	>16	64	>128	>64	>16	>16	32	>1024	<=1	4	2	8	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728780	BfR-CA-16039	Vietnam	broiler, feces	CG122	13.02.2017	Campylobacter jejuni	16	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728781	BfR-CA-16040	Vietnam	broiler, feces	CG123	13.02.2017	Campylobacter coli	>16	>64	128	>64	>16	>16				64		>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728782	BfR-CA-16041	Vietnam	broiler, feces	CG124	13.02.2017	Campylobacter jejuni	>16	>64	<=1	1	0,5	2	256	8	<=1	<=2	8	8	16	CIP, NAL	1-fold
PRJNA872862	SAMN34728783	BfR-CA-16042	Vietnam	broiler, feces	CG125	13.02.2017	Campylobacter jejuni	8	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728784	BfR-CA-16043	Vietnam	broiler, feces	CG126	13.02.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728785	BfR-CA-16044	Vietnam	broiler, feces	CG127	13.02.2017	Campylobacter jejuni	>16	64	>128	>64	>16	1	256	>1024		8		<=2	>128	CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34728786	BfR-CA-16045	Vietnam	broiler, feces	CG128	13.02.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,25	>16								CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728787	BfR-CA-16046	Vietnam	broiler, feces	CG129	13.02.2017	Campylobacter coli	16	>64	>128	32	>16	>16	>512	>1024	<=1	64	4	>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728788	BfR-CA-16048	Vietnam	broiler, feces	CG131	13.02.2017	Campylobacter coli	16	64	<=1	64	>16	>16								CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728789	BfR-CA-16052	Vietnam	broiler, feces	CG137	13.02.2017	Campylobacter coli	>16	64	>128	64	>16	>16	>512	>1024		128		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728790	BfR-CA-16053	Vietnam	broiler, feces	CG141	13.02.2017	Campylobacter coli	16	64	>128	64	>16	>16				128	>16	>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728791	BfR-CA-16056	Vietnam	broiler, feces	CG145	10.03.2017	Campylobacter jejuni	>16	>64	2	>64	0,5	1	>512	>1024		<=2				CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728792	BfR-CA-16057	Vietnam	broiler, feces	CG147	10.03.2017	Campylobacter coli	16	64	>128	64	>16	>16	>512	>1024	<=1	128	>16	>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728793	BfR-CA-16058	Vietnam	broiler, feces	CG148	10.03.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728794	BfR-CA-16059	Vietnam	broiler, feces	CG149	10.03.2017	Campylobacter coli	>16	64	>128	>64	>16	>16	>512	>1024	<=1	128	>16	>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728795	BfR-CA-16060	Vietnam	broiler, feces	CG150	10.03.2017	Campylobacter coli	16	64	>128	>64	>16	>16				128	>16	>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728796	BfR-CA-16062	Vietnam	broiler, feces	CG154	10.03.2017	Campylobacter coli	>16	>64	>128	>64	>16	>16	256	>1024		4				CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728797	BfR-CA-16063	Vietnam	broiler, feces	CG155	10.03.2017	Campylobacter jejuni	>16	>64	<=1	>64	1	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728798	BfR-CA-16064	Vietnam	broiler, feces	CG156	10.03.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728799	BfR-CA-16065	Vietnam	broiler, feces	CG157	10.03.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728800	BfR-CA-16068	Vietnam	broiler, feces	CG160	10.03.2017	Campylobacter coli	16	64	>128	>64	>16	2	>512	>1024		64		>512		CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34728801	BfR-CA-16069	Vietnam	broiler, feces	CG161	10.03.2017	Campylobacter coli	16	32	>128	64	>16	1	>512	>1024		64		>512		CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34728802	BfR-CA-16070	Vietnam	broiler, feces	CG162	10.03.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728803	BfR-CA-16071	Vietnam	broiler, feces	CG165	10.03.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728804	BfR-CA-16072	Vietnam	broiler, feces	CG166	10.03.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728805	BfR-CA-16073	Vietnam	broiler, feces	CG167	10.03.2017	Campylobacter coli	>16	64	>128	>64	>16	>16	512	>1024		64		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold

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PRJNA872862	SAMN34728806	BfR-CA-16077	Vietnam	broiler, feces	CG171	10.03.2017	Campylobacter jejuni	>16	32	2	64	>16	16	>512	>1024		128		>512	>128	CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728807	BfR-CA-16078	Vietnam	broiler, feces	CG172	09.04.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728808	BfR-CA-16079	Vietnam	broiler, feces	CG174	09.04.2017	Campylobacter jejuni	>16	>64	2	>64	0,5	1		>1024		>128	>16		>128	CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728809	BfR-CA-16080	Vietnam	broiler, feces	CG175	09.04.2017	Campylobacter jejuni	16	32	<=1	16	<=0,12	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728810	BfR-CA-16081	Vietnam	broiler, feces	CG176	09.04.2017	Campylobacter jejuni	>16	>64	2	>64	0,5	1	512	>1024	<=1	>128	>16	8	>128	CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728811	BfR-CA-16088	Vietnam	broiler, feces	CG183	09.04.2017	Campylobacter jejuni	>16	32	>128	64	>16	>16	>512	>1024		128		>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728812	BfR-CA-16089	Vietnam	broiler, feces	CG184	09.04.2017	Campylobacter jejuni	>16	>64	>128	>64	>16	>16	>512	>1024		64		>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728813	BfR-CA-16090	Vietnam	broiler, feces	CG185	09.04.2017	Campylobacter jejuni	>16	>64	>128	>64	>16	>16	>512	>1024		128		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728814	BfR-CA-16091	Vietnam	broiler, feces	CG186	09.04.2017	Campylobacter jejuni	>16	>64	>128	>64	2	4								CIP, ERY, NAL, TET	3-fold
PRJNA872862	SAMN34728815	BfR-CA-16092	Vietnam	broiler, feces	CG187	09.04.2017	Campylobacter jejuni	>16	64	>128	>64	>16	>16	>512	>1024	<=1	128	16	>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728816	BfR-CA-16095	Vietnam	broiler, feces	CG190	09.04.2017	Campylobacter jejuni	>16	64	>128	64	>16	16				128		>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728817	BfR-CA-16096	Vietnam	broiler, feces	CG191	09.04.2017	Campylobacter jejuni	>16	32	>128	64	>16	>16				128		>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728818	BfR-CA-16099	Vietnam	broiler, feces	CG194	09.04.2017	Campylobacter jejuni	>16	64	<=1	>64	0,5	>16								CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728819	BfR-CA-16103	Vietnam	broiler, feces	CG97	12.01.2017	Campylobacter coli	>16	64	128	>64	>16	>16	512	>1024		64		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728820	BfR-CA-16104	Vietnam	broiler, feces	CG98	12.01.2017	Campylobacter jejuni	8	>64	4	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728821	BfR-CA-16105	Vietnam	broiler, feces	CG100	12.01.2017	Campylobacter jejuni	>16	>64	>128	>64	0,25	1								CIP, ERY, NAL, TET	3-fold
PRJNA872862	SAMN34728822	BfR-CA-16106	Vietnam	broiler, feces	CG103	12.01.2017	Campylobacter coli	>16	64	128	>64	>16	>16	512	>1024		128		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728823	BfR-CA-16107	Vietnam	broiler, feces	CG104	12.01.2017	Campylobacter coli	>16	>64	>128	>64	>16	>16	64	>1024	32	<=2	4	>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728824	BfR-CA-16108	Vietnam	broiler, feces	CG105	12.01.2017	Campylobacter jejuni	>16	>64	<=1	>64	>16	4	256	>1024		64		>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728825	BfR-CA-16109	Vietnam	broiler, feces	CG121	13.02.2017	Campylobacter coli	>16	>64	>128	>64	1	>16	>512	>1024		64		>512		CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34728826	BfR-CA-16110	Vietnam	broiler, feces	CG142	13.02.2017	Campylobacter coli	>16	64	>128	>64	0,5	>16						>512		CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34728827	BfR-CA-16111	Vietnam	broiler, feces	CG152	10.03.2017	Campylobacter coli	16	>64	>128	>64	>16	>16				>128	>16	>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728828	BfR-CA-16112	Vietnam	broiler, feces	CG153	10.03.2017	Campylobacter jejuni	>16	>64	2	>64	1	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728829	BfR-CA-16190	Vietnam	broiler, feces	CG198	09.04.2017	Campylobacter jejuni	8	64	<=1	32	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728830	BfR-CA-16191	Vietnam	broiler, feces	CG200	03.05.2017	Campylobacter coli	16	64	>128	64	>16	>16	>512	>1024		32		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728831	BfR-CA-16193	Vietnam	broiler, feces	CG202	03.05.2017	Campylobacter jejuni	>16	>64	<=1	>64	>16	>16	>512	>1024		128		>512		CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728832	BfR-CA-16196	Vietnam	broiler, feces	CG205	03.05.2017	Campylobacter coli	16	64	>128	32	>16	>16	>512	>1024	<=1	128	>16	>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728833	BfR-CA-16197	Vietnam	broiler, feces	CG206	03.05.2017	Campylobacter jejuni	>16	>64	<=1	64	0,25	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728834	BfR-CA-16198	Vietnam	broiler, feces	CG208	03.05.2017	Campylobacter jejuni	16	16	<=1	64	0,25	1								CIP, TET	2-fold
PRJNA872862	SAMN34728835	BfR-CA-16201	Vietnam	broiler, feces	CG213	03.05.2017	Campylobacter coli	>16	64	>128	>64	>16	>16	512	>1024	<=1	64		256		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728836	BfR-CA-16203	Vietnam	broiler, feces	CG215	03.05.2017	Campylobacter coli	>16	64	>128	>64	>16	16				128		512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728837	BfR-CA-16204	Vietnam	broiler, feces	CG216	03.05.2017	Campylobacter jejuni	>16	>64	<=1	>64	>16	1	>512	>1024		>128		>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728838	BfR-CA-16207	Vietnam	broiler, feces	CG219	03.05.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,25	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728839	BfR-CA-16208	Vietnam	broiler, feces	CG220	03.05.2017	Campylobacter jejuni	>16	32	<=1	64	<=0,12	0,5		>1024	<=1					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728840	BfR-CA-16209	Vietnam	broiler, feces	CG222	03.05.2017	Campylobacter jejuni	>16	64	<=1	>64	0,25	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728841	BfR-CA-16210	Vietnam	broiler, feces	CG223	15.05.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728842	BfR-CA-16211	Vietnam	broiler, feces	CG224	15.05.2017	Campylobacter coli	>16	64	<=1	64	>16	1				128		>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728843	BfR-CA-16215	Vietnam	broiler, feces	CG229	15.05.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728844	BfR-CA-16216	Vietnam	broiler, feces	CG230	15.05.2017	Campylobacter coli	16	64	<=1	<=0,5	<=0,12	0,5								CIP, NAL	1-fold
PRJNA872862	SAMN34728845	BfR-CA-16217	Vietnam	broiler, feces	CG231	15.05.2017	Campylobacter jejuni	4	64	<=1	64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728846	BfR-CA-16220	Vietnam	broiler, feces	CG236	15.05.2017	Campylobacter jejuni	>16	64	<=1	64	0,25	16	>512	>1024	512					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728847	BfR-CA-16221	Vietnam	broiler, feces	CG237	15.05.2017	Campylobacter coli	>16	>64	>128	>64	>16	>16	64	>1024		64		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728848	BfR-CA-16222	Vietnam	broiler, feces	CG238	15.05.2017	Campylobacter jejuni	16	64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728849	BfR-CA-16245	Vietnam	broiler, feces	CG234	15.05.2017	Campylobacter coli	>16	>64	>128	>64	>16	>16	256	>1024		4				CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728850	BfR-CA-16246	Vietnam	broiler, feces	CG239	15.05.2017	Campylobacter jejuni	>16	64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728851	BfR-CA-16247	Vietnam	broiler, feces	CG240	15.05.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728852	BfR-CA-16248	Vietnam	broiler, feces	CG241	15.05.2017	Campylobacter jejuni	>16	64	<=1	>64	<=0,12	16		4				>512		CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728853	BfR-CA-16249	Vietnam	broiler, feces	CG242	15.05.2017	Campylobacter coli	>16	64	>128	>64	>16	>16	128	>1024		8				CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728854	BfR-CA-16251	Vietnam	broiler, feces	CG247	18.06.2017	Campylobacter jejuni	4	16	<=1	16	<=0,12	0,5								CIP, TET	2-fold
PRJNA872862	SAMN34728855	BfR-CA-16252	Vietnam	broiler, feces	CG248	18.06.2017	Campylobacter jejuni	16	64	<=1	64	0,25	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728856	BfR-CA-16253	Vietnam	broiler, feces	CG252	18.06.2017	Campylobacter coli	16	64	64	>64	>16	>16	64	>1024		128		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold

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PRJNA872862	SAMN34728857	BfR-CA-16254	Vietnam	broiler, feces	CG253	18.06.2017	Campylobacter jejuni	>16	32	<=1	32	<=0,12	<=0,25								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728858	BfR-CA-16257	Vietnam	broiler, feces	CG261	16.07.2017	Campylobacter coli	>16	64	>128	>64	>16	2	512	>1024		8		>512		CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34728859	BfR-CA-16258	Vietnam	broiler, feces	CG263	16.07.2017	Campylobacter coli	>16	>64	>128	>64	0,5	>16		4				>512	16	CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34728860	BfR-CA-16259	Vietnam	broiler, feces	CG264	16.07.2017	Campylobacter coli	>16	>64	>128	>64	>16	>16	>512	>1024		8		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728861	BfR-CA-16261	Vietnam	broiler, feces	CG267	16.07.2017	Campylobacter coli	>16	>64	64	>64	>16	>16	>512	>1024	<=1	128	>16	>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728862	BfR-CA-16264	Vietnam	broiler, feces	CG270	16.07.2017	Campylobacter coli	>16	>64	>128	>64	>16	2			<=1			>512		CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34728863	BfR-CA-16265	Vietnam	broiler, feces	CG271	16.07.2017	Campylobacter jejuni	>16	>64	2	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728864	BfR-CA-16272	Vietnam	broiler, feces	CG272	16.07.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728865	BfR-CA-16273	Vietnam	broiler, feces	CG273	16.07.2017	Campylobacter jejuni	8	>64	<=1	64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728866	BfR-CA-16275	Vietnam	broiler, feces	CG275	14.08.2017	Campylobacter coli	16	64	>128	>64	>16	>16	512	>1024		64		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728867	BfR-CA-16277	Vietnam	broiler, feces	CG277	14.08.2017	Campylobacter jejuni	16	32	<=1	16	16	1	256	>1024		64		>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728868	BfR-CA-16278	Vietnam	broiler, feces	CG278	14.08.2017	Campylobacter jejuni	>16	>64	2	>64	>16	1	256	>1024		64	8	>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728869	BfR-CA-16279	Vietnam	broiler, feces	CG279	14.08.2017	Campylobacter jejuni	8	32	<=1	8	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728870	BfR-CA-16280	Vietnam	broiler, feces	CG280	14.08.2017	Campylobacter jejuni	>16	>64	2	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728871	BfR-CA-16281	Vietnam	broiler, feces	CG281	14.08.2017	Campylobacter jejuni	16	32	<=1	16	<=0,12	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728872	BfR-CA-16282	Vietnam	broiler, feces	CG282	14.08.2017	Campylobacter coli	16	64	2	32	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728873	BfR-CA-16283	Vietnam	broiler, feces	CG283	14.08.2017	Campylobacter jejuni	8	16	<=1	8	<=0,12	0,5								CIP, TET	2-fold
PRJNA872862	SAMN34728874	BfR-CA-16284	Vietnam	broiler, feces	CG284	14.08.2017	Campylobacter jejuni	8	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728875	BfR-CA-16287	Vietnam	broiler, feces	CG287	14.08.2017	Campylobacter jejuni	16	>64	<=1	>64	0,25	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728876	BfR-CA-16292	Vietnam	broiler, feces	CG294	11.09.2017	Campylobacter coli	>16	64	>128	>64	>16	>16	32	>1024		64	8	>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728877	BfR-CA-16296	Vietnam	broiler, feces	CG302	11.09.2017	Campylobacter jejuni	>16	64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728878	BfR-CA-16297	Vietnam	broiler, feces	CG303	11.09.2017	Campylobacter coli	>16	64	>128	>64	>16	>16	512	>1024		4		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728879	BfR-CA-16298	Vietnam	broiler, feces	CG304	11.09.2017	Campylobacter coli	8	64	>128	>64	0,5	>16			<=1			>512		CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34728880	BfR-CA-16299	Vietnam	broiler, feces	CG305	11.09.2017	Campylobacter jejuni	8	>64	<=1	32	0,5	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728881	BfR-CA-16300	Vietnam	broiler, feces	CG306	11.09.2017	Campylobacter coli	>16	64	>128	>64	0,5	16			<=1			>512		CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34728882	BfR-CA-16303	Vietnam	broiler, feces	CG310	09.10.2017	Campylobacter jejuni	8	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728883	BfR-CA-16305	Vietnam	broiler, feces	CG313	09.10.2017	Campylobacter jejuni	8	>64	<=1	32	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728884	BfR-CA-16307	Vietnam	broiler, feces	CG315	09.10.2017	Campylobacter jejuni	8	64	<=1	>64	0,25	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728885	BfR-CA-16309	Vietnam	broiler, feces	CG317	09.10.2017	Campylobacter jejuni	16	>64	<=1	64	1	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728886	BfR-CA-16311	Vietnam	broiler, feces	CG319	09.10.2017	Campylobacter coli	16	>64	4	>64	>16	2	256	>1024		64	2	>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728887	BfR-CA-16329	Vietnam	broiler, feces	CG292	11.09.2017	Campylobacter jejuni	8	>64	<=1	>64	0,25	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728888	BfR-CA-16330	Vietnam	broiler, feces	CG293	11.09.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728889	BfR-CA-16348	Vietnam	broiler, feces	CG322	09.10.2017	Campylobacter jejuni	>16	>64	2	>64	1	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728890	BfR-CA-16349	Vietnam	broiler, feces	CG325	09.10.2017	Campylobacter jejuni	16	>64	<=1	64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728891	BfR-CA-16350	Vietnam	broiler, feces	CG329	09.10.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728892	BfR-CA-16351	Vietnam	broiler, feces	CG330	09.10.2017	Campylobacter coli	16	>64	4	>64	>16	2	256	>1024		128	2	>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728893	BfR-CA-16352	Vietnam	broiler, feces	CG338	09.10.2017	Campylobacter coli	16	64	>128	>64	>16	>16	>512	>1024		64	8	>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728894	BfR-CA-16353	Vietnam	broiler, feces	CG348	02.11.2017	Campylobacter coli	>16	>64	>128	>64	>16	>16	64	>1024		16		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34728895	BfR-CA-16354	Vietnam	broiler, feces	CG352	02.11.2017	Campylobacter coli	16	64	4	>64	1	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728896	BfR-CA-16360	Vietnam	broiler, feces	CG324	09.10.2017	Campylobacter jejuni	>16	>64	2	>64	1	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728897	BfR-CA-16361	Vietnam	broiler, feces	CG326	09.10.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728898	BfR-CA-16362	Vietnam	broiler, feces	CG327	09.10.2017	Campylobacter jejuni	>16	>64	<=1	>64	1	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728899	BfR-CA-16365	Vietnam	broiler, feces	CG332	09.10.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	>16		8				>512		CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728900	BfR-CA-16370	Vietnam	broiler, feces	CG344	09.10.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728901	BfR-CA-16372	Vietnam	broiler, feces	CG346	09.10.2017	Campylobacter coli	16	64	4	>64	>16	>16	32	>1024		8				CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728902	BfR-CA-16373	Vietnam	broiler, feces	CG349	02.11.2017	Campylobacter jejuni	>16	>64	2	>64	1	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728903	BfR-CA-16374	Vietnam	broiler, feces	CG350	02.11.2017	Campylobacter jejuni	>16	>64	2	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728904	BfR-CA-16375	Vietnam	broiler, feces	CG351	02.11.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728905	BfR-CA-16376	Vietnam	broiler, feces	CG353	02.11.2017	Campylobacter coli	16	>64	2	>64	>16	>16	512	>1024		64	4	>512		CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728906	BfR-CA-16378	Vietnam	broiler, feces	CG355	02.11.2017	Campylobacter jejuni	8	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728907	BfR-CA-16381	Vietnam	broiler, feces	CG361	02.11.2017	Campylobacter jejuni	<=0,12	4	<=1	>64	0,5	1								TET	1-fold
PRJNA872862	SAMN34728908	BfR-CA-16383	Vietnam	broiler, feces	CG363	02.11.2017	Campylobacter jejuni	4	>64	<=1	64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728909	BfR-CA-16385	Vietnam	broiler, feces	CG337	09.10.2017	Campylobacter jejuni	>16	>64	2	>64	>16	2	256	>1024		64	8	>512		CIP, GEN, NAL, TET	3-fold

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PRJNA872862	SAMN34728910	BfR-CA-16387	Vietnam	broiler, feces	CG341	09.10.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728911	BfR-CA-16389	Vietnam	broiler, feces	CG357	02.11.2017	Campylobacter jejuni	>16	>64	4	>64	>16	2	256	>1024		64	8	>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34728912	BfR-CA-16491	Germany	broiler, cecum		20.08.2018	Campylobacter jejuni	8	64	<=1	>64	0,5	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728913	BfR-CA-16671	Germany	broiler, meat		19.09.2018	Campylobacter coli	>16	>64	>128	>64	0,5	>16								CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34728914	BfR-CA-16677	Germany	broiler, cecum		11.10.2018	Campylobacter jejuni	>16	64	>128	>64	0,25	>16	>512	>1024	256					CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34728915	BfR-CA-16708	Germany	broiler, cecum		25.09.2018	Campylobacter coli	16	64	>128	>64	0,5	>16	>512	>1024	128					CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34728916	BfR-CA-16732	Germany	turkey, cecum		10.09.2018	Campylobacter coli	16	64	>128	>64	0,5	>16								CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34728917	BfR-CA-16737	Germany	turkey, cecum		18.09.2018	Campylobacter jejuni	>16	>64	<=1	>64	0,25	1	>512	>1024	256					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728918	BfR-CA-16743	Germany	turkey, cecum		25.09.2018	Campylobacter coli	>16	>64	>128	64	1	>16								CIP, ERY, NAL, STR, TET	4-fold
PRJNA595957	SAMN13577915	BfR-CA-16767	Germany	turkey, cecum		18.09.2018	Campylobacter coli	>16	64	<=1	>64	0,25	0,5	>512	>1024	8					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728919	BfR-CA-16783	Germany	broiler, cecum		22.10.2018	Campylobacter jejuni	8	>64	2	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728920	BfR-CA-16800	Germany	broiler, meat		23.10.2018	Campylobacter jejuni	<=0,12	2	<=1	<=0,5	0,5	1								sensitive	sensitive
PRJNA595957	SAMN13577916	BfR-CA-16822	Germany	turkey, cecum		08.10.2018	Campylobacter coli	16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728921	BfR-CA-16831	Germany	turkey, cecum		16.10.2018	Campylobacter coli	16	64	>128	>64	0,5	>16	>512	>1024	128					CIP, ERY, NAL, STR, TET	4-fold
PRJNA595957	SAMN13577917	BfR-CA-16834	Germany	turkey, cecum		15.10.2018	Campylobacter coli	16	>64	<=1	>64	0,5	1	512	>1024	512					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728922	BfR-CA-16888	Germany	broiler, meat		16.10.2018	Campylobacter jejuni	8	>64	<=1	64	0,25	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728923	BfR-CA-16930	Germany	broiler, meat		22.11.2018	Campylobacter jejuni	16	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577918	BfR-CA-16942	Germany	turkey, meat		21.11.2018	Campylobacter coli	16	64	2	2	1	2	512	8	<=1	<=2	2	8	8	CIP, NAL	1-fold
PRJNA872862	SAMN34728924	BfR-CA-17056	Germany	turkey, cecum		13.11.2018	Campylobacter coli	>16	64	>128	>64	1	>16								CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34728925	BfR-CA-17071	Germany	turkey, cecum		26.11.2018	Campylobacter coli	>16	>64	>128	>64	0,5	>16			<=1			>512		CIP, ERY, NAL, STR, TET	4-fold
PRJNA595957	SAMN13577919	BfR-CA-17078	Germany	turkey, cecum		27.11.2018	Campylobacter coli	0,5	8	<=1	<=0,5	0,5	2								sensitive	sensitive
PRJNA872862	SAMN34728926	BfR-CA-17105	Germany	turkey, meat		06.12.2018	Campylobacter jejuni	<=0,12	4	<=1	>64	0,5	1								TET	1-fold
PRJNA872862	SAMN34728927	BfR-CA-17107	Germany	turkey, meat		07.05.2018	Campylobacter jejuni	>16	>64	<=1	64	0,5	1								CIP, NAL, TET	2-fold
PRJNA595957	SAMN13577920	BfR-CA-17110	Germany	turkey, meat		15.05.2018	Campylobacter coli	8	>64	<=1	>64	1	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728928	BfR-CA-17153	Germany	broiler, egg		08.02.2019	Campylobacter coli	16	64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA872862	SAMN34728929	BfR-CA-17156	Germany	broiler, meat		04.02.2019	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728930	BfR-CA-17157	Germany	broiler, meat		24.01.2019	Campylobacter jejuni	>16	>64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA872862	SAMN34728931	BfR-CA-17159	Germany	broiler, meat		05.02.2019	Campylobacter coli	8	>64	<=1	>64	1	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728932	BfR-CA-17160	Germany	broiler, meat		05.02.2019	Campylobacter jejuni	<=0,12	4	<=1	<=0,5	0,5	1								sensitive	sensitive
PRJNA872862	SAMN34728933	BfR-CA-17230	Germany	turkey, cecum		03.12.2018	Campylobacter coli	16	64	>128	>64	0,5	>16	512	>1024	256					CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34728934	BfR-CA-17247	Germany	broiler, meat		11.04.2019	Campylobacter coli	16	>64	<=1	>64	1	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728935	BfR-CA-17249	Germany	broiler, egg		06.05.2019	Campylobacter coli	<=0,12	4	<=1	>64	1	2								TET	1-fold
PRJNA872862	SAMN34728936	BfR-CA-17288	Germany	broiler, meat		11.06.2019	Campylobacter jejuni	4	2	<=1	32	0,25	0,5								CIP, TET	2-fold
PRJNA872862	SAMN34728937	BfR-CA-17356	Germany	broiler, meat		15.07.2019	Campylobacter jejuni	8	>64	<=1	16	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728938	BfR-CA-17379	Germany	broiler, meat		17.07.2019	Campylobacter jejuni	>16	>64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728939	BfR-CA-17395	Germany	broiler, meat		06.08.2019	Campylobacter jejuni	16	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728940	BfR-CA-17405	Germany	broiler, meat		15.08.2019	Campylobacter jejuni	16	>64	<=1	>64	0,5	>16	256	>1024	256					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728941	BfR-CA-17407	Germany	broiler, skin		19.08.2019	Campylobacter jejuni	8	>64	<=1	64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728942	BfR-CA-17415	Germany	broiler, meat		26.08.2019	Campylobacter jejuni	>16	>64	<=1	>64	0,5	>16	256	1024	128					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728943	BfR-CA-17424	Germany	broiler, skin		02.09.2019	Campylobacter jejuni	8	>64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA872862	SAMN34728944	BfR-CA-17549	Germany	broiler, meat		29.10.2019	Campylobacter jejuni	>16	>64	<=1	>64	0,5	>16	256	>1024	256					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728945	BfR-CA-17788	Germany	broiler, meat		08.01.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	>16	256	>1024	256					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728946	BfR-CA-17799	Germany	broiler, meat		16.01.2020	Campylobacter jejuni	8	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728947	BfR-CA-17805	Germany	poultry, meat		29.01.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728948	BfR-CA-17822	Germany	broiler, meat		04.02.2020	Campylobacter jejuni	16	>64	2	>64	0,5	>16	256	>1024	256					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728949	BfR-CA-17824	Germany	broiler, meat		03.02.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728950	BfR-CA-17827	Germany	broiler, egg		29.01.2020	Campylobacter coli	16	64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728951	BfR-CA-17832	Germany	broiler, meat		13.02.2020	Campylobacter jejuni	8	>64	<=1	64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728952	BfR-CA-17836	Germany	broiler, meat		18.02.2020	Campylobacter coli	8	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728953	BfR-CA-17840	Germany	broiler, meat		17.02.2020	Campylobacter jejuni	<=0,12	4	<=1	<=0,5	0,5	2								sensitive	sensitive
PRJNA872862	SAMN34728954	BfR-CA-17860	Germany	broiler, meat		27.02.2020	Campylobacter jejuni	16	>64	<=1	64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728955	BfR-CA-17861	Germany	turkey, cecum		03.03.2020	Campylobacter coli	16	>64	>128	>64	1	4								CIP, ERY, NAL, TET	3-fold
PRJNA872862	SAMN34728956	BfR-CA-17869	Germany	broiler, meat		10.03.2020	Campylobacter jejuni	<=0,12	4	<=1	<=0,5	1	2								sensitive	sensitive

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PRJNA872862	SAMN34728957	BfR-CA-17890	Germany	broiler, meat		10.03.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	>16	256	>1024	256	<=2	2		8	CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728958	BfR-CA-17905	Germany	turkey, cecum		17.03.2020	Campylobacter coli	16	64	<=1	64	1	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728959	BfR-CA-17949	Germany	broiler, liver		21.04.2020	Campylobacter coli	<=0,12	4	<=1	<=0,5	0,5	1								sensitive	sensitive
PRJNA872862	SAMN34728960	BfR-CA-17950	Germany	broiler, liver		21.04.2020	Campylobacter coli	<=0,12	4	<=1	<=0,5	0,5	2								sensitive	sensitive
PRJNA872862	SAMN34728961	BfR-CA-17951	Germany	broiler, skin		08.05.2020	Campylobacter coli	<=0,12	4	<=1	<=0,5	0,5	2								sensitive	sensitive
PRJNA872862	SAMN34728962	BfR-CA-17959	Germany	broiler, skin		08.05.2020	Campylobacter jejuni	16	>64	<=1	<=0,5	0,5	1								CIP, NAL	1-fold
PRJNA872862	SAMN34728963	BfR-CA-17965	Germany	broiler, cecum		11.05.2020	Campylobacter coli	>16	64	>128	>64	1	4	512	>1024	128					CIP, ERY, NAL, TET	3-fold
PRJNA872862	SAMN34728964	BfR-CA-17971	Germany	turkey, cecum		21.04.2020	Campylobacter coli	8	>64	<=1	>64	1	4								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728965	BfR-CA-17991	Germany	broiler, skin		08.05.2020	Campylobacter coli	<=0,12	8	2	<=0,5	0,25	1								sensitive	sensitive
PRJNA872862	SAMN34728966	BfR-CA-17992	Germany	broiler, cecum		08.05.2020	Campylobacter coli	<=0,12	4	<=1	<=0,5	0,5	1								sensitive	sensitive
PRJNA872862	SAMN34728967	BfR-CA-18000	Germany	broiler, skin		23.05.2020	Campylobacter coli	>16	>64	>128	>64	0,5	2	>512	>1024	32					CIP, ERY, NAL, TET	3-fold
PRJNA872862	SAMN34728968	BfR-CA-18036	Germany	turkey, cecum		27.05.2020	Campylobacter coli	16	64	>128	>64	0,5	2	512	>1024	64					CIP, ERY, NAL, TET	3-fold
PRJNA872862	SAMN34728969	BfR-CA-18037	Germany	broiler, meat		26.05.2020	Campylobacter jejuni	16	>64	<=1	>64	0,25	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728970	BfR-CA-18038	Germany	broiler, meat		06.05.2020	Campylobacter jejuni	16	>64	<=1	<=0,5	0,5	1								CIP, NAL	1-fold
PRJNA872862	SAMN34728971	BfR-CA-18039	Germany	broiler, meat		02.06.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728972	BfR-CA-18045	Germany	broiler, meat		08.06.2020	Campylobacter coli	<=0,12	4	<=1	<=0,5	0,5	2								sensitive	sensitive
PRJNA872862	SAMN34728973	BfR-CA-18060	Germany	broiler, egg		10.06.2020	Campylobacter jejuni	<=0,12	2	<=1	64	0,5	1								TET	1-fold
PRJNA872862	SAMN34728974	BfR-CA-18061	Germany	broiler, meat		15.06.2020	Campylobacter jejuni	8	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728975	BfR-CA-18064	Germany	broiler, liver		21.04.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728976	BfR-CA-18096	Germany	broiler, meat		24.06.2020	Campylobacter jejuni	8	>64	<=1	8	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728977	BfR-CA-18102	Germany	broiler, skin		29.06.2020	Campylobacter coli	>16	>64	8	>64	1	4								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728978	BfR-CA-18104	Germany	broiler, meat		22.06.2020	Campylobacter jejuni	0,25	4	<=1	<=0,5	1	2								sensitive	sensitive
PRJNA872862	SAMN34728979	BfR-CA-18143	Germany	broiler, meat		06.07.2020	Campylobacter jejuni	<=0,12	4	<=1	<=0,5	0,5	>16	>512	>1024	128					STR	1-fold
PRJNA872862	SAMN34728980	BfR-CA-18167	Germany	broiler, meat		06.07.2020	Campylobacter jejuni	8	>64	<=1	<=0,5	0,5	1								CIP, NAL	1-fold
PRJNA872862	SAMN34728981	BfR-CA-18197	Germany	broiler, meat		21.07.2020	Campylobacter jejuni	<=0,12	4	<=1	<=0,5	1	2	8	4	<=1	<=2	1	8	4	sensitive	sensitive
PRJNA872862	SAMN34728982	BfR-CA-18248	Germany	broiler, meat		30.06.2020	Campylobacter jejuni	<=0,12	8	<=1	<=0,5	0,5	1								sensitive	sensitive
PRJNA872862	SAMN34728983	BfR-CA-18264	Germany	broiler, egg		22.07.2020	Campylobacter coli	0,25	8	2	<=0,5	1	1								sensitive	sensitive
PRJNA872862	SAMN34728984	BfR-CA-18277	Germany	broiler, meat		08.07.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	>16	512	>1024	128					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728985	BfR-CA-18280	Germany	broiler, meat		20.07.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	>16	512	>1024	128					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728986	BfR-CA-18322	Germany	broiler, meat		22.07.2020	Campylobacter jejuni	0,25	4	<=1	<=0,5	1	2								sensitive	sensitive
PRJNA872862	SAMN34728987	BfR-CA-18353	Germany	turkey, cecum		27.07.2020	Campylobacter coli	16	64	<=1	2	0,5	1								CIP, NAL	1-fold
PRJNA872862	SAMN34728988	BfR-CA-18372	Germany	broiler, meat		11.08.2020	Campylobacter jejuni	<=0,12	4	<=1	>64	0,5	1								TET	1-fold
PRJNA872862	SAMN34728989	BfR-CA-18391	Germany	broiler, meat		10.08.2020	Campylobacter jejuni	16	>64	<=1	64	0,5	1	512							CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728990	BfR-CA-18407	Germany	broiler, meat		11.08.2020	Campylobacter jejuni	16	>64	<=1	<=0,5	0,5	0,5	32	>1024	64					CIP, NAL	1-fold
PRJNA872862	SAMN34728991	BfR-CA-18408	Germany	duck, meat		12.08.2020	Campylobacter coli	16	>64	<=1	>64	0,5	2		>1024	<=1					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728992	BfR-CA-18548	Germany	broiler, meat		24.08.2020	Campylobacter jejuni	8	>64	<=1	>64	0,25	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728993	BfR-CA-18564	Germany	broiler, meat		31.08.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	16	256	>1024	256					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728994	BfR-CA-18580	Germany	broiler, meat		08.09.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728995	BfR-CA-18585	Germany	broiler, meat		01.09.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	>16	128	>1024	256	<=2	2	16	8	CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34728996	BfR-CA-18592	Germany	broiler, skin		25.08.2020	Campylobacter coli	>16	>64	<=1	>64	0,5	1	>512	>1024	32					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728997	BfR-CA-18665	Germany	broiler, meat		02.09.2020	Campylobacter jejuni	>16	>64	4	<=0,5	0,5	>16	256	>1024	256					CIP, NAL, STR	2-fold
PRJNA872862	SAMN34728998	BfR-CA-18683	Vietnam	broiler, feces	CG96	25.12.2016	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34728999	BfR-CA-18684	Vietnam	broiler, feces	CG110	12.01.2017	Campylobacter jejuni	>16	>64	<=1	>64	>16	1				64		>512		CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34729000	BfR-CA-18685	Vietnam	broiler, feces	CG118	12.01.2017	Campylobacter coli	>16	>64	>128	>64	0,5	>16		>1024		64		>512		CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34729001	BfR-CA-18686	Vietnam	broiler, feces	CG136	13.02.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729002	BfR-CA-18687	Vietnam	broiler, feces	CG138	13.02.2017	Campylobacter coli	>16	>64	>128	>64	>16	>16				128		512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729003	BfR-CA-18689	Vietnam	broiler, feces	CG146	10.03.2017	Campylobacter jejuni	>16	>64	<=1	>64	>16	0,5	>512	>1024	<=1	>128	>16	8	64	CIP, GEN, NAL, TET	3-fold
PRJNA872862	SAMN34729004	BfR-CA-18691	Vietnam	broiler, feces	CG199	09.04.2017	Campylobacter jejuni	16	>64	<=1	32	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729005	BfR-CA-18694	Vietnam	broiler, feces	CG243	15.05.2017	Campylobacter coli	16	>64	>128	>64	0,5	>16		>1024		64		>512		CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34729006	BfR-CA-18695	Vietnam	broiler, feces	CG250	18.06.2017	Campylobacter jejuni	8	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729007	BfR-CA-18717	Vietnam	broiler, feces	CG70	24.11.2016	Campylobacter jejuni	16	>64	<=1	64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729008	BfR-CA-18718	Vietnam	broiler, feces	CG210	03.05.2017	Campylobacter coli	>16	>64	2	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729009	BfR-CA-18719	Vietnam	broiler, feces	CG211	03.05.2017	Campylobacter jejuni	>16	>64	2	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729010	BfR-CA-18728	Vietnam	broiler, feces	CG251	18.06.2017	Campylobacter coli	>16	>64	>128	>64	>16	>16				128	>16	>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729011	BfR-CA-18729	Vietnam	broiler, feces	CG254	18.06.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,25	16		1024		128		>512		CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729012	BfR-CA-18731	Vietnam	broiler, feces	CG262	16.07.2017	Campylobacter jejuni	>16	>64	<=1	>64	>16	>16				>128		>512		CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729013	BfR-CA-18732	Vietnam	broiler, feces	CG266	16.07.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	>16						>512		CIP, NAL, STR, TET	3-fold

PRJNA872862	SAMN34729014	BfR-CA-18734	Vietnam	broiler, feces	CG320	09.10.2017	Campylobacter jejuni	>16	>64	<=1	>64	>16	>16				128		>512		CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729015	BfR-CA-18735	Vietnam	broiler, feces	CG364	02.11.2017	Campylobacter jejuni	8	>64	<=1	64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729016	BfR-CA-18736	Vietnam	broiler, feces	CG365	02.11.2017	Campylobacter coli	>16	>64	>128	>64	>16	>16				>128		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729017	BfR-CA-18737	Vietnam	broiler, feces	CG366	15.11.2017	Campylobacter coli	16	>64	>128	>64	>16	>16	>512	>1024		128	>16	>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729018	BfR-CA-18738	Vietnam	broiler, feces	CG367	15.11.2017	Campylobacter coli	>16	>64	>128	>64	>16	>16	>512	>1024		>128	>16	>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729019	BfR-CA-18743	Germany	broiler, meat		18.08.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	>16	256	>1024	256					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729020	BfR-CA-18748	Germany	turkey, cecum		04.09.2020	Campylobacter coli	>16	>64	<=1	>64	0,5	2	>512	>1024	16					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729021	BfR-CA-18820	Vietnam	broiler, feces	CG369	15.11.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729022	BfR-CA-18821	Vietnam	broiler, feces	CG371	15.11.2017	Campylobacter coli	16	>64	>128	>64	>16	>16	>512	>1024		128	>16	>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729023	BfR-CA-18822	Vietnam	broiler, feces	CG372	15.11.2017	Campylobacter coli	>16	64	2	>64	1	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729024	BfR-CA-18825	Vietnam	broiler, feces	CG378	15.11.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729025	BfR-CA-18826	Vietnam	broiler, feces	CG380	15.11.2017	Campylobacter coli	16	>64	>128	>64	>16	2				64		>512		CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34729026	BfR-CA-18834	Germany	turkey, cecum		19.09.2020	Campylobacter coli	8	64	64	<=0,5	0,5	2								CIP, ERY, NAL	2-fold
PRJNA872862	SAMN34729027	BfR-CA-18839	Vietnam	broiler, feces	CG368	15.11.2017	Campylobacter jejuni	16	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729028	BfR-CA-18840	Vietnam	broiler, feces	CG370	15.11.2017	Campylobacter jejuni	8	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729029	BfR-CA-18841	Vietnam	broiler, feces	CG373	15.11.2017	Campylobacter jejuni	>16	>64	2	>64	1	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729030	BfR-CA-18842	Vietnam	broiler, feces	CG375	15.11.2017	Campylobacter coli	16	>64	2	>64	>16	>16								CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729031	BfR-CA-18843	Vietnam	broiler, feces	CG377	15.11.2017	Campylobacter coli	16	>64	>128	>64	>16	>16				128	>16	>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729032	BfR-CA-18844	Vietnam	broiler, feces	CG379	15.11.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729033	BfR-CA-18869	Germany	broiler, meat		28.09.2020	Campylobacter jejuni	<=0,12	16	4	<=0,5	0,5	2								sensitive	sensitive
PRJNA872862	SAMN34729034	BfR-CA-18879	Vietnam	broiler, feces	CG390	15.11.2017	Campylobacter coli	>16	64	>128	>64	>16	>16			<=1	64		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729035	BfR-CA-18880	Vietnam	broiler, feces	CG391	01.12.2017	Campylobacter coli	>16	>64	8	>64	0,5	>16								CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729036	BfR-CA-18881	Vietnam	broiler, feces	CG392	01.12.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729037	BfR-CA-18883	Vietnam	broiler, feces	CG396	01.12.2017	Campylobacter coli	>16	>64	>128	>64	>16	>16			<=1			>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729038	BfR-CA-18884	Vietnam	broiler, feces	CG397	01.12.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729039	BfR-CA-18885	Vietnam	broiler, feces	CG398	01.12.2017	Campylobacter coli	>16	>64	>128	>64	>16	>16				128		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729040	BfR-CA-18886	Vietnam	broiler, feces	CG399	01.12.2017	Campylobacter coli	16	>64	>128	>64	0,5	>16		8	<=1			>512		CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34729041	BfR-CA-18887	Vietnam	broiler, feces	CG400	01.12.2017	Campylobacter coli	>16	>64	4	>64	>16	>16								CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729042	BfR-CA-18889	Vietnam	broiler, feces	CG404	01.12.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729043	BfR-CA-18891	Vietnam	broiler, feces	CG406	01.12.2017	Campylobacter jejuni	>16	>64	2	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729044	BfR-CA-18892	Vietnam	broiler, feces	CG407	01.12.2017	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729045	BfR-CA-18894	Germany	broiler, meat		06.10.2020	Campylobacter jejuni	<=0,12	4	<=1	<=0,5	0,25	1								sensitive	sensitive
PRJNA872862	SAMN34729046	BfR-CA-18901	Germany	broiler, meat		15.10.2020	Campylobacter jejuni	16	>64	<=1	<=0,5	0,5	1								CIP, NAL	1-fold
PRJNA872862	SAMN34729047	BfR-CA-19025	Vietnam	broiler, cecum	CG408	15.01.2018	Campylobacter coli	16	>64	2	>64	>16	>16	64			4		>512		CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729048	BfR-CA-19026	Vietnam	broiler, cecum	CG409	15.01.2018	Campylobacter coli	16	>64	2	>64	0,5	>16				8		>512		CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729049	BfR-CA-19027	Vietnam	broiler, cecum	CG410	15.01.2018	Campylobacter coli	16	>64	>128	>64	>16	>16				128		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729050	BfR-CA-19028	Vietnam	broiler, cecum	CG411	15.01.2018	Campylobacter coli	16	>64	2	>64	>16	>16						>512		CIP, GEN, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729051	BfR-CA-19029	Vietnam	broiler, cecum	CG412	15.01.2018	Campylobacter coli	16	64	64	>64	>16	>16				64		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729052	BfR-CA-19030	Vietnam	broiler, cecum	CG413	15.01.2018	Campylobacter coli	16	>64	64	>64	>16	>16				128		>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729053	BfR-CA-19031	Vietnam	broiler, cecum	CG414	15.01.2018	Campylobacter coli	16	64	64	>64	>16	>16				64	4	>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729054	BfR-CA-19032	Vietnam	broiler, meat	CG415	15.01.2018	Campylobacter coli	>16	>64	>128	>64	>16	>16	64			64	4	>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729055	BfR-CA-19033	Vietnam	broiler, meat	CG416	15.01.2018	Campylobacter coli	>16	>64	64	>64	>16	>16	64	>1024	64	<=2	8	>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729056	BfR-CA-19034	Vietnam	broiler, meat	CG417	15.01.2018	Campylobacter coli	>16	>64	>128	>64	>16	>16				128	4	>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729057	BfR-CA-19035	Vietnam	broiler, cecum	CG418	01.02.2018	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729058	BfR-CA-19036	Vietnam	broiler, cecum	CG419	01.02.2018	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729059	BfR-CA-19037	Vietnam	broiler, cecum	CG420	01.02.2018	Campylobacter coli	>16	>64	>128	>64	>16	>16		>1024		64		>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729060	BfR-CA-19038	Vietnam	broiler, cecum	CG421	01.02.2018	Campylobacter coli	16	64	>128	>64	>16	>16								CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729061	BfR-CA-19039	Vietnam	broiler, cecum	CG422	01.02.2018	Campylobacter coli	8	>64	>128	>64	0,5	>16		8	<=1			>512		CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34729062	BfR-CA-19040	Vietnam	broiler, meat	CG423	01.02.2018	Campylobacter coli	>16	>64	>128	>64	0,5	16		8	<=1			>512		CIP, ERY, NAL, STR, TET	4-fold
PRJNA872862	SAMN34729063	BfR-CA-19044	Germany	broiler, meat		28.10.2020	Campylobacter coli	16	64	>128	>64	0,5	2		>1024	256			8		CIP, ERY, NAL, TET	3-fold
PRJNA872862	SAMN34729064	BfR-CA-19052	Germany	broiler, cecum		02.11.2020	Campylobacter jejuni	8	>64	<=1	<=0,5	0,5	0,5								CIP, NAL	1-fold
PRJNA872862	SAMN34729065	BfR-CA-19053	Germany	broiler, cecum		02.11.2020	Campylobacter jejuni	8	2	<=1	<=0,5	0,5	1								CIP	1-fold
PRJNA872862	SAMN34729066	BfR-CA-19055	Germany	broiler, skin		02.11.2020	Campylobacter jejuni	16	2	<=1	<=0,5	0,5	1								CIP	1-fold
PRJNA872862	SAMN34729067	BfR-CA-19058	Germany	turkey, cecum		12.10.2020	Campylobacter coli	>16	>64	<=1	>64	0,5	1	>512	>1024	16					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729068	BfR-CA-19082	Germany	broiler, skin		02.11.2020	Campylobacter jejuni	>16	>64	<=1	>64	0,25	>16	512	>1024	128					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729069	BfR-CA-19085	Germany	broiler, cecum		04.11.2020	Campylobacter jejuni	16	>64	<=1	<=0,5	0,5	1								CIP, NAL	1-fold

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PRJNA872862	SAMN34729070	BfR-CA-19086	Germany	broiler, meat		02.11.2020	Campylobacter jejuni	4	<=1	<=1	32	0,25	1								CIP, TET	2-fold
PRJNA872862	SAMN34729071	BfR-CA-19087	Germany	broiler, meat		02.11.2020	Campylobacter coli	8	64	<=1	>64	>16	>16	8	>1024	2	<=2	1	>512	16	CIP, GEN, NAL, STR, TET	4-fold
PRJNA872862	SAMN34729072	BfR-CA-19088	Germany	broiler, meat		02.11.2020	Campylobacter coli	8	64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729073	BfR-CA-19089	Germany	broiler, meat		04.11.2020	Campylobacter jejuni	<=0,12	4	<=1	<=0,5	0,5	2								sensitive	sensitive
PRJNA872862	SAMN34729074	BfR-CA-19092	Germany	broiler, meat		05.11.2020	Campylobacter jejuni	8	>64	<=1	<=0,5	0,5	1								CIP, NAL	1-fold
PRJNA872862	SAMN34729075	BfR-CA-19102	Vietnam	broiler, meat	CG424	01.02.2018	Campylobacter jejuni	>16	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729076	BfR-CA-19104	Vietnam	broiler, cecum	CG426	01.03.2018	Campylobacter coli	>16	>64	2	>64	0,5	>16	32	4	<=1	<=2	4	16	16	CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729077	BfR-CA-19106	Vietnam	broiler, cecum	CG428	01.03.2018	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729078	BfR-CA-19107	Vietnam	broiler, cecum	CG429	01.03.2018	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729079	BfR-CA-19108	Vietnam	broiler, cecum	CG430	01.03.2018	Campylobacter jejuni	>16	>64	128	>64	>16	1	256	>1024		64	4	512		CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34729080	BfR-CA-19110	Vietnam	broiler, meat	CG433	01.03.2018	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729081	BfR-CA-19111	Vietnam	broiler, cecum	CG434	01.03.2018	Campylobacter jejuni	>16	>64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729082	BfR-CA-19112	Vietnam	broiler, cecum	CG435	01.03.2018	Campylobacter coli	>16	>64	>128	>64	>16	>16			32			>512		CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729083	BfR-CA-19115	Vietnam	broiler, cecum	CG439	15.03.2018	Campylobacter jejuni	>16	>64	64	>64	>16	1	256	>1024		64	8	256		CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34729084	BfR-CA-19116	Vietnam	broiler, cecum	CG440	15.03.2018	Campylobacter jejuni	>16	>64	128	>64	>16	0,5	256	>1024		64	8	256		CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34729085	BfR-CA-19117	Vietnam	broiler, cecum	CG441	15.03.2018	Campylobacter jejuni	>16	>64	64	>64	>16	1	256	>1024		64		256		CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34729086	BfR-CA-19118	Vietnam	broiler, meat	CG442	15.03.2018	Campylobacter jejuni	>16	>64	64	>64	>16	1	256	>1024		64		256		CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34729087	BfR-CA-19119	Vietnam	broiler, meat	CG432	01.03.2018	Campylobacter coli	>16	>64	>128	>64	>16	>16	64	>1024	32	<=2	8	>512	>128	CIP, ERY, GEN, NAL, STR, TE	4-fold
PRJNA872862	SAMN34729088	BfR-CA-19120	Vietnam	broiler, meat	CG443	15.03.2018	Campylobacter jejuni	>16	>64	64	>64	>16	2	256	>1024		64		256		CIP, ERY, GEN, NAL, TET	4-fold
PRJNA872862	SAMN34729089	BfR-CA-19137	Germany	turkey, cecum		26.10.2020	Campylobacter coli	>16	>64	<=1	>64	0,5	1	>512	64	16					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729090	BfR-CA-19154	Germany	broiler, meat		05.10.2020	Campylobacter jejuni	8	>64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729091	BfR-CA-19155	Germany	broiler, meat		12.10.2020	Campylobacter coli	<=0,12	8	<=1	64	1	4								TET	1-fold
PRJNA872862	SAMN34729092	BfR-CA-19156	Germany	broiler, meat		13.10.2020	Campylobacter coli	>16	>64	<=1	<=0,5	1	2								CIP, NAL	1-fold
PRJNA872862	SAMN34729093	BfR-CA-19164	Germany	broiler, skin		10.11.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729094	BfR-CA-19165	Germany	broiler, cecum		10.11.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729095	BfR-CA-19166	Germany	broiler, meat		11.11.2020	Campylobacter coli	8	64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA872862	SAMN34729096	BfR-CA-19171	Germany	broiler, cecum		04.11.2020	Campylobacter coli	<=0,12	8	<=1	>64	0,5	2								TET	1-fold
PRJNA872862	SAMN34729097	BfR-CA-19180	Germany	broiler, skin		09.11.2020	Campylobacter jejuni	>16	>64	<=1	>64	0,5	>16	512	>1024	256					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729098	BfR-CA-19181	Germany	broiler, skin		09.11.2020	Campylobacter jejuni	16	>64	<=1	8	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729099	BfR-CA-19192	Germany	broiler, skin		18.11.2020	Campylobacter jejuni	>16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729100	BfR-CA-19204	Germany	broiler, skin		02.11.2020	Campylobacter jejuni	8	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729101	BfR-CA-19206	Germany	broiler, skin		02.11.2020	Campylobacter jejuni	>16	>64	2	>64	0,5	>16	256	>1024	128					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729102	BfR-CA-19207	Germany	broiler, skin		02.11.2020	Campylobacter jejuni	8	>64	<=1	>64	0,5	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729103	BfR-CA-19209	Germany	broiler, skin		02.11.2020	Campylobacter jejuni	8	>64	<=1	>64	0,5	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729104	BfR-CA-19211	Germany	broiler, skin		02.11.2020	Campylobacter jejuni	<=0,12	4	<=1	<=0,5	0,5	0,5								sensitive	sensitive
PRJNA872862	SAMN34729105	BfR-CA-19213	Germany	turkey, cecum		02.11.2020	Campylobacter coli	16	64	<=1	>64	0,5	2	512	>1024	32					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729106	BfR-CA-19217	Germany	broiler, cecum		10.11.2020	Campylobacter jejuni	>16	64	<=1	>64	0,25	>16	>512	>1024	256					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729107	BfR-CA-19218	Germany	broiler, cecum		10.11.2020	Campylobacter jejuni	>16	>64	<=1	>64	0,5	>16	>512	>1024	128					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729108	BfR-CA-19219	Germany	broiler, cecum		09.11.2020	Campylobacter jejuni	16	>64	<=1	64	0,5	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729109	BfR-CA-19226	Germany	turkey, cecum		09.11.2020	Campylobacter coli	16	64	<=1	>64	0,5	>16	512	>1024	256					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729110	BfR-CA-19231	Germany	broiler, meat		18.11.2020	Campylobacter coli	8	64	<=1	<=0,5	0,5	2								CIP, NAL	1-fold
PRJNA872862	SAMN34729111	BfR-CA-19235	Germany	broiler, cecum		16.11.2020	Campylobacter jejuni	8	>64	<=1	<=0,5	0,5	0,5								CIP, NAL	1-fold
PRJNA872862	SAMN34729112	BfR-CA-19239	Germany	turkey, cecum		13.11.2020	Campylobacter coli	16	>64	<=1	>64	0,25	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729113	BfR-CA-19241	Germany	turkey, cecum		14.11.2020	Campylobacter jejuni	8	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729114	BfR-CA-19250	Germany	broiler, skin		23.11.2020	Campylobacter jejuni	8	>64	<=1	8	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729115	BfR-CA-19254	Germany	broiler, meat		30.11.2020	Campylobacter coli	16	64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729116	BfR-CA-19256	Germany	broiler, cecum		17.11.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729117	BfR-CA-19257	Germany	broiler, cecum		23.11.2020	Campylobacter jejuni	<=0,12	4	<=1	<=0,5	0,25	0,5								sensitive	sensitive
PRJNA872862	SAMN34729118	BfR-CA-19259	Germany	broiler, cecum		23.11.2020	Campylobacter coli	>16	>64	<=1	>64	0,5	2								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729119	BfR-CA-19269	Germany	broiler, meat		18.11.2020	Campylobacter jejuni	8	>64	<=1	>64	0,25	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729120	BfR-CA-19273	Germany	turkey, meat		16.11.2020	Campylobacter jejuni	>16	>64	<=1	>64	0,25	>16	>512	>1024	256					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729121	BfR-CA-19275	Germany	broiler, skin		17.11.2020	Campylobacter jejuni	<=0,12	4	<=1	<=0,5	0,5	1								sensitive	sensitive
PRJNA872862	SAMN34729122	BfR-CA-19279	Germany	turkey, cecum		30.11.2020	Campylobacter coli	>16	>64	>128	>64	0,5	1		>1024	64	8		8		CIP, ERY, NAL, TET	3-fold
PRJNA872862	SAMN34729123	BfR-CA-19281	Germany	turkey, cecum		30.11.2020	Campylobacter coli	>16	>64	>128	>64	0,5	2		>1024	16	16		8		CIP, ERY, NAL, TET	3-fold
PRJNA872862	SAMN34729124	BfR-CA-19282	Germany	turkey, cecum		30.11.2020	Campylobacter jejuni	8	>64	<=1	<=0,5	1	4								CIP, NAL	1-fold
PRJNA872862	SAMN34729125	BfR-CA-19284	Germany	turkey, cecum		30.11.2020	Campylobacter coli	>16	>64	>128	>64	0,5	1		>1024	16			8		CIP, ERY, NAL, TET	3-fold
PRJNA872862	SAMN34729126	BfR-CA-19285	Germany	broiler, meat		24.11.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold

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PRJNA872862	SAMN34729127	BfR-CA-19286	Germany	poultry, meat		09.09.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	>16	256	>1024	256					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729128	BfR-CA-19287	Germany	broiler, meat		08.12.2020	Campylobacter jejuni	<=0,12	4	<=1	<=0,5	0,5	1								sensitive	sensitive
PRJNA872862	SAMN34729129	BfR-CA-19288	Germany	broiler, cecum		08.12.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729130	BfR-CA-19289	Germany	broiler, cecum		07.12.2020	Campylobacter coli	<=0,12	4	<=1	>64	0,5	2								TET	1-fold
PRJNA872862	SAMN34729131	BfR-CA-19290	Germany	broiler, skin		08.12.2020	Campylobacter coli	<=0,12	8	<=1	>64	0,5	2								TET	1-fold
PRJNA872862	SAMN34729132	BfR-CA-19295	Germany	broiler, skin		17.11.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729133	BfR-CA-19298	Germany	broiler, meat		29.10.2020	Campylobacter jejuni	4	>64	<=1	<=0,5	0,25	0,5								CIP, NAL	1-fold
PRJNA872862	SAMN34729134	BfR-CA-19301	Germany	broiler, meat		12.11.2020	Campylobacter jejuni	16	>64	<=1	>64	0,5	>16	256	>1024	256					CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729135	BfR-CA-19311	Germany	broiler, cecum		01.12.2020	Campylobacter jejuni	>16	64	<=1	>64	0,25	0,5	>512	>1024	256					CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729136	BfR-CA-19312	Germany	broiler, skin		16.11.2020	Campylobacter coli	16	64	<=1	>64	0,5	>16								CIP, NAL, STR, TET	3-fold
PRJNA872862	SAMN34729137	BfR-CA-19318	Germany	broiler, skin		02.11.2020	Campylobacter jejuni	<=0,12	8	<=1	32	0,5	1								TET	1-fold
PRJNA872862	SAMN34729138	BfR-CA-19320	Germany	broiler, meat		09.11.2020	Campylobacter jejuni	8	>64	<=1	<=0,5	0,5	1								CIP, NAL	1-fold
PRJNA872862	SAMN34729139	BfR-CA-19328	Germany	broiler, meat		04.11.2020	Campylobacter coli	<=0,12	4	<=1	64	0,5	2								TET	1-fold
PRJNA872862	SAMN34729140	BfR-CA-19329	Germany	broiler, meat		10.11.2020	Campylobacter jejuni	8	>64	<=1	>64	0,5	0,5								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729141	BfR-CA-19336	Germany	broiler, meat		12.01.2021	Campylobacter jejuni	8	>64	<=1	<=0,5	0,5	1								CIP, NAL	1-fold
PRJNA872862	SAMN34729142	BfR-CA-19362	Germany	broiler, meat		16.02.2021	Campylobacter jejuni	8	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold
PRJNA872862	SAMN34729143	BfR-CA-19364	Germany	broiler, meat		17.02.2021	Campylobacter jejuni	8	>64	<=1	>64	0,5	1								CIP, NAL, TET	2-fold

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Sample overview Samples highlighted in blue were additionally sequenced with Oxford Nanopore Technology	Resistance determinants as reported by AMRFinderPlus Genes not found are highlighted in red Genes that were falsely annotated are struck through (e.g. ~~tet(O)~~) Genes only partially found, but manually confirmed as full-length are in **bold**. Partial genes correctly found are annotated as such (e.g. aadE2_Δ1-415) aad9 falsely annotated as truncated due to frame-shifting in the poly-C tract are shown in **bold and blue**																															
	(Fluoro-)Quinolone	Macrolide/Lincosamide				Tetracycline Additional full-length or partial allelic variants of *tet* (O) genes identified through read mapping using Geneious Prime Software are illustrated as "+ tet(O)x".					Aminoglycoside										Phenicol					β-lactam	Streptothricin		
isolate No.	GyrA	23S	50S_L22	ermB	lnu(C)	tet(O)	tet(O/32/O)	tet(O/M/O)	tet(L)	tet(W)	aph(2'')-If	aac(6')-Ie/aph(2'')-Ia	aph(2'')-Ii	aadE	aadE-Cc	RpsL_K43R	RpsL_K88R	aph(3')-IIIa	aad9	catA9	catA13	cat-TC	optrA	fexA	blaOXA	sat4	amr genecount	amr count classes
BfR-CA-11843	GyrA_T86I					~~tet(O)-~~	~~tet(O/32/O)~~																		blaOXA-489		3	3
BfR-CA-11858	GyrA_T86I	23S_A2075G				tet(O)																			blaOXA-193		4	4
BfR-CA-11892	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-11893																											0	0
BfR-CA-11930	<=0,12					tet(O)																			blaOXA-193		2	1
BfR-CA-12208	GyrA_T86I		50S_L22_A103V			tet(O)												aph(3')-IIIa							blaOXA-193	sat4	6	6
BfR-CA-12658	GyrA_T86I	23S_A2075G				tet(O)																			blaOXA-595		5	4
BfR-CA-12887	GyrA_T86I																								blaOXA-61 family		2	2
BfR-CA-12897	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-12906	GyrA_T86I					~~tet(O)-~~	~~tet(O/32/O)~~																		blaOXA-489		3	3
BfR-CA-12973	<=0,12					tet(O)																			blaOXA-193		2	2
BfR-CA-13310	GyrA_T86I																								blaOXA-489		2	2
BfR-CA-13470	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-13526	GyrA_T86I	23S_A2075G				tet(O)									aadE-Cc										blaOXA-193		5	5
BfR-CA-13528	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-13537	GyrA_T86I					tet(O)																			blaOXA-489		3	3
BfR-CA-13895																									blaOXA-450		1	1
BfR-CA-13918	<=0,12																								blaOXA-625		1	1
BfR-CA-13919	GyrA_T86I																								blaOXA-594		2	2
BfR-CA-13937	GyrA_T86I																								blaOXA-193		2	2
BfR-CA-13938	GyrA_T86I		50S_L22_A103V															aph(3')-IIIa							blaOXA-193		4	4
BfR-CA-13939	GyrA_T86I					tet(O)																					2	2
BfR-CA-13953	GyrA_T86I					tet(O)												aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-13971	GyrA_T86I	23S_A2075G				~~tet(O)-~~	~~tet(O/32/O)~~																		blaOXA-489		4	4
BfR-CA-13985	GyrA_T86I					tet(O)								aadE3				aph(3')-IIIa							blaOXA-184	sat4	5	5
BfR-CA-14088	GyrA_T86I																								blaOXA-193		2	2
BfR-CA-14109																									blaOXA-193		1	1
BfR-CA-14180	GyrA_T86I					tet(O)																			blaOXA-460		3	3
BfR-CA-14181	GyrA_T86I																										1	1
BfR-CA-14216	GyrA_T86I					tet(O)																			blaOXA-489		3	3
BfR-CA-14226	GyrA_T86I					tet(O)																			blaOXA-584		3	3
BfR-CA-14373	GyrA_T86I					tet(O)																			blaOXA-184		3	3
BfR-CA-14430	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-14582	GyrA_T86I																										1	1
BfR-CA-14583	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-14610	GyrA_T86I																										1	1
BfR-CA-14731																									blaOXA-193		1	1
BfR-CA-14781	GyrA_T86I					tet(O)																			blaOXA-630		3	3
BfR-CA-14810														aadE3				aph(3')-IIIa							blaOXA-594	sat4	3	3
BfR-CA-14815	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-14825	GyrA_T86I																								blaOXA-594		2	2
BfR-CA-14833																									blaOXA-450		1	1
BfR-CA-14857	GyrA_T86I					tet(O)																			blaOXA-632		3	3
BfR-CA-14872	GyrA_T86I																								blaOXA-184		2	2
BfR-CA-14940																									blaOXA-193		1	1
BfR-CA-14943	GyrA_T86I																								blaOXA-594		2	2
BfR-CA-14958	GyrA_T86I					~~tet(O)-~~	~~tet(O/32/O)~~																		blaOXA-489		3	3
BfR-CA-14973	GyrA_T86I													aadE3				aph(3')-IIIa							blaOXA-61 family	sat4	4	4
BfR-CA-14974	GyrA_T86I																								blaOXA-193		2	2
BfR-CA-15005	GyrA_T86I																										1	1
BfR-CA-15035	<=0,12																								blaOXA-184 family		1	1
BfR-CA-15062	GyrA_T86I			erm(B)				tet(O/M/O)			aph(2'')-If			aadE1	aadE-Cc			aph(3')-IIIa	aad9		catA13				blaOXA-61 family		10	6
BfR-CA-15077	GyrA_T86I	23S_A2075G						tet(O/M/O)			aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-61 family		8	6
BfR-CA-15078	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)					aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-15080	GyrA_T86I		50S_L22_A103V			tet(O)																					3	3
BfR-CA-15124	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-61 family		4	4
BfR-CA-15245	<=0,12																								blaOXA-193		1	1
BfR-CA-15246	GyrA_T86I																								blaOXA-489		2	2
BfR-CA-15267										tet(W)															blaOXA-193		2	2
BfR-CA-15268	GyrA_T86I		50S_L22_A103V																						blaOXA-193		3	3
BfR-CA-15281	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-15282	<=0,12					tet(O)																			blaOXA-61		2	2
BfR-CA-15286	GyrA_T86I																								blaOXA-193		2	2
BfR-CA-15287	GyrA_T86I																								blaOXA-193		2	2
BfR-CA-15324	GyrA_T86I		50S_L22_A103V																						blaOXA-184		3	3
BfR-CA-15396	GyrA_T86I					tet(O)												aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-15403	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-15426	GyrA_T86I		50S_L22_A103V																						blaOXA-193		3	3
BfR-CA-15489	GyrA_T86I					tet(O)																			blaOXA-489		3	3
BfR-CA-15500	<=0,12					tet(O)																			blaOXA-184 family		2	2
BfR-CA-15532	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-15533	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-15629	GyrA_T86I					tet(O)																					2	2
BfR-CA-15630	GyrA_T86I					tet(O)												aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-15687	GyrA_T86I					**tet(O)**																			blaOXA-489		3	3
BfR-CA-15892	GyrA_T86I					tet(O)												aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-15913	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-15968	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-15978	GyrA_T86I					tet(O)																					2	2
BfR-CA-15985	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-15986	GyrA_T86I	23S_A2075G						**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa							blaOXA-193		7	5
BfR-CA-15987	GyrA_T86I			erm(B)		tet(O)								aadE1					aad9						blaOXA-193		5	4

9 Appendix

BfR-CA-15988	GyrA_T86I							**tet(O/M/O)** + tet(O)x					aadE1					aad9							blaOXA-193		5	4
BfR-CA-15989	GyrA_T86I			erm(B)				tet(O/M/O)	tet(L)	aph(2'')-If			aadE1				aph(3')-IIIa	aad9	catA9	catA13			fexA	blaOXA-193		12	6
BfR-CA-15990	GyrA_T86I	23S_A2075G						**tet(O/M/O)** + tet(O)x	tet(L)		aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9	catA9	catA13		optrA	fexA	blaOXA-489		13	7
BfR-CA-15991	GyrA_T86I	23S_A2075G						**tet(O/M/O) Taiwanes** tet(L)			aac(6')-Ie/aph(2'')-Ia		aadE1						catA9			optrA	fexA	blaOXA-193		10	7
BfR-CA-15992	GyrA_T86I							**tet(O/M/O)** + tet(O)x			aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa			catA13				blaOXA-61 family		7	5
BfR-CA-15993	GyrA_T86I					tet(O)																		blaOXA-460		3	3
BfR-CA-15994	GyrA_T86I			erm(B)				tet(O/M/O)		aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		9	6
BfR-CA-15995	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)																blaOXA-184		4	4
BfR-CA-15996	GyrA_T86I					tet(O)				aph(2'')-If					RpsL_K43R		aph(3')-IIIa	aad9		catA13				blaOXA-193		8	5
BfR-CA-15997	<=0.12					tet(O)																		blaOXA-193		2	2
BfR-CA-15998	GyrA_T86I							tet(O/M/O)							RpsL_K43R									blaOXA-193		4	4
BfR-CA-15999	GyrA_T86I	23S_A2075G	S0S_L22_A103V			tet(O)																		blaOXA-193		5	4
BfR-CA-16000	GyrA_T86I							tet(O/M/O)																blaOXA-460		3	3
BfR-CA-16001	GyrA_T86I		S0S_L22_A103V			tet(O)																		blaOXA-193		4	4
BfR-CA-16002	GyrA_T86I					tet(O)																		blaOXA-193		3	3
BfR-CA-16003	GyrA_T86I		S0S_L22_A103V			tet(O)																		blaOXA-594		4	4
BfR-CA-16004	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)																blaOXA-193		4	4
BfR-CA-16006	GyrA_T86I	23S_A2075G						tet(O/M/O)		aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		9	6
BfR-CA-16007	GyrA_T86I							tet(O/M/O) Taiwanese variant		aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-577		7	5
BfR-CA-16008	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)																blaOXA-193		4	4
BfR-CA-16010	GyrA_T86I							tet(O/M/O)					aadE1					aad9						blaOXA-193		5	4
BfR-CA-16011						tet(O)																		blaOXA-193		2	2
BfR-CA-16012	GyrA_T86I					tet(O)																		blaOXA-193		3	3
BfR-CA-16013	GyrA_T86I		S0S_L22_A103V					**tet(O/M/O)** + tet(O)x		aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-184		9	6
BfR-CA-16014	GyrA_T86I							tet(O/M/O) Taiwanese variant																blaOXA-193		3	3
BfR-CA-16015	GyrA_T86I		S0S_L22_A103V			tet(O)																		blaOXA-594		4	4
BfR-CA-16016	GyrA_T86I			erm(B)				tet(O/M/O)		aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		9	6
BfR-CA-16021	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)		aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-16022	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)																blaOXA-61 family		4	4
BfR-CA-16023	GyrA_T86I							**tet(O/M/O)** + tet(O)x			aac(6')-Ie/aph(2'')-Ia		aadE1					aad9						blaOXA-489		6	4
BfR-CA-16024	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)									aph(3')-IIIa							blaOXA-193		5	5
BfR-CA-16026	GyrA_T86I							tet(O/M/O)																blaOXA-193		3	3
BfR-CA-16027	GyrA_T86I	23S_A2075G						tet(O/M/O)		aph(2'')-If				aadE-Cc			aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-16028	GyrA_T86I							**tet(O/M/O)** + tet(O)x			aac(6')-Ie/aph(2'')-Ia		aadE1					aad9						blaOXA-489		6	4
BfR-CA-16029	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)		aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-16030	GyrA_T86I							tet(O/M/O)		aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		7	5
BfR-CA-16031	GyrA_T86I					tet(O)																		blaOXA-193		3	3
BfR-CA-16032	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)																blaOXA-184		4	4
BfR-CA-16033	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)		aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-16034	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)		aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-16035	GyrA_T86I					tet(O)																		blaOXA-193		3	3
BfR-CA-16036	GyrA_T86I	23S_A2075G				**tet(O)** + tet(O)x					aac(6')-Ie/aph(2'')-Ia		aadE1											blaOXA-193		6	5
BfR-CA-16039	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)																blaOXA-193		4	4
BfR-CA-16040	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x			aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-16041	GyrA_T86I							tet(O/M/O)																blaOXA-61 family		2	2
BfR-CA-16042	GyrA_T86I							tet(O/M/O)																blaOXA-460		3	3
BfR-CA-16043	GyrA_T86I		S0S_L22_A103V			tet(O)																		blaOXA-193		4	4
BfR-CA-16044	GyrA_T86I	23S_A2075G	S0S_L22_A103V					tet(O/M/O)		aph(2'')-If														blaOXA-193		6	5
BfR-CA-16045	GyrA_T86I					tet(O)									RpsL_K43R									blaOXA-193		4	4
BfR-CA-16046	GyrA_T86I			erm(B)				tet(O/M/O)		aph(2'')-If			aadE1	aadE-Cc			aph(3')-IIIa	aad9		catA13				blaOXA-193		10	6
BfR-CA-16048	GyrA_T86I							**tet(O/M/O)** + tet(O)x			aac(6')-Ie/aph(2'')-Ia		aadE1											blaOXA-193		5	4
BfR-CA-16052	GyrA_T86I	23S_A2075G						tet(O/M/O)		aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		9	6
BfR-CA-16053	GyrA_T86I	23S_A2075G						tet(O/M/O) Taiwanese	tet(L)	aph(2'')-If				aadE-Cc			aph(3')-IIIa	aad9	catA9	catA13		optrA	fexA	blaOXA-61 family		13	7
BfR-CA-16056	GyrA_T86I							tet(O/M/O)									aph(3')-IIIa							blaOXA-184		4	4
BfR-CA-16057	GyrA_T86I	23S_A2075G						tet(O/M/O)	tet(L)	aph(2'')-If					RpsL_K43R		aph(3')-IIIa	aad9	catA9	catA13		optrA	fexA	blaOXA-193		13	7
BfR-CA-16058	GyrA_T86I					tet(O)																		blaOXA-193		3	3
BfR-CA-16059	GyrA_T86I	23S_A2075G						tet(O/M/O)	tet(L)	aph(2'')-If					RpsL_K43R		aph(3')-IIIa	aad9	catA9	catA13		optrA	fexA	blaOXA-193		13	7
BfR-CA-16060	GyrA_T86I	23S_A2075G						tet(O/M/O)	tet(L)	aph(2'')-If					RpsL_K43R		aph(3')-IIIa	aad9	catA9	catA13		optrA	fexA	blaOXA-193		13	7
BfR-CA-16062	GyrA_T86I	23S_A2075G				~~**tet(O)**~~		tet(O/M/O) Shanghai variant + tet(O)x			aac(6')-Ie/aph(2'')-Ia		aadE1											blaOXA-193		6	5
BfR-CA-16063	GyrA_T86I		S0S_L22_A103V					tet(O/M/O) Taiwanese Variant																blaOXA-193		4	4
BfR-CA-16064	GyrA_T86I		S0S_L22_A103V			tet(O)																		blaOXA-193		4	4
BfR-CA-16065	GyrA_T86I							tet(O/M/O)																blaOXA-631		3	3
BfR-CA-16068	GyrA_T86I	23S_A2075G						tet(O/M/O)		aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-16069	GyrA_T86I	23S_A2075G						tet(O/M/O)		aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-16070	GyrA_T86V							tet(O/M/O)																blaOXA-193		3	3
BfR-CA-16071	GyrA_T86V							tet(O/M/O)																blaOXA-193		3	3
BfR-CA-16072	GyrA_T86I							tet(O/M/O)																blaOXA-193		3	3
BfR-CA-16073	GyrA_T86I		S0S_L22_A103V	erm(B)				**tet(O/M/O)** + tet(O)x		aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		10	6
BfR-CA-16077	GyrA_T86I				lnu(C)			**tet(O/M/O) Henan variant** + tet(O)x		aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-184 family		9	6
BfR-CA-16078	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)																blaOXA-193		4	4
BfR-CA-16079	GyrA_T86I				lnu(C)	~~tet(O)~~	tet(O/32/O)		tet(L)								aph(3')-IIIa		catA9			optrA	fexA	blaOXA-184 family		9	7
BfR-CA-16080	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)																blaOXA-193		4	4
BfR-CA-16081	GyrA_T86I				lnu(C)	~~tet(O)~~	tet(O/32/O)		tet(L)								aph(3')-IIIa		catA9			optrA	fexA	blaOXA-184 family		9	7
BfR-CA-16088	GyrA_T86I	23S_A2075G			lnu(C)			**tet(O/M/O) Henan variant** + tet(O)x		aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-184 family		10	7
BfR-CA-16089	GyrA_T86I	23S_A2075G			lnu(C)			**tet(O/M/O) Henan**		aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-184 family		10	7
BfR-CA-16090	GyrA_T86I	23S_A2075G				**tet(O)** + tet(O)x				aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-184 family		9	6
BfR-CA-16091	GyrA_T86I	23S_A2075G	S0S_L22_A103V					tet(O/M/O)																blaOXA-184		5	4
BfR-CA-16092	GyrA_T86I	23S_A2075G			lnu(C)			**variant** + tet(O)x		aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-184 family		10	7
BfR-CA-16095	GyrA_T86I	23S_A2075G				**tet(O)** + tet(O)x				aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-184 family		9	6
BfR-CA-16096	GyrA_T86I	23S_A2075G			lnu(C)			**tet(O/M/O) Henan**		aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-184 family		10	7
BfR-CA-16099	GyrA_T86I					tet(O)									RpsL_K43R									blaOXA-193		4	4
BfR-CA-16103	GyrA_T86I			erm(B)				tet(O/M/O)		aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		9	6
BfR-CA-16104	GyrA_T86I		S0S_L22_A103V					tet(O/M/O)																blaOXA-61 family		4	4
BfR-CA-16105	GyrA_T86I	23S_A2075G	S0S_L22_A103V			tet(O)																		blaOXA-489		5	4

BfR-CA-16106	GyrA_T86I			erm(B)				tet(O/M/O)			aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		9	6
BfR-CA-16107	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1, aadE2_Δ1-109				aph(3')-IIIa	aad9						blaOXA-193	sat4	10	6
BfR-CA-16108	GyrA_T86I		50S_L22_A103V					tet(O/M/O)			aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-16109	GyrA_T86I	23S_A2075G						tet(O/M/O)							aadE-Cc			aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-16110	GyrA_T86I			erm(B)		tet(O)								aadE1					aad9						blaOXA-193		6	5
BfR-CA-16111	GyrA_T86I	23S_A2075G						tet(O/M/O) Taiwanese	tet(L)		aph(2'')-If				aadE-Cc			aph(3')-IIIa	aad9	catA9	catA13		optrA	fexA	blaOXA-489		13	7
BfR-CA-16112	GyrA_T86V							tet(O/M/O)																	blaOXA-193		3	3
BfR-CA-16190	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-16191	GyrA_T86I	23S_A2075G						**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		9	6
BfR-CA-16193	GyrA_T86I					tet(O)					aph(2'')-If					RpsL_K43R		aph(3')-IIIa	aad9		catA13				blaOXA-193		8	5
BfR-CA-16196	GyrA_T86I	23S_A2075G						tet(O/M/O)	tet(L)		aph(2'')-If					RpsL_K43R		aph(3')-IIIa	aad9	catA9	catA13		optrA	fexA	blaOXA-193		13	7
BfR-CA-16197	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-16198	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-16201	GyrA_T86I		50S_L22_A103V	erm(B)		tet(O)					aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		10	6
BfR-CA-16203	GyrA_T86I		50S_L22_A103V	erm(B)		tet(O)					aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		10	6
BfR-CA-16204	GyrA_T86I							tet(O/M/O)			aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		7	5
BfR-CA-16207	GyrA_T86I							tet(O/M/O)																	blaOXA-193		3	3
BfR-CA-16208	GyrA_T86I		50S_L22_A103V			tet(O)												aph(3')-IIIa							blaOXA-61 family		5	5
BfR-CA-16209	GyrA_T86I							tet(O/M/O)																	blaOXA-193		3	3
BfR-CA-16210	GyrA_T86I							tet(O/M/O)																	blaOXA-184		3	3
BfR-CA-16211	GyrA_T86I							tet(O/M/O)			aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		7	5
BfR-CA-16215	GyrA_T86I							tet(O/M/O)																	blaOXA-193		3	3
BfR-CA-16216	GyrA_T86I		50S_L22_A103V																						blaOXA-193		3	3
BfR-CA-16217	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-61 family		4	4
BfR-CA-16220	GyrA_T86I							**tet(O/M/O)** + tet(O)x						aadE1, aadE2_Δ1-415				aph(3')-IIIa							blaOXA-184	sat4	7	5
BfR-CA-16221	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-16222	GyrA_T86I							tet(O/M/O)																	blaOXA-193		3	3
BfR-CA-16245	GyrA_T86I	23S_A2075G						**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1											blaOXA-193		6	5
BfR-CA-16246	GyrA_T86I							tet(O/M/O)																	blaOXA-631		3	3
BfR-CA-16247	GyrA_T86I							tet(O/M/O)																	blaOXA-61 family		3	3
BfR-CA-16248	GyrA_T86I					tet(O)x		tet(O/M/O)						aadE1					aad9						blaOXA-193		6	4
BfR-CA-16249	GyrA_T86I	23S_A2075G				**tet(O)**						aac(6')-Ie/aph(2'')-Ia		aadE1	aadE-Cc										blaOXA-489		7	5
BfR-CA-16251	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-16252	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-16253	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-16254	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-594		4	4
BfR-CA-16257	GyrA_T86I	23S_A2075G				tet(O)					aph(2'')-If							aph(3')-IIIa	aad9						blaOXA-193		7	5
BfR-CA-16258	GyrA_T86I		50S_L22_A103V	erm(B)		**tet(O)**								aadE1					aad9						blaOXA-193		7	5
BfR-CA-16259	GyrA_T86I			erm(B)				tet(O/M/O)			aph(2'')-If			aadE1				aph(3')-IIIa	aad9		**catA13_p.L180-K207delins180-262**				blaOXA-193		9	6
BfR-CA-16261	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x	tet(L)			aac(6')-Ie/aph(2'')-Ia		aadE1					aad9	catA9_G589A; p.A197T		~~cat-TC~~	optrA		blaOXA-193		10	7
BfR-CA-16264	GyrA_T86I	23S_A2075G				tet(O)					aph(2'')-If							aph(3')-IIIa	aad9						blaOXA-193		7	5
BfR-CA-16265	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-61 family		4	4
BfR-CA-16272	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-61 family		4	4
BfR-CA-16273	GyrA_T86I							tet(O/M/O)																	blaOXA-591		3	3
BfR-CA-16275	GyrA_T86I	23S_A2075G						tet(O/M/O)			aph(2'')-If					RpsL_K43R		aph(3')-IIIa	aad9		catA13				blaOXA-193		9	6
BfR-CA-16277	GyrA_T86I		50S_L22_A103V			tet(O)					aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-16278	GyrA_T86I		50S_L22_A103V			tet(O)					aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-16279	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-16280	GyrA_T86I							tet(O/M/O)																	blaOXA-184		3	3
BfR-CA-16281	GyrA_T86I							tet(O/M/O)																	blaOXA-193		3	3
BfR-CA-16282	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-16283	GyrA_T86I							tet(O/M/O)																	blaOXA-61 family		3	3
BfR-CA-16284	GyrA_T86I							tet(O/M/O)																	blaOXA-61 family		3	3
BfR-CA-16287	GyrA_T86I							tet(O/M/O)																	blaOXA-61 family		3	3
BfR-CA-16292	GyrA_T86I	23S_A2075G						**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		9	6
BfR-CA-16296	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-16297	GyrA_T86I			erm(B)				tet(O/M/O) + tet(O)x			aph(2'')-If	aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9						blaOXA-193		8	4
BfR-CA-16298	GyrA_T86V			erm(B)		tet(O)								aadE1					aad9						blaOXA-193		6	5
BfR-CA-16299	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-16300	GyrA_T86I			erm(B)		**tet(O)**								aadE1					aad9						blaOXA-193		6	5
BfR-CA-16303	GyrA_T86I							tet(O/M/O)																	blaOXA-61 family		3	3
BfR-CA-16305	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-184		4	4
BfR-CA-16307	GyrA_T86I							tet(O/M/O)																	blaOXA-61 family		3	3
BfR-CA-16309	GyrA_T86I		50S_L22_A103V			tet(O)																					3	3
BfR-CA-16311	GyrA_T86I							tet(O/M/O)			aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		7	5
BfR-CA-16329	GyrA_T86I							tet(O/M/O)																	blaOXA-61 family		3	3
BfR-CA-16330	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-16348	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-61 family		4	4
BfR-CA-16349	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-184		4	4
BfR-CA-16350	GyrA_T86I		50S_L22_A103V			tet(O)																					3	3
BfR-CA-16351	GyrA_T86I							tet(O/M/O)			aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		7	5
BfR-CA-16352	GyrA_T86I	23S_A2075G						tet(O/M/O)			aph(2'')-If					RpsL_K43R		aph(3')-IIIa	aad9		catA13				blaOXA-61 family		9	6
BfR-CA-16353	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9						blaOXA-193		8	5
BfR-CA-16354	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-16360	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-184		4	4
BfR-CA-16361	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-16362	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-16365	GyrA_T86I					tet(O)x		tet(O/M/O)						aadE1					aad9						blaOXA-193		6	4
BfR-CA-16370	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-16372	GyrA_T86I					**tet(O)** + tet(O)x						aac(6')-Ie/aph(2'')-Ia		aadE1											blaOXA-193		5	4
BfR-CA-16373	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-16374	GyrA_T86I							tet(O/M/O)																	blaOXA-193		3	3
BfR-CA-16375	GyrA_T86I		50S_L22_A103V			tet(O)																					3	3
BfR-CA-16376	GyrA_T86I							tet(O/M/O)			aph(2'')-If				aadE-Cc			aph(3')-IIIa	aad9		catA13				blaOXA-193		8	5
BfR-CA-16378	GyrA_T86I							tet(O/M/O)																	blaOXA-460		3	3
BfR-CA-16381	<=0,12							tet(O/M/O)																	blaOXA-193		2	2
BfR-CA-16383	GyrA_T86I		50S_L22_A103V			tet(O)																					3	3
BfR-CA-16385	GyrA_T86I		50S_L22_A103V			tet(O)					aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-16387	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-61 family		4	4
BfR-CA-16389	GyrA_T86I		50S_L22_A103V			tet(O)					aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-16491	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)																				3	3

BfR-CA-16671	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)									aadE-Cc										blaOXA-193		6	5
BfR-CA-16677	GyrA_T86I	23S_A2075G				tet(O)								aadE3				aph(3')-IIIa							blaOXA-184 family	sat4	6	6
BfR-CA-16708	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)								aadE3				aph(3')-IIIa							blaOXA-193	sat4	7	6
BfR-CA-16732	GyrA_T86I	23S_A2075G				tet(O)									aadE-Cc										blaOXA-193		5	5
BfR-CA-16737	GyrA_T86I						tet(O/32/O) + tet(O)x							aadE2_Δ1-415				aph(3')-IIIa							blaOXA-184 family	sat4	5	4
BfR-CA-16743	GyrA_T86I	23S_A2075G				tet(O)									aadE-Cc										blaOXA-489		5	5
BfR-CA-16767	GyrA_T86I					tet(O)												aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-16783	GyrA_T86I					tet(O)																			blaOXA-461		3	3
BfR-CA-16800	<=0,12																								blaOXA-193		1	1
BfR-CA-16822	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-16831	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)								aadE3				aph(3')-IIIa							blaOXA-193	sat4	7	6
BfR-CA-16834	GyrA_T86I		50S_L22_A103V			tet(O)								aadE2_Δ1-415				aph(3')-IIIa							blaOXA-193	sat4	7	6
BfR-CA-16888	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)																		blaOXA-595		4	4
BfR-CA-16930	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-16942	GyrA_T86I									tet(W)_G511A, G1736A; p.D171N, G579D															blaOXA-584		3	3
BfR-CA-17056	GyrA_T86I	23S_A2075G				tet(O)									aadE-Cc										blaOXA-193		5	5
BfR-CA-17071	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)								aadE1					aad9						blaOXA-193		7	5
BfR-CA-17078			50S_L22_A103V			~~tet(O)_G1475A; p.W492Ter~~	tet(O/32/O)_G1475A; p.W492Ter																				2	2
BfR-CA-17105	<=0,12					tet(O) x2																			blaOXA-630		3	2
BfR-CA-17107	GyrA_T86I					tet(O)																			blaOXA-184 family		3	3
BfR-CA-17110	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)																		blaOXA-489		4	4
BfR-CA-17153	GyrA_T86I																								blaOXA-61 family		2	2
BfR-CA-17156	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-17157	GyrA_T86I		50S_L22_A103V																						blaOXA-184		3	3
BfR-CA-17159	GyrA_T86I					tet(O)																			blaOXA-489		3	3
BfR-CA-17160	<=0,12		50S_L22_A103V																								1	1
BfR-CA-17230	GyrA_T86I	23S_A2075G				~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-489	sat4	6	6
BfR-CA-17247	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-17249	<=0,12					tet(O)																			blaOXA-489		2	2
BfR-CA-17288	GyrA_T86V					tet(O)																			blaOXA-193		3	3
BfR-CA-17356	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-17379	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-17395	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-17405	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	6	6
BfR-CA-17407	GyrA_T86I					tet(O)																					2	2
BfR-CA-17415	GyrA_T86I					~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-17424	GyrA_T86I																								blaOXA-449		2	2
BfR-CA-17549	GyrA_T86I					~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-17788	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	6	6
BfR-CA-17799	GyrA_T86I					tet(O)																			blaOXA-461		3	3
BfR-CA-17805	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-17822	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	6	6
BfR-CA-17824	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-17827	GyrA_T86I					tet(O)																			blaOXA-450		3	3
BfR-CA-17832	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)																		blaOXA-505		4	4
BfR-CA-17836	GyrA_T86I					~~tet(O)~~	tet(O/32/O)																		blaOXA-489		3	3
BfR-CA-17840	<=0,12																								blaOXA-193		1	1
BfR-CA-17860	GyrA_T86I					tet(O)																			blaOXA-460		3	3
BfR-CA-17861	GyrA_T86I	23S_A2075G				tet(O)									aadE-Cc_ΔA558; p.A187LfsTer188										blaOXA-193		5	5
BfR-CA-17869	<=0,12																								blaOXA-447		1	1
BfR-CA-17890	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	6	6
BfR-CA-17905	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-17949	<=0,12																										0	0
BfR-CA-17950	<=0,12																										0	0
BfR-CA-17951	<=0,12																								blaOXA-193		1	1
BfR-CA-17959	GyrA_T86I																								blaOXA-193		2	2
BfR-CA-17965	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)												aph(3')-IIIa							blaOXA-193	sat4	7	6
BfR-CA-17971	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-17991	<=0,12																								blaOXA-193		1	1
BfR-CA-17992	<=0,12																								blaOXA-193		1	1
BfR-CA-18000	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)												aph(3')-IIIa							blaOXA-193	sat4	7	6
BfR-CA-18036	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)												aph(3')-IIIa							blaOXA-193	sat4	7	6
BfR-CA-18037	GyrA_T86I					tet(O)																			blaOXA-460		3	3
BfR-CA-18038	GyrA_T86I																								blaOXA-61		2	2
BfR-CA-18039	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)																				3	3
BfR-CA-18045	<=0,12																								blaOXA-489		1	1
BfR-CA-18060	<=0,12					~~tet(O)~~	tet(O/32/O)																		blaOXA-193		2	2
BfR-CA-18061	GyrA_T86I					tet(O)																			blaOXA-460		3	3
BfR-CA-18064	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-18096	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-18102	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-489		4	4
BfR-CA-18104																									blaOXA-193		1	1
BfR-CA-18143	,12													aadE3				aph(3')-IIIa							blaOXA-184	sat4	3	3
BfR-CA-18167	GyrA_T86I		50S_L22_A103V																								2	2
BfR-CA-18197	<=0,12																										0	0
BfR-CA-18248	<=0,12																								blaOXA-193		1	1
BfR-CA-18264																									blaOXA-450		1	1
BfR-CA-18277	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	6	6
BfR-CA-18280	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	6	6
BfR-CA-18322																									blaOXA-61		1	1
BfR-CA-18353	GyrA_T86I									tet(W)_G511A, G1736A; p.D171N, G579D															blaOXA-584		3	3
BfR-CA-18372	<=0,12					tet(O)																			blaOXA-193		2	2
BfR-CA-18391	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)																		blaOXA-193		4	4
BfR-CA-18407	GyrA_T86I																	aph(3')-IIIa							blaOXA-193	sat4	4	4
BfR-CA-18408	GyrA_T86I					tet(O)												aph(3')-IIIa									3	3
BfR-CA-18548	GyrA_T86I		50S_L22_A103V				tet(O/32/O) + tet(O)x																		blaOXA-61 family		3	3
BfR-CA-18564	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	6	6
BfR-CA-18580	GyrA_T86I					tet(O)																			blaOXA-460		3	3
BfR-CA-18585	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	6	6
BfR-CA-18592	GyrA_T86I					tet(O)												aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-18665	GyrA_T86I													aadE3				aph(3')-IIIa							blaOXA-193	sat4	4	4
BfR-CA-18683	GyrA_T86I							tet(O/M/O)																	blaOXA-193		3	3

9 Appendix

BfR-CA-18684	GyrA_T86I							tet(O/M/O)			aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		7	5
BfR-CA-18685	GyrA_T86I	23S_A2075G						tet(O/M/O)							aadE-Cc			aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-18686	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-18687	GyrA_T86I		50S_L22_A103V	erm(B)				tet(O/M/O) + tet(O)x			aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		9	5
BfR-CA-18689	GyrA_T86I				lnu(C)			tet(O/M/O)	tet(L)		aph(2'')-If							aph(3')-IIIa		catA9			optrA	fexA	blaOXA-184		10	7
BfR-CA-18691	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-18694	GyrA_T86I	23S_A2075G						tet(O/M/O)							aadE-Cc			aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-18695	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-18717	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-18718	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-18719	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-18728	GyrA_T86I	23S_A2075G						tet(O/M/O) + tet(O)x	tet(L)		aph(2'')-If	aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9	catA9_G589A; p.A197T	catA13	cat-TC	optrA		blaOXA-193		12	7
BfR-CA-18729	GyrA_T86I							**tet(O/M/O)** + tet(O)x						aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		7	5
BfR-CA-18731	GyrA_T86I							**tet(O/M/O)** + tet(O)x	tet(L)		aph(2'')-If			aadE1				aph(3')-IIIa	aad9	catA9	catA13				blaOXA-184		10	5
BfR-CA-18732	GyrA_T86I					tet(O)x		tet(O/M/O)						aadE1					aad9						blaOXA-193		6	4
BfR-CA-18734	GyrA_T86I					**tet(O)** + tet(O)x					aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-184 family		8	5
BfR-CA-18735	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-184		4	4
BfR-CA-18736	GyrA_T86I		50S_L22_A103V	erm(B)		tet(O)					aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		10	6
BfR-CA-18737	GyrA_T86I	23S_A2075G						tet(O/M/O)	tet(L)		aph(2'')-If					RpsL_K43R		aph(3')-IIIa	aad9	catA9	catA13		optrA	fexA	blaOXA-193		13	7
BfR-CA-18738	GyrA_T86I	23S_A2075G						**tet(O/M/O)** + tet(O)x	tet(L)			aac(6')-Ie/aph(2'')-Ia		aadE1		RpsL_K43R		aph(3')-IIIa	aad9	catA9	catA13		optrA	fexA	blaOXA-193		14	7
BfR-CA-18743	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	6	6
BfR-CA-18748	GyrA_T86I					tet(O)												aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-18820	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-18821	GyrA_T86I	23S_A2075G						tet(O/M/O)	tet(L)		aph(2'')-If					RpsL_K43R		aph(3')-IIIa	aad9	catA9	catA13		optrA	fexA	blaOXA-193		13	7
BfR-CA-18822	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-18825	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-61 family		4	4
BfR-CA-18826	GyrA_T86I	23S_A2075G						tet(O/M/O)			aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-193		8	6
BfR-CA-18834	GyrA_T86I	23S_A2075G	50S_L22_A103V																						blaOXA-193		4	3
BfR-CA-18839	GyrA_T86I							tet(O/M/O)																	blaOXA-460		3	3
BfR-CA-18840	GyrA_T86I							tet(O/M/O)																	blaOXA-460		3	3
BfR-CA-18841	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-594		4	4
BfR-CA-18842	GyrA_T86I							**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1											blaOXA-193		5	4
BfR-CA-18843	GyrA_T86I	23S_A2075G						tet(O/M/O)	tet(L)		aph(2'')-If					RpsL_K43R		aph(3')-IIIa	aad9	catA9	catA13		optrA	fexA	blaOXA-193		13	7
BfR-CA-18844	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-18869	<=0,12																								blaOXA-193		1	1
BfR-CA-18879	GyrA_T86I		50S_L22_A103V	erm(B)		**tet(O)**		tet(O/M/O)			aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		10	6
BfR-CA-18880	GyrA_T86I					tet(O)											RpsL_K88R								blaOXA-193		4	4
BfR-CA-18881	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-18883	GyrA_T86I		50S_L22_A103V	erm(B)				**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9						blaOXA-193		9	5
BfR-CA-18884	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-18885	GyrA_T86I	23S_A2075G						tet(O/M/O)			aph(2'')-If			aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		9	6
BfR-CA-18886	GyrA_T86I			erm(B)		tet(O) + tet(O)x								aadE1					aad9								4	3
BfR-CA-18887	GyrA_T86I					**tet(O)** + tet(O)x						aac(6')-Ie/aph(2'')-Ia		aadE1											blaOXA-193		5	4
BfR-CA-18889	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-18891	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-18892	GyrA_T86I							tet(O/M/O) Taiwanese variant																	blaOXA-193		3	3
BfR-CA-18894	<=0,12																								blaOXA-461		1	1
BfR-CA-18901	GyrA_T86I																								blaOXA-193		2	2
BfR-CA-19025	GyrA_T86I							**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1					aad9						blaOXA-489		6	4
BfR-CA-19026	GyrA_T86I							**tet(O/M/O)** + tet(O)x						aadE1					aad9						blaOXA-193		5	4
BfR-CA-19027	GyrA_T86I	23S_A2075G						tet(O/M/O)			aph(2'')-If				aadE-Cc			aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-19028	GyrA_T86I							**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1					aad9						blaOXA-489		6	4
BfR-CA-19029	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-19030	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-19031	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-19032	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-19033	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1, aadE2_Δ1-109				aph(3')-IIIa	aad9						blaOXA-193	sat4	10	6
BfR-CA-19034	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-19035	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-594		4	4
BfR-CA-19036	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-19037	GyrA_T86I	23S_A2075G						tet(O/M/O) + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1				aph(3')-IIIa	aad9		catA13				blaOXA-193		8	5
BfR-CA-19038	GyrA_T86I	23S_A2075G						**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		aadE1											blaOXA-193		7	5
BfR-CA-19039	GyrA_T86V			erm(B)		tet(O)								aadE1					aad9						blaOXA-193		6	5
BfR-CA-19040	GyrA_T86I			erm(B)		tet(O)								aadE1					aad9						blaOXA-193		6	5
BfR-CA-19044	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)												aph(3')-IIIa							blaOXA-193	sat4	7	6
BfR-CA-19052	GyrA_T86I																								blaOXA-193		2	2
BfR-CA-19053	GyrA_T86I																								blaOXA-184 family		2	2
BfR-CA-19055	GyrA_T86I																								blaOXA-184 family		2	2
BfR-CA-19058	GyrA_T86I					tet(O)												aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-19082	GyrA_T86I					~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-19085	GyrA_T86I																								blaOXA-184 family		2	2
BfR-CA-19086	GyrA_T86V					tet(O)																			blaOXA-193		3	3
BfR-CA-19087	GyrA_T86I						tet(O/32/O) + tet(O)x						aph(2'')-Ii$_1$	aadE1	aadE-Cc			aph(3')-IIIa	aad9								5	2
BfR-CA-19088	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-19089	<=0,12																								blaOXA-193		1	1
BfR-CA-19092	GyrA_T86I		50S_L22_A103V																						blaOXA-193		3	3
BfR-CA-19102	GyrA_T86I		50S_L22_A103V					tet(O/M/O)																	blaOXA-193		4	4
BfR-CA-19104	GyrA_T86I					tet(O)x		tet(O/M/O) Taiwanese variant						aadE1													4	3
BfR-CA-19106	GyrA_T86I		50S_L22_A103V			tet(O)																					3	3
BfR-CA-19107	GyrA_T86I		50S_L22_A103V			tet(O)																					3	3
BfR-CA-19108	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)					aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-19110	GyrA_T86I		50S_L22_A103V			tet(O)																					3	3
BfR-CA-19111	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-19112	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		**aadE1**, aadE2_Δ1-109				aph(3')-IIIa	aad9						blaOXA-193	sat4	10	6
BfR-CA-19115	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)					aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-19116	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)					aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-19117	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)					aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-19118	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)					aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-19119	GyrA_T86I			erm(B)				**tet(O/M/O)** + tet(O)x				aac(6')-Ie/aph(2'')-Ia		**aadE1**, aadE2_Δ1-109				aph(3')-IIIa	aad9						blaOXA-193	sat4	10	6
BfR-CA-19120	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)					aph(2'')-If							aph(3')-IIIa	aad9		catA13				blaOXA-489		9	6
BfR-CA-19137	GyrA_T86I					tet(O)												aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-19154	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-184 family		4	4

BfR-CA-19155	<=0,12					tet(O)																			blaOXA-193		2	2
BfR-CA-19156	GyrA_T86I																										1	1
BfR-CA-19164	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)																				3	3
BfR-CA-19165	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)																				3	3
BfR-CA-19166	GyrA_T86I																								blaOXA-579		2	2
BfR-CA-19171	<=0,12					tet(O)																			blaOXA-193		2	2
BfR-CA-19180	GyrA_T86I					~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-19181	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-19192	GyrA_T86I					tet(O)																			blaOXA-460		3	3
BfR-CA-19204	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-19206	GyrA_T86I					~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-19207	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-184 family		4	4
BfR-CA-19209	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-184 family		4	4
BfR-CA-19211	<=0,12																								blaOXA-448		1	1
BfR-CA-19213	GyrA_T86I					tet(O)												aph(3')-IIIa							blaOXA-489	sat4	5	5
BfR-CA-19217	GyrA_T86I					tet(O)								aadE3				aph(3')-IIIa							blaOXA-184 family	sat4	5	5
BfR-CA-19218	GyrA_T86I					~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	5	5
BfR-CA-19219	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-19226	GyrA_T86I					~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-489	sat4	5	5
BfR-CA-19231	GyrA_T86I		50S_L22_A103V																						blaOXA-193		3	3
BfR-CA-19235	GyrA_T86I		50S_L22_A103V																						blaOXA-184		3	3
BfR-CA-19239	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-193		4	4
BfR-CA-19241	GyrA_T86I					tet(O)																			blaOXA-461		3	3
BfR-CA-19250	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-19254	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-19256	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-19257	<=0,12																								blaOXA-452		1	1
BfR-CA-19259	GyrA_T86I		50S_L22_A103V			tet(O)																					3	3
BfR-CA-19269	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)																		blaOXA-595		4	4
BfR-CA-19273	GyrA_T86I					~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-184 family	sat4	5	5
BfR-CA-19275	<=0,12																								blaOXA-193		1	1
BfR-CA-19279	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)												aph(3')-IIIa							blaOXA-193	sat4	7	6
BfR-CA-19281	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)												aph(3')-IIIa							blaOXA-193	sat4	7	6
BfR-CA-19282	GyrA_T86I																								blaOXA-61		2	2
BfR-CA-19284	GyrA_T86I	23S_A2075G	50S_L22_A103V			tet(O)												aph(3')-IIIa							blaOXA-193	sat4	7	6
BfR-CA-19285	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-19286	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	6	6
BfR-CA-19287	<=0,12																										0	0
BfR-CA-19288	GyrA_T86I					tet(O)																			blaOXA-460		3	3
BfR-CA-19289	<=0,12					tet(O)																			blaOXA-489		2	2
BfR-CA-19290	<=0,12					tet(O)																			blaOXA-489		2	2
BfR-CA-19295	GyrA_T86I					tet(O)																			blaOXA-193		3	3
BfR-CA-19298	GyrA_T86I		50S_L22_A103V																						blaOXA-184		3	3
BfR-CA-19301	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)							aadE3				aph(3')-IIIa							blaOXA-193	sat4	6	6
BfR-CA-19311	GyrA_T86I					~~tet(O)~~	tet(O/32/O)							aadE2_Δ1-415				aph(3')-IIIa							blaOXA-184 family	sat4	6	5
BfR-CA-19312	GyrA_T86I					tet(O)									aadE-Cc												3	3
BfR-CA-19318	<=0,12		50S_L22_A103V			tet(O)																			blaOXA-184		3	3
BfR-CA-19320	GyrA_T86I		50S_L22_A103V																						blaOXA-184		3	3
BfR-CA-19328	<=0,12					tet(O)																			blaOXA-193		2	2
BfR-CA-19329	GyrA_T86I		50S_L22_A103V			tet(O)																			blaOXA-184 family		4	4
BfR-CA-19336	GyrA_T86I		50S_L22_A103V																						blaOXA-184		3	3
BfR-CA-19362	GyrA_T86I		50S_L22_A103V			tet(O)-	tet(O/32/O)																		blaOXA-193		4	4
BfR-CA-19364	GyrA_T86I		50S_L22_A103V			~~tet(O)~~	tet(O/32/O)																		blaOXA-193		4	4

9 Appendix

Sample overview Samples highlighted in blue were additionally sequenced with Oxford Nanopore Technology		**mobile AMR genes and putative plasmids as predicted by platon v1.6**						**Multi-Locus Sequence Typing (MLST)** new allele variants and ST-Types are highlighted in yellow								**Illumina Short-Read Sequencing overview and QC data**							
isolate No.	**amr count by mobility**	**plasmids contigs**	**plasmids cumulativelength**	**plasmids circular**	**plasmids mobilization elements**	**plasmids conjugation elements**	**Sum circ, mob, conj**	**ST**	**CC**	**aspA**	**glnA**	**gltA**	**glyA**	**pgm**	**tkt**	**uncA**	**Total length**	**coverage depth**	**number contigs**	**Read Fraction Majority**	**Library Preparation Kit**	**DNA extraction kit**	**NGS method**	**cycle number**
BfR-CA-11843	chromosome (3)	0	0	0	0	0	0	5150		292	66	30	82	113	206	17	1645861	97,5	66	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-11858	chromosome (4)	1	6302	0	1	0	1	7159	ST-828 complex	33	39	418	82	104	85	17	1664776	97,7	38	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-11892	chromosome (3)	0	0	0	0	0	0	1585	ST-828 complex	33	39	30	82	189	43	17	1682675	97,2	53	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-11893		0	0	0	0	0	0	1585	ST-828 complex	33	39	30	82	189	43	17	1685169	97,2	68	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-11930	chromosome (2)	0	0	0	0	0	0	1595	ST-828 complex	33	38	30	79	104	43	17	1684720	97,5	40	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-12208	chromosome (6)	1	5417	0	1	0	1	8053	ST-828 complex	33	39	30	79	113	625	17	1692385	97,2	66	0,93	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-12658	chromosome (5)	2	8696	0	1	0	1	832	ST-828 complex	33	39	30	79	113	43	17	1692031	96,8	46	0,95	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-12887	chromosome (2)	0	0	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1700507	97,1	45	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-12897	chromosome (3)	2	32454	0	2	10	12	1595	ST-828 complex	33	38	30	79	104	43	17	1801810	96,8	40	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-12906	chromosome (3)	0	0	0	0	0	0	8509		292	66	30	79	113	43	17	1651791	97,3	38	0,95	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-12973	chromosome (2)	0	0	0	0	0	0	1595	ST-828 complex	33	38	30	79	104	43	17	1683652	97,4	24	0,92	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-13310	chromosome (2)	0	0	0	0	0	0	5150		292	66	30	82	113	206	17	1636608	97,3	52	0,95	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-13470	chromosome (4)	0	0	0	0	0	0	3018	ST-828 complex	33	39	30	79	188	43	17	1707966	97,1	43	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-13526	chromosome (5)	1	30564	0	1	10	11	872	ST-828 complex	33	39	30	82	113	44	17	1734510	97,4	53	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-13528	chromosome (3)	0	0	0	0	0	0	1055	ST-828 complex	33	39	30	82	104	47	17	1695006	97,9	31	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-13537	chromosome (3)	1	29421	0	1	10	11	829	ST-828 complex	33	39	30	82	113	43	17	1750236	92,9	114	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-13895	chromosome (1)	0	0	0	0	0	0	5439		114	406	103	140	459	164	79	1736539	94,9	40	0,75	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-13918	chromosome (1)	0	0	0	0	0	0	1003	ST-45 complex	8	7	4	4	125	7	1	1620744	99,8	20	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-13919	chromosome (2)	0	0	0	0	0	0	4148		114	195	103	140	459	164	79	1734346	93,4	43	0,75	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-13937	chromosome (2)	0	0	0	0	0	0	1519	ST-21 complex	8	1	5	3	2	1	1	1649010	84,6	29	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-13938	chromosome (4)	0	0	0	0	0	0	3018	ST-828 complex	33	39	30	79	188	43	17	1732290	71,2	29	0,94	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-13939	chromosome (2)	0	0	0	0	0	0	607	ST-607 complex	8	2	5	53	11	3	1	1794954	92,5	40	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-13953	chromosome (5)	1	6963	1	0	0	1	10183		114	110	30	140	104	625	79	1762543	94,7	25	0,72	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-13971	chromosome (4)	5	71302	1	2	16	19	8509		292	66	30	79	113	43	17	1808400	94,7	68	0,93	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-13985	chromosome (5)	3	12866	0	1	0	1	4754		37	61	57	64	519	430	23	1805268	95,4	109	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14088	chromosome (2)	0	0	0	0	0	0	48	ST-48 complex	2	4	1	2	7	1	5	1644285	98,5	18	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14109	chromosome (1)	0	0	0	0	0	0	45	ST-45 complex	4	7	10	4	1	7	1	1645767	101,1	17	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14180	chromosome (3)	0	0	0	0	0	0	354	ST-354 complex	8	10	2	2	11	12	6	1703363	93,1	17	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14181	chromosome (1)	0	0	0	0	0	0	2066	ST-52 complex	9	10	5	10	22	3	6	1747434	95,2	44	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14216	chromosome (3)	0	0	0	0	0	0	10049		292	66	30	79	113	47	17	1649723	80	41	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-14226	chromosome (3)	0	0	0	0	0	0	10184		114	110	103	140	1041	164	342	1738033	94,3	45	0,75	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14373	chromosome (3)	0	0	0	0	0	0	977	ST-1034 complex	22	61	4	64	74	25	23	1691214	95,5	73	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-14430	chromosome (2);plasmid (1)	1	41863	0	1	6	7	44	ST-21 complex	8	1	6	3	2	1	1	1667778	96,8	33	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14582	chromosome (1)	1	13935	1	0	0	1	830	ST-828 complex	33	39	30	79	104	47	17	1656703	92,5	46	0,95	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14583	chromosome (3)	0	0	0	0	0	0	1055	ST-828 complex	33	39	30	82	104	47	17	1696609	77,9	21	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-14610	chromosome (1)	2	13706	1	1	0	2	1586	ST-828 complex	33	176	30	82	113	43	17	1693819	96,7	88	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14731	chromosome (1)	1	5506	1	0	0	1	10185		265	195	103	140	113	164	79	1725152	81,3	21	0,79	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14781	chromosome (3)	0	0	0	0	0	0	7000		7	21	2	62	525	48	1	1704481	91,5	29	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14810	chromosome (3)	1	3405	1	0	0	1	10186		541	195	30	140	1041	164	79	1754842	93,5	45	0,74	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14815	chromosome (3)	1	25179	1	1	10	12	1595	ST-828 complex	33	38	30	79	104	43	17	1767921	84,3	28	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-14825	chromosome (2)	1	3588	1	0	0	1	4148		114	195	103	140	459	164	79	1734756	91,4	34	0,73	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14833	chromosome (1)	1	5517	1	0	0	1	5439		114	406	103	140	459	164	79	1735954	90,6	33	0,74	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14857	chromosome (3)	2	13243	0	0	0	0	2368		22	28	4	28	363	99	35	1748928	79,4	62	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14872	chromosome (2)	0	0	0	0	0	0	905		2	15	4	3	154	25	35	1623935	93,2	35	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14940	chromosome (1)	0	0	0	0	0	0	267	ST-283 complex	4	7	40	4	42	51	1	1597079	90,3	16	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-14943	chromosome (2)	1	3605	1	0	0	1	4148		114	195	103	140	459	164	79	1747482	89,2	35	0,77	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14958	chromosome (3)	0	0	0	0	0	0	5150		292	66	30	82	113	206	17	1682809	86,6	34	0,95	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-14973	chromosome (4)	0	0	0	0	0	0	10187		2	195	103	140	459	164	79	1783879	93,1	88	0,74	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-14974	chromosome (2)	1	4704	1	0	0	1	11858	ST-1150 complex	103	110	30	140	188	99	17	1705768	68,2	24	0,78	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-15005	chromosome (1)	0	0	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1703192	91,5	51	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-15035	chromosome (1)	1	43026	0	1	6	7	5203		2	15	4	28	20	34	35	1651264	58,3	26	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-15062	chromosome (10)	0	0	0	0	0	0	5695		303	39	30	79	113	47	17	1677243	98,3	37	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-15077	chromosome (8)	0	0	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1742658	89	29	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-15078	chromosome (8);plasmid (1)	2	50589	2	1	6	9	11990		2	114	12	2	2	894	6	1688187	96,1	24	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-15080	chromosome (3)	5	43368	0	1	6	7	11991	ST-460 complex	24	30	2	2	1197	59	6	1750655	95,7	57	1,00	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-15124	chromosome (4)	1	1127	1	0	0	1	832	ST-828 complex	33	39	30	79	113	43	17	1663034	41,6	116	0,94	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 251
BfR-CA-15245	chromosome (1)	0	0	0	0	0	0	45	ST-45 complex	4	7	10	4	1	7	1	1609974	102,2	32	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-15246	chromosome (2)	0	0	0	0	0	0	2823		55	172	21	49	125	48	51	1621126	86,4	30	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-15267	chromosome (2)	0	0	0	0	0	0	5903	ST-1150 complex	2	195	103	140	188	164	79	1737894	102,1	39	0,68	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq	2 x 151
BfR-CA-15268	chromosome (3)	0	0	0	0	0	0	1595	ST-828 complex	33	38	30	79	104	43	17	1684203	97,7	45	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-15281	chromosome (4)	0	0	0	0	0	0	832	ST-828 complex	33	39	30	79	113	43	17	1688106	95	32	0,93	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-15282	chromosome (1);plasmid (1)	1	44953	1	1	6	8	48	ST-48 complex	2	4	1	2	7	1	5	1691145	96,7	19	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-15286	chromosome (2)	0	0	0	0	0	0	9168	ST-828 complex	33	38	30	82	918	43	17	1733945	91,8	38	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-15287	chromosome (2)	0	0	0	0	0	0	9168	ST-828 complex	33	38	30	82	918	43	17	1734707	97,6	33	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-15324	chromosome (3)	0	0	0	0	0	0	3628	ST-443 complex	7	17	2	337	23	3	12	1673576	99,5	20	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq	2 x 151
BfR-CA-15396	chromosome (5)	1	6833	1	0	0	1	10183		114	110	30	140	104	625	79	1763778	99,2	19	0,71	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301

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BfR-CA-15403	chromosome (4)	1	5543	0	1	0	1	832	ST-828 complex	33	39	30	79	113	43	17	1743626	82,7	29	0,84	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-15426	chromosome (3)	0	0	0	0	0	0	1595	ST-828 complex	33	38	30	79	104	43	17	1680091	85,9	25	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-15489	chromosome (3)	0	0	0	0	0	0	10190	ST-828 complex	33	39	30	79	104	35	670	1730176	85,5	39	0,88	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-15500	chromosome (2)	4	13931	0	0	0	0	905		2	15	4	3	154	25	35	1702965	96,8	47	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq	2 x 151
BfR-CA-15532	chromosome (3)	0	0	0	0	0	0	3926	ST-21 complex	2	2	12	3	2	1	5	1658043	89,2	25	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-15533	chromosome (3)	0	0	0	0	0	0	1595	ST-828 complex	33	38	30	79	104	43	17	1658800	97,5	26	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq	2 x 151
BfR-CA-15629	chromosome (2)	1	26872	1	1	10	12	3016	ST-828 complex	33	39	103	79	104	35	17	1732393	85,4	31	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-15630	chromosome (5)	0	0	0	0	0	0	10183		114	110	30	140	104	625	79	1759614	102,6	31	0,71	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq	2 x 151
BfR-CA-15687	chromosome (3)	1	42602	0	1	6	7	10049		292	66	30	79	113	47	17	1736253	91,8	41	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 149
BfR-CA-15892	chromosome (5)	0	0	0	0	0	0	10183		114	110	30	140	104	625	79	1770276	84,2	443	0,66	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 149
BfR-CA-15913	chromosome (3)	1	27120	1	1	10	12	1595	ST-828 complex	33	38	30	79	104	43	17	1767715	83,3	42	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-15969	chromosome (4)	1	5543	0	1	0	1	832	ST-828 complex	33	39	30	79	113	43	17	1739479	85,1	23	0,90	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-15978	chromosome (2)	0	0	0	0	0	0	825	ST-828 complex	33	39	30	82	113	47	17	1660644	83	33	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 301
BfR-CA-15985	chromosome (3)	1	3701	0	0	0	0	8920		9	2	2	10	11	253	147	1739716	97,5	119	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-15986	chromosome (7)	1	39258	1	1	6	8	11994	ST-828 complex	33	176	30	82	1198	43	17	1699972	98,5	32	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-15987	chromosome (5)	3	23389	0	1	10	11	860	ST-828 complex	33	39	30	79	113	47	17	1737477	98,3	32	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-15988	chromosome (5)	1	38986	0	1	6	7	3119	ST-828 complex	33	39	30	82	188	47	17	1739357	103,3	68	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-15989	chromosome (12)	0	0	0	0	0	0	3753	ST-828 complex	33	176	30	82	104	43	17	1714244	99	27	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-15990	chromosome (13)	3	40135	0	1	6	7	860	ST-828 complex	33	39	30	79	113	47	17	1754549	104,1	74	0,94	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-15991	chromosome (10)	0	0	0	0	0	0	829	ST-828 complex	33	39	30	82	113	43	17	1668403	97,3	46	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-15992	chromosome (7)	4	42057	0	1	6	7	9867	ST-828 complex	33	491	30	82	113	43	17	1745071	97,3	80	0,93	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-15993	chromosome (3)	1	3952	0	0	0	0	1723	ST-354 complex	8	17	2	2	11	12	6	1700597	97,7	51	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-15994	chromosome (9)	0	0	0	0	0	0	3753	ST-828 complex	33	176	30	82	104	43	17	1708486	96,2	16	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-15995	chromosome (3);plasmid (1)	2	44205	2	1	6	9	5799	ST-443 complex	7	2	2	15	23	3	12	1675983	95,8	28	1,00	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-15996	chromosome (8)	0	0	0	0	0	0	7280		406	114	2	2	2	3	147	1681172	98,9	25	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-15997	chromosome (2)	2	7713	0	0	0	0	5229		8	2	2	212	10	253	147	1777563	97,4	127	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-15998	chromosome (4)	3	9341	0	0	0	0	5229		8	2	2	212	10	253	147	1768992	97,2	109	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-15999	chromosome (4);plasmid (1)	1	50476	0	1	6	7	11851		7	114	12	2	2	676	6	1683341	99,1	15	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16000	chromosome (3)	0	0	0	0	0	0	11999	ST-354 complex	8	812	2	2	11	12	6	1700252	98,4	37	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16001	chromosome (4)	3	10538	0	0	0	0	4395	ST-353 complex	24	17	1	2	11	3	6	1791477	98,9	42	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16002	chromosome (2);plasmid (1)	1	39835	1	1	6	8	4831		166	2	1	10	151	3	1	1826018	98,1	60	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16003	chromosome (4)	0	0	0	0	0	0	9649	ST-464 complex	24	2	2	2	10	3	629	1709998	98,3	57	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16004	chromosome (3);plasmid (1)	7	48676	0	1	6	7	9131	ST-460 complex	24	30	2	2	11	716	6	1790494	98,5	50	1,00	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16006	chromosome (9)	0	0	0	0	0	0	829	ST-828 complex	33	39	30	82	113	43	17	1761239	94,8	44	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16007	chromosome (6);plasmid (1)	1	43331	0	1	6	7	11870	ST-354 complex	8	364	2	2	11	12	6	1645840	99,7	36	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16008	chromosome (3);plasmid (1)	4	47864	0	1	6	7	11852	ST-574 complex	9	30	2	2	11	3	3	1738828	98,3	47	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16010	chromosome (5)	0	0	0	0	0	0	966	ST-828 complex	33	39	30	79	112	47	17	1709102	98,2	45	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16011	chromosome (2)	0	0	0	0	0	0	11864		9	17	5	10	23	3	3	1.776.183	97,2	35	0,987	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16012	chromosome (3)	1	2645	0	0	0	0	8920		9	2	2	10	11	253	147	1.734.619	96,1	184	0,985	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16013	chromosome (9)	1	4390	0	1	0	1	11859		22	15	4	64	777	3	35	1.602.663	96,9	46	0,936	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16014	chromosome (2);plasmid (1)	1	43491	0	1	6	7	11878	ST-354 complex	8	3	2	2	11	12	6	1.637.237	99,3	34	0,988	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16015	chromosome (4)	1	2564	0	0	0	0	9649	ST-464 complex	24	2	2	2	10	3	629	1.741.845	97,2	78	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16016	chromosome (9)	0	0	0	0	0	0	3753	ST-828 complex	33	176	30	82	104	43	17	1710925	85,1	33	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16021	chromosome (7);plasmid (1)	1	46291	0	1	5	6	7268	ST-464 complex	7	2	358	2	188	3	1	1764944	98,3	56	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16022	chromosome (4)	0	0	0	0	0	0	4108	ST-464 complex	24	2	2	2	11	3	1	1695926	78,7	77	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16023	chromosome (6)	0	0	0	0	0	0	829	ST-828 complex	33	39	30	82	113	43	17	1658652	97,9	56	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16024	chromosome (5)	3	11289	0	0	0	0	1919	ST-52 complex	9	2	2	10	10	3	5	1.772.252	96,8	138	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16026	chromosome (3)	0	0	0	0	0	0	3930		7	78	42	4	11	12	8	1619741	98,1	23	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16027	chromosome (9)	0	0	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1696026	92,9	19	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16028	chromosome (6)	0	0	0	0	0	0	829	ST-828 complex	33	39	30	82	113	43	17	1658640	98	55	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16029	chromosome (7);plasmid (1)	2	45256	0	1	6	7	7433	ST-353 complex	7	17	358	2	22	3	1	1761229	97,5	72	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16030	chromosome (7)	2	5817	0	0	0	0	5229		8	2	2	212	10	253	147	1824454	93,4	86	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16031	chromosome (3)	1	44085	0	1	6	7	11989		166	2	1	10	11	3	733	1.843.896	96,8	68	0,989	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16032	chromosome (3);plasmid (1)	2	44206	2	1	6	9	9762	ST-443 complex	7	2	2	15	982	3	12	1685013	90,2	21	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16033	chromosome (7);plasmid (1)	1	42534	0	1	6	7	7433	ST-353 complex	7	17	358	2	22	3	1	1.762.997	96,8	56	0,991	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16034	chromosome (7);plasmid (1)	1	42564	0	1	6	7	7433	ST-353 complex	7	17	358	2	22	3	1	1.763.130	96,2	56	0,991	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16035	chromosome (3)	0	0	0	0	0	0	11861		166	1	1	10	151	3	1	1782244	92,9	33	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16036	chromosome (6)	1	27995	1	1	10	12	11863	ST-828 complex	32	39	30	544	112	43	17	1684183	96,2	47	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16039	chromosome (4)	0	0	0	0	0	0	2895	ST-574 complex	9	53	5	10	11	3	3	1.696.019	97,1	39	0,991	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16040	chromosome (8);plasmid (1)	1	2126	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1.712.289	96,2	117	0,962	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16041	chromosome (2)	1	20473	0	0	0	0	6175	ST-21 complex	2	1	5	10	608	1	5	1.738.619	96,3	36	0,989	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16042	chromosome (3)	0	0	0	0	0	0	354	ST-354 complex	8	10	2	2	11	12	6	1.702.271	97,2	38	0,987	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16043	chromosome (4)	1	2441	1	0	0	1	9943		7	2	5	10	13	408	1	1737779	87,6	67	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16044	chromosome (6)	0	0	0	0	0	0	11851		7	114	12	2	2	676	6	1648210	93,5	13	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16045	chromosome (4)	0	0	0	0	0	0	7280		406	114	2	2	2	3	147	1656609	99,9	25	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16046	chromosome (8);plasmid (2)	2	43460	1	1	6	8	11993	ST-828 complex	353	176	30	82	1199	43	17	1814331	91,8	47	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16048	chromosome (5)	0	0	0	0	0	0	829	ST-828 complex	33	39	30	82	113	43	17	1.702.901	96,8	39	0,962	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16052	chromosome (9)	1	1017	1	0	0	1	1586	ST-828 complex	33	176	30	82	113	43	17	1699959	98,6	46	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16053	chromosome (13)	0	0	0	0	0	0	1055	ST-828 complex	33	39	30	82	104	47	17	1.742.692	105,4	44	0,966	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16056	chromosome (4)	1	1048	0	0	0	0	11849		37	490	5	64	694	3	412	1646050	95,2	44	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16057	chromosome (13)	1	39305	1	1	6	8	10873		33	284	30	79	113	47	17	1763872	91,8	47	0,93	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201

9 Appendix

BfR-CA-16058	chromosome (3)	1	1909	0	0	0	0	8920		9	2	2	10	11	253	147	1731585	86	163	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16059	chromosome (13)	2	39436	0	1	6	7	10873		33	284	30	79	113	47	17	1765524	98	50	0,92	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16060	chromosome (13)	1	39269	0	1	6	7	10873		33	284	30	79	113	47	17	1.764.096	96,4	51	0,945	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16062	chromosome (6)	2	4815	0	0	0	0	9976	ST-828 complex	33	39	631	544	104	43	17	1719703	90,2	59	0,86	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16063	chromosome (3);plasmid (1)	1	43607	0	1	6	7	653	ST-354 complex	9	17	2	2	11	12	6	1.651.130	97,6	36	0,993	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16064	chromosome (4)	0	0	0	0	0	0	9943		7	2	5	10	13	408	1	1.698.584	96,3	67	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16065	chromosome (3)	0	0	0	0	0	0	11866	ST-354 complex	9	10	2	37	11	12	6	1.654.034	96,8	29	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16068	chromosome (8)	0	0	0	0	0	0	10873		33	284	30	79	113	47	17	1735989	98,2	29	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16069	chromosome (8)	0	0	0	0	0	0	10873		33	284	30	79	113	47	17	1732226	97,6	51	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16070	chromosome (3)	0	0	0	0	0	0	3611	ST-607 complex	9	2	5	333	11	3	1	1782900	101,8	52	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16071	chromosome (3)	0	0	0	0	0	0	3611	ST-607 complex	9	2	5	333	11	3	1	1789401	98,7	43	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16072	chromosome (3)	2	7035	0	0	0	0	5229		8	2	2	212	10	253	147	1763746	72,9	117	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16073	chromosome (10)	0	0	0	0	0	0	4360	ST-1150 complex	103	110	30	140	210	164	79	1762769	90	54	0,74	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16077	chromosome (8);plasmid (1)	1	1082	0	0	0	0	8089		8	455	291	668	127	24	19	1598879	97,5	42	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16078	chromosome (3);plasmid (1)	3	46747	0	1	6	7	1213	ST-460 complex	7	30	2	2	89	59	6	1.830.802	97,3	52	0,996	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16079	chromosome (9)	0	0	0	0	0	0	9560		8	455	291	494	127	24	35	1.611.117	96,9	35	0,953	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16080	chromosome (3);plasmid (1)	4	49386	0	1	6	7	1213	ST-460 complex	7	30	2	2	89	59	6	1.831.519	97,1	46	0,996	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16081	chromosome (9)	0	0	0	0	0	0	9560		8	455	291	494	127	24	35	1653984	96,8	20	0,94	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16088	chromosome (9);plasmid (1)	1	1082	0	0	0	0	8089		8	455	291	668	127	24	19	1636320	97	43	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16089	chromosome (9);plasmid (1)	1	1082	0	0	0	0	8089		8	455	291	668	127	24	19	1635976	97,5	38	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16090	chromosome (9)	0	0	0	0	0	0	7476		37	476	4	28	682	25	147	1675797	98,2	57	0,94	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16091	chromosome (5)	1	4410	1	1	0	2	8887		22	15	4	735	777	3	35	1591057	98,5	35	0,93	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16092	chromosome (9);plasmid (1)	1	1082	0	0	0	0	8089		8	455	291	668	127	24	19	1637736	98,1	35	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16095	chromosome (9)	0	0	0	0	0	0	7476		37	476	4	28	682	25	147	1.676.203	96,3	55	0,942	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16096	chromosome (9);plasmid (1)	1	1082	0	0	0	0	8089		8	455	291	668	127	24	19	1.636.365	96,7	35	0,953	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16099	chromosome (4)	0	0	0	0	0	0	7280		406	114	2	2	2	3	147	1654493	98,7	26	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16103	chromosome (9)	0	0	0	0	0	0	3753	ST-828 complex	33	176	30	82	104	43	17	1703929	97,6	37	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16104	chromosome (4)	0	0	0	0	0	0	4108	ST-464 complex	24	2	2	2	11	3	1	1693316	91,9	66	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16105	chromosome (4);plasmid (1)	1	50457	0	1	6	7	11851		7	114	12	2	2	676	6	1681038	98,4	27	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16106	chromosome (9)	0	0	0	0	0	0	3753	ST-828 complex	33	176	30	82	104	43	17	1704957	98,2	32	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16107	chromosome (10)	1	30063	1	1	10	12	1145	ST-828 complex	33	39	30	82	104	44	17	1698312	98,5	54	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16108	chromosome (7);plasmid (1)	2	45256	0	1	6	7	7433	ST-353 complex	7	17	358	2	22	3	1	1761790	91,8	73	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16109	chromosome (8)	1	47200	0	1	6	7	829	ST-828 complex	33	39	30	82	113	43	17	1764366	97,9	42	0,94	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16110	chromosome (6)	0	0	0	0	0	0	5507	ST-828 complex	33	39	30	79	112	64	17	1655341	98,8	25	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16111	chromosome (13)	0	0	0	0	0	0	3020	ST-828 complex	33	176	30	79	113	43	17	1.668.361	96,9	46	0,976	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16112	chromosome (3)	0	0	0	0	0	0	3611	ST-607 complex	9	2	5	333	11	3	1	1787311	97	66	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16190	chromosome (4)	0	0	0	0	0	0	6607		9	22	173	146	11	3	6	1.743.017	97,6	26	0,992	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16191	chromosome (9)	2	34194	1	1	10	12	829	ST-828 complex	33	39	30	82	113	43	17	1816813	97,3	61	0,92	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16193	chromosome (8)	0	0	0	0	0	0	7280		406	114	2	2	2	3	147	1672985	97,4	35	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16196	chromosome (13)	0	0	0	0	0	0	10873		33	284	30	79	113	47	17	1725376	98,2	40	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16197	chromosome (3)	1	3479	0	0	0	0	8920		9	2	2	10	11	253	147	1.734.834	95,9	177	0,984	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16198	chromosome (3);plasmid (1)	8	53960	0	1	6	7	113	ST-460 complex	24	30	2	2	11	3	6	1.744.409	97,1	76	0,993	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16201	chromosome (10)	0	0	0	0	0	0	1121	ST-1150 complex	103	110	30	140	188	164	79	1723247	98	34	0,75	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 149
BfR-CA-16203	chromosome (10)	0	0	0	0	0	0	1121	ST-1150 complex	103	110	30	140	188	164	79	1720584	97,6	45	0,72	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16204	chromosome (7)	1	2636	0	0	0	0	2328		8	2	2	212	153	253	147	1761160	96,3	153	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16207	chromosome (2);plasmid (1)	1	47704	0	1	6	7	161	ST-52 complex	14	21	2	10	86	3	6	1.750.596	97,5	59	0,991	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16208	chromosome (5)	2	9733	0	0	0	0	4258		2	2	2	10	10	59	5	1.777.718	96,7	137	0,989	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16209	chromosome (2);plasmid (1)	1	47587	0	1	6	7	161	ST-52 complex	14	21	2	10	86	3	6	1.750.337	97,3	65	0,992	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16210	chromosome (3)	0	0	0	0	0	0	11867		2	10	292	26	127	25	541	1589588	94,6	24	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16211	chromosome (7)	1	70890	0	2	16	18	11993	ST-828 complex	33	176	30	82	1200	43	17	1.758.639	96,9	72	0,962	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16215	chromosome (3)	1	3299	0	0	0	0	2328		8	2	2	212	153	253	147	1.748.154	59,8	142	0,979	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16216	chromosome (3)	0	0	0	0	0	0	1121	ST-1150 complex	103	110	30	140	188	164	79	1.741.266	97	43	0,717	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16217	chromosome (3);plasmid (1)	1	44066	0	1	6	7	11997	ST-353 complex	7	2	5	2	1201	395	6	1.741.525	88,4	38	0,993	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16220	chromosome (4);plasmid (3)	1	3345	0	0	0	0	11996		597	2	292	26	90	3	541	1612401	97,1	52	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16221	chromosome (8);plasmid (1)	1	2126	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1712053	95,9	116	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16222	chromosome (3)	3	7277	0	0	0	0	2328		8	2	2	212	153	253	147	1761599	90,7	126	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16245	chromosome (6)	0	0	0	0	0	0	829	ST-828 complex	33	39	30	82	113	43	17	1741237	98,3	33	0,94	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16246	chromosome (2);plasmid (1)	1	48348	0	1	6	7	161	ST-52 complex	14	21	2	10	86	3	6	1757969	71,5	84	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16247	chromosome (3)	1	21095	0	0	0	0	6175	ST-21 complex	2	1	5	10	608	1	5	1745794	97,6	39	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16248	chromosome (6)	1	2541	0	0	0	0	11865		8	2	2	212	2	253	147	1788687	84,8	115	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16249	chromosome (7)	1	3416	1	0	0	1	1016	ST-828 complex	33	38	30	82	118	43	17	1652922	98,1	40	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16251	chromosome (3)	0	0	0	0	0	0	12240		625	17	5	10	350	3	3	1801707	98,4	71	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16252	chromosome (3)	0	0	0	0	0	0	2274		9	17	5	10	350	3	3	1802746	90,3	68	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16253	chromosome (9)	0	0	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1711813	107,3	106	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16254	chromosome (4)	1	2564	0	0	0	0	9649	ST-464 complex	24	2	2	2	10	3	629	1741693	97,9	79	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16257	chromosome (7)	1	1194	0	0	0	0	899	ST-828 complex	33	39	30	82	113	35	17	1676471	98,4	39	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16258	chromosome (7)	1	6667	1	0	0	1	1121	ST-1150 complex	103	110	30	140	188	164	79	1713929	97,8	35	0,74	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16259	chromosome (9)	0	0	0	0	0	0	3753	ST-828 complex	33	176	30	82	104	43	17	1706398	96,8	26	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16261	chromosome (9);plasmid (1)	1	3849	0	0	0	0	5191	ST-828 complex	33	176	30	82	113	47	17	1662462	97,5	42	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149

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BfR-CA-16264	chromosome (7)	0	0	0	0	0	0	899	ST-828 complex	33	39	30	82	113	35	17	1.673.657	66,7	45	0,967	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16265	chromosome (4)	0	0	0	0	0	0	4108	ST-464 complex	24	2	2	2	11	3	1	1.704.538	97,1	76	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16272	chromosome (4)	2	5676	0	0	0	0	8906	ST-52 complex	9	2	2	10	13	3	5	1.773.827	96,1	115	0,989	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16273	chromosome (3)	0	0	0	0	0	0	298	ST-21 complex	9	1	12	3	2	1	5	1.668.745	97	29	0,996	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16275	chromosome (9)	0	0	0	0	0	0	11874		33	284	30	79	113	35	17	1654348	93,9	14	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16277	chromosome (7);plasmid (1)	1	45480	0	1	6	7	7433	ST-353 complex	7	17	358	2	22	3	1	1832181	96,8	115	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16278	chromosome (7);plasmid (1)	1	46010	0	1	6	7	7433	ST-353 complex	7	17	358	2	22	3	1	1833057	96,2	106	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16279	chromosome (3)	1	2574	0	0	0	0	11988		14	21	2	918	86	3	6	1.712.646	96,5	55	0,991	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16280	chromosome (2);plasmid (1)	1	44708	0	1	6	7	6497	ST-353 complex	7	17	371	10	151	3	6	1.758.269	97,4	43	0,987	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16281	chromosome (3)	1	3179	0	0	0	0	2328		8	2	2	212	153	253	147	1.749.132	96,2	145	0,977	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16282	chromosome (4)	3	34519	0	1	10	11	854	ST-828 complex	33	38	30	82	104	43	17	1812432	97,4	64	0,91	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16283	chromosome (3)	0	0	0	0	0	0	354	ST-354 complex	8	10	2	2	11	12	6	1.728.807	99	35	0,987	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16284	chromosome (3)	0	0	0	0	0	0	354	ST-354 complex	8	10	2	2	11	12	6	1.728.411	97,4	31	0,987	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16287	chromosome (3)	0	0	0	0	0	0	354	ST-354 complex	8	10	2	2	11	12	6	1733248	92,5	16	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16292	chromosome (9)	0	0	0	0	0	0	1625	ST-828 complex	33	39	30	82	104	47	139	1679673	82,8	29	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16296	chromosome (3);plasmid (1)	1	47418	1	1	6	8	6494	ST-353 complex	2	114	5	2	2	3	6	1671064	94,4	22	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16297	chromosome (8)	0	0	0	0	0	0	5511	ST-828 complex	33	39	30	82	113	47	139	1678420	97,6	50	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16298	chromosome (6)	1	27721	0	1	10	11	5507	ST-828 complex	33	39	30	79	112	64	17	1.759.430	97,1	31	0,966	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16299	chromosome (3)	0	0	0	0	0	0	2274		9	17	5	10	350	3	3	1.825.735	69,3	75	0,984	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16300	chromosome (6)	3	70472	0	2	16	18	860	ST-828 complex	33	39	30	79	113	47	17	1.772.771	82,5	45	0,944	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16303	chromosome (3)	0	0	0	0	0	0	354	ST-354 complex	8	10	2	2	11	12	6	1727607	97,6	35	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16305	chromosome (3);plasmid (1)	1	38963	0	1	6	7	2865	ST-443 complex	199	17	2	15	23	3	12	1667703	97,9	35	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16307	chromosome (3)	0	0	0	0	0	0	354	ST-354 complex	8	10	2	2	11	12	6	1732991	92,4	19	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16309	chromosome (2);plasmid (1)	4	47124	0	1	6	7	11991	ST-460 complex	24	30	2	2	1197	59	6	1744675	98,1	63	1,00	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16311	chromosome (7)	0	0	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1753278	98,2	51	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16329	chromosome (3)	0	0	0	0	0	0	354	ST-354 complex	8	10	2	2	11	12	6	1.729.342	82,8	32	0,987	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16330	chromosome (3)	2	6051	0	0	0	0	8920		9	2	2	10	11	253	147	1.766.449	95,7	125	0,988	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16348	chromosome (4)	1	2718	0	0	0	0	464	ST-464 complex	24	2	2	2	10	3	1	1.711.422	97,2	80	0,989	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16349	chromosome (3);plasmid (1)	1	44056	0	1	6	7	5799	ST-443 complex	7	2	2	15	23	3	12	1.667.942	95,9	40	0,995	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16350	chromosome (2);plasmid (1)	4	47124	0	1	6	7	11991	ST-460 complex	24	30	2	2	1197	59	6	1.745.671	98,5	58	0,995	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16351	chromosome (7)	0	0	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1753742	97,2	46	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16352	chromosome (9)	1	30465	1	1	10	12	830	ST-828 complex	33	39	30	79	104	47	17	1740104	98,4	39	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16353	chromosome (8)	1	2390	0	0	0	0	1145	ST-828 complex	33	39	30	82	104	44	17	1758290	107,9	46	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16354	chromosome (4)	1	4182	0	0	0	0	2172	ST-828 complex	32	38	30	82	104	35	17	1.785.342	96,8	60	0,925	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16360	chromosome (4)	1	4390	0	1	0	1	8887		22	15	4	735	777	3	35	1.583.500	97,9	32	0,853	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16361	chromosome (4)	0	0	0	0	0	0	4108	ST-464 complex	24	2	2	2	11	3	1	1.707.756	96,4	47	0,991	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16362	chromosome (3);plasmid (1)	1	47255	0	1	6	7	8986		9	114	16	10	13	3	3	1.723.110	67,8	23	0,973	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16365	chromosome (6)	2	6407	0	0	0	0	2328		8	2	2	212	153	253	147	1777971	96,6	149	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16370	chromosome (3)	0	0	0	0	0	0	11855		166	1	1	10	22	3	1	1.739.625	99,7	46	0,991	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16372	chromosome (5)	4	66632	0	2	16	18	1586	ST-828 complex	33	176	30	82	113	43	17	1788292	98,7	74	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16373	chromosome (3);plasmid (1)	1	45481	0	1	6	7	7433	ST-353 complex	7	17	358	2	22	3	1	1797101	87,2	142	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16374	chromosome (3)	0	0	0	0	0	0	8881		8	2	2	212	894	253	147	1812499	55,9	165	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16375	chromosome (2);plasmid (1)	4	47124	0	1	6	7	11991	ST-460 complex	24	30	2	2	1197	59	6	1750401	82,6	60	1,00	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16376	chromosome (8)	0	0	0	0	0	0	830	ST-828 complex	33	39	30	79	104	47	17	1691791	99,3	35	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16378	chromosome (3)	0	0	0	0	0	0	354	ST-354 complex	8	10	2	2	11	12	6	1.703.732	86,3	33	0,987	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16381	chromosome (2)	0	0	0	0	0	0	12002		9	17	690	10	350	3	3	1.800.964	97,2	56	0,986	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16383	chromosome (3)	0	0	0	0	0	0	11998	ST-353 complex	7	2	691	2	10	3	6	1.762.344	73,4	40	0,994	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16385	chromosome (7);plasmid (1)	1	46010	0	1	6	7	10320	ST-353 complex	7	17	52	2	22	3	1	1769994	97,8	64	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16387	chromosome (4)	0	0	0	0	0	0	4108	ST-464 complex	24	2	2	2	11	3	1	1.746.118	72,3	67	0,991	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16389	chromosome (7);plasmid (1)	1	45480	0	1	6	7	7433	ST-353 complex	7	17	358	2	22	3	1	1809604	95,3	67	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-16491	chromosome (3)	0	0	0	0	0	0	400	ST-353 complex	8	17	5	2	10	59	6	1748895	77,3	72	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16671	chromosome (6)	0	0	0	0	0	0	829	ST-828 complex	33	39	30	82	113	43	17	1700973	92,7	26	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16677	chromosome (6)	0	0	0	0	0	0	10628		37	61	12	64	363	24	23	1636718	95,9	22	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16708	chromosome (7)	9	77777	3	3	16	22	11876	ST-828 complex	33	39	30	82	104	29	17	1892552	94,6	86	0,89	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16732	chromosome (5)	1	30596	1	1	10	12	872	ST-828 complex	33	39	30	82	113	44	17	1787726	90,1	46	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16737	chromosome (2);plasmid (3)	2	47910	0	1	6	7	5973	ST-1034 complex	22	15	4	64	360	25	23	1803358	100,2	56	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq	2 x 151
BfR-CA-16743	chromosome (5)	3	71605	3	2	16	21	1109		33	38	30	173	104	35	68	1768339	101,5	44	0,95	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-16767	chromosome (5)	0	0	0	0	0	0	10183		114	110	30	140	104	625	79	1758632	101	35	0,71	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq	2 x 151
BfR-CA-16783	chromosome (3)	0	0	0	0	0	0	2254	ST-257 complex	8	2	4	62	4	5	6	1717873	82,9	29	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16800	chromosome (1)	0	0	0	0	0	0	19	ST-21 complex	2	1	5	3	2	1	5	1664765	87,2	26	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16822	chromosome (4)	1	6092	0	1	0	1	832	ST-828 complex	33	39	30	79	113	43	17	1687930	96,1	30	0,93	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq	2 x 151
BfR-CA-16831	chromosome (7)	6	74999	1	3	16	20	11876	ST-828 complex	33	39	30	82	104	29	17	1939348	55,6	91	0,87	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16834	chromosome (4);plasmid (3)	3	54333	0	2	6	8	832	ST-828 complex	33	39	30	79	113	43	17	1735505	98,9	42	0,93	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq	2 x 151
BfR-CA-16888	chromosome (4)	0	0	0	0	0	0	464	ST-464 complex	24	2	2	2	10	3	1	1735704	90,4	38	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16930	chromosome (3)	1	20459	0	0	0	0	6175	ST-21 complex	2	1	5	10	608	1	5	1762658	82,9	48	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-16942	chromosome (3)	1	10795	1	0	0	1	10194		114	195	103	140	1040	164	120	1770515	103,5	36	0,73	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq	2 x 151
BfR-CA-17056	chromosome (5)	1	30570	0	1	10	11	872	ST-828 complex	33	39	30	82	113	44	17	1736316	82,3	35	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17071	chromosome (7)	1	27130	1	1	10	12	860	ST-828 complex	33	39	30	79	113	47	17	1850010	100	27	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-17078	chromosome (1);plasmid (1)	9	72223	1	2	15	18	10195	ST-828 complex	33	39	65	140	189	43	17	1736895	95,1	52	0,93	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq	2 x 151
BfR-CA-17105	chromosome (3)	0	0	0	0	0	0	1399		8	21	2	62	67	48	6	1722739	87,5	38	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17107	chromosome (3)	1	6784	1	1	0	2	5973	ST-1034 complex	22	15	4	64	360	25	23	1759375	66,6	51	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17110	chromosome (4)	1	30592	1	1	10	12	1769	ST-828 complex	33	176	30	115	113	43	17	1770648	95	32	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq	2 x 151

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BfR-CA-17153	chromosome (2)	0	0	0	0	0	0	4148		114	195	103	140	459	164	79	1739887	72,5	30	0,76	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17156	chromosome (2);plasmid (1)	1	41864	0	1	6	7	44	ST-21 complex	8	1	6	3	2	1	1	1704948	81,1	35	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17157	chromosome (3)	0	0	0	0	0	0	51	ST-443 complex	7	17	2	15	23	3	12	1634272	71,4	25	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17159	chromosome (3)	1	37482	0	1	1	2	855	ST-828 complex	33	39	30	79	104	35	17	1689414	62,7	29	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17160	chromosome (1)	2	8381	0	0	0	0	670	ST-460 complex	77	30	2	2	89	59	6	1747204	79,9	42	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17230	chromosome (6)	5	67868	1	2	15	18	8509		292	66	30	79	113	43	17	1812144	95,2	48	0,93	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-17247	chromosome (3)	1	5536	1	0	0	1	8858		103	195	30	140	104	164	79	1772593	98,8	22	0,78	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17249	chromosome (2)	0	0	0	0	0	0	855	ST-828 complex	33	39	30	79	104	35	17	1653247	94,4	20	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-17288	chromosome (3)	0	0	0	0	0	0	2274		9	17	5	10	350	3	3	1785248	96,2	32	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-17356	chromosome (3)	0	0	0	0	0	0	50	ST-21 complex	2	1	12	3	2	1	5	1689392	95,9	46	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-17379	chromosome (2);plasmid (1)	1	41899	1	1	5	7	44	ST-21 complex	8	1	6	3	2	1	1	1648372	98,5	30	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17395	chromosome (3)	1	20491	0	0	0	0	6175	ST-21 complex	2	1	5	10	608	1	5	1732952	98,8	32	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-17405	chromosome (6)	0	0	0	0	0	0	7355	ST-353 complex	8	17	5	2	10	59	23	1777906	97,7	54	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 149
BfR-CA-17407	chromosome (1);plasmid (1)	1	46278	1	1	6	8	356	ST-353 complex	14	17	5	2	11	3	6	1760725	99,8	24	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-17415	chromosome (5)	0	0	0	0	0	0	10025	ST-353 complex	2	17	5	2	23	59	6	1699779	94,8	36	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-17424	chromosome (2)	0	0	0	0	0	0	45	ST-45 complex	4	7	10	4	1	7	1	1662206	80	15	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 201
BfR-CA-17549	chromosome (5)	0	0	0	0	0	0	10025	ST-353 complex	2	17	5	2	23	59	6	1695815	66,5	33	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17788	chromosome (6)	0	0	0	0	0	0	7355	ST-353 complex	8	17	5	2	10	59	23	1778622	97,4	47	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-17799	chromosome (3)	0	0	0	0	0	0	2254	ST-257 complex	8	2	4	62	4	5	6	1691413	97,9	19	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-17805	chromosome (3)	1	20459	0	0	0	0	6175	ST-21 complex	2	1	5	10	608	1	5	1735898	98	39	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17822	chromosome (6)	0	0	0	0	0	0	7355	ST-353 complex	8	17	5	2	10	59	23	1778707	105,3	51	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-17824	chromosome (3)	1	20443	0	0	0	0	6175	ST-21 complex	2	1	5	10	608	1	5	1734257	98,4	43	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17827	chromosome (3)	2	8137	0	1	0	1	5439		114	406	103	140	459	164	79	1750166	97,8	51	0,68	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17832	chromosome (4)	0	0	0	0	0	0	464	ST-464 complex	24	2	2	2	10	3	1	1737544	98,1	94	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17836	chromosome (3)	0	0	0	0	0	0	5150		292	66	30	82	113	206	17	1634360	105,7	53	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17840	chromosome (1)	0	0	0	0	0	0	475	ST-48 complex	2	4	1	4	19	62	5	1669174	101,6	72	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17860	chromosome (3)	0	0	0	0	0	0	354	ST-354 complex	8	10	2	2	11	12	6	1737910	97,8	36	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-17861	chromosome (5)	1	30403	0	1	10	11	872	ST-828 complex	33	39	30	82	113	44	17	1740467	98,4	39	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17869	chromosome (1)	0	0	0	0	0	0	677	ST-677 complex	10	81	50	99	120	76	52	1661876	97,7	32	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-17890	chromosome (6)	0	0	0	0	0	0	7355	ST-353 complex	8	17	5	2	10	59	23	1778661	97,7	55	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-17905	chromosome (3)	1	25843	1	1	10	12	1595	ST-828 complex	33	38	30	79	104	43	17	1717792	97,7	18	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17949	<=0,12	0	0	0	0	0	0	8466		121	651	38	695	836	72	601	1580590	98,6	32	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17950	<=0,12	0	0	0	0	0	0	8466		121	651	38	695	836	72	601	1580591	98,3	27	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17951	chromosome (1)	2	11309	1	1	0	2	11857	ST-1150 complex	103	406	103	140	459	164	79	1746660	92	24	0,74	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17959	chromosome (2)	4	13245	0	0	0	0	11875		2	28	4	762	463	99	35	1702845	98	69	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17965	chromosome (7)	2	32431	1	2	10	13	8053	ST-828 complex	33	39	30	79	113	625	17	1713198	98,2	23	0,93	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17971	chromosome (3)	1	25825	0	1	10	11	1595	ST-828 complex	33	38	30	79	104	43	17	1716128	97,1	31	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17991	chromosome (1)	2	9857	1	0	2	2	11857	ST-1150 complex	103	406	103	140	459	164	79	1780220	95,8	69	0,80	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-17992	chromosome (1)	1	5555	0	1	0	1	11857	ST-1150 complex	103	406	103	140	459	164	79	1744015	98	46	0,68	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-18000	chromosome (7)	2	30376	0	2	9	11	8053	ST-828 complex	33	39	30	79	113	625	17	1708051	95,7	21	0,94	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-18036	chromosome (7)	2	32431	1	2	10	13	8053	ST-828 complex	33	39	30	79	113	625	17	1749688	98,9	27	0,92	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-18037	chromosome (3)	0	0	0	0	0	0	354	ST-354 complex	8	10	2	2	11	12	6	1768092	97,7	35	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18038	chromosome (2)	0	0	0	0	0	0	48	ST-48 complex	2	4	1	2	7	1	5	1639981	98,8	36	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-18039	chromosome (3)	0	0	0	0	0	0	400	ST-353 complex	8	17	5	2	10	59	6	1726316	47,9	41	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-18045	chromosome (1)	1	28757	0	1	10	11	855	ST-828 complex	33	39	30	79	104	35	17	1718962	96,6	53	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18060	chromosome (2)	1	37628	0	1	6	7	6089	ST-21 complex	2	1	12	3	2	226	5	1739221	98	45	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-18061	chromosome (3)	2	3918	2	0	0	2	354	ST-354 complex	8	10	2	2	11	12	6	1756451	105,8	63	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-18064	chromosome (3)	1	20419	0	0	0	0	6175	ST-21 complex	2	1	5	10	608	1	5	1732339	97,2	50	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18096	chromosome (4)	0	0	0	0	0	0	353	ST-353 complex	7	17	5	2	10	3	6	1804944	97,1	92	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18102	chromosome (4)	0	0	0	0	0	0	10190	ST-828 complex	33	39	30	79	104	35	670	1733360	99,1	37	0,83	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-18104	chromosome (1)	0	0	0	0	0	0	45	ST-45 complex	4	7	10	4	1	7	1	1654544	97,6	38	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18143	chromosome (3)	0	0	0	0	0	0	2663	ST-45 complex	4	7	10	3	1	7	1	1597462	97,6	27	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18167	chromosome (2)	1	2751	1	0	0	1	6657	ST-353 complex	7	112	5	2	10	3	6	1748781	96,9	64	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18197	<=0,12	0	0	0	0	0	0	45	ST-45 complex	4	7	10	4	1	7	1	1616297	97,6	24	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18248	chromosome (1)	0	0	0	0	0	0	267	ST-283 complex	4	7	40	4	42	51	1	1595995	99,3	28	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-18264	chromosome (1)	1	10895	1	0	0	1	5439		114	406	103	140	459	164	79	1746450	41,9	38	0,77	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-18277	chromosome (6)	0	0	0	0	0	0	7355	ST-353 complex	8	17	5	2	10	59	23	1782019	98,6	44	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-18280	chromosome (6)	0	0	0	0	0	0	7355	ST-353 complex	8	17	5	2	10	59	23	1789785	97,2	137	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18322	chromosome (1)	0	0	0	0	0	0	48	ST-48 complex	2	4	1	2	7	1	5	1641631	97,3	32	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18353	chromosome (3)	0	0	0	0	0	0	11854		103	195	103	140	1040	164	120	1783969	96,6	62	0,75	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 151
BfR-CA-18372	chromosome (2)	0	0	0	0	0	0	2123	ST-362 complex	1	2	42	4	2	25	8	1599931	97,6	32	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18391	chromosome (4)	0	0	0	0	0	0	464	ST-464 complex	24	2	2	2	10	3	1	1801072	96,8	147	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18407	chromosome (2);plasmid (2)	1	43124	0	1	6	7	305	ST-574 complex	9	53	2	10	11	3	3	1734431	98	42	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18408	chromosome (3)	0	0	0	0	0	0	832	ST-828 complex	33	39	30	79	113	43	17	1702724	97,3	20	0,95	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18548	chromosome (3)	1	39472	0	1	6	7	464	ST-464 complex	24	2	2	2	10	3	1	1769324	97,5	69	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18564	chromosome (6)	0	0	0	0	0	0	7355	ST-353 complex	8	17	5	2	10	59	23	1776196	97,4	47	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18580	chromosome (3)	0	0	0	0	0	0	2988	ST-354 complex	8	10	2	2	10	12	6	1771911	97,7	34	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18585	chromosome (6)	0	0	0	0	0	0	7355	ST-353 complex	8	17	5	2	10	59	23	1778361	98,1	60	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18592	chromosome (5)	0	0	0	0	0	0	10183		114	110	30	140	104	625	79	1761957	97,5	31	0,75	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18665	chromosome (4)	0	0	0	0	0	0	10025	ST-353 complex	2	17	5	2	23	59	6	1731581	97,8	53	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18683	chromosome (3)	0	0	0	0	0	0	4259	ST-354 complex	8	10	2	2	13	12	6	1.698.867	97,2	32	0,991	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18684	chromosome (7)	2	7812	0	0	0	0	5229		8	2	2	212	10	253	147	1.813.339	96,3	117	0,972	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18685	chromosome (8)	1	47208	0	1	6	7	829	ST-828 complex	33	39	30	82	113	43	17	1.760.174	97	56	0,944	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18686	chromosome (3);plasmid (1)	1	42682	0	1	6	7	5815	ST-353 complex	7	17	358	2	10	3	354	1.755.106	96,5	59	0,978	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18687	chromosome (9)	1	6669	1	0	0	1	1121	ST-1150 complex	103	110	30	140	188	164	79	1.760.229	96,5	38	0,75	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18689	chromosome (10)	0	0	0	0	0	0	11869		22	490	292	10	694	29	412	1610910	96,8	29	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18691	chromosome (3)	2	4645	0	0	0	0	9037	ST-353 complex	9	2	5	2	13	3	6	1.811.781	97	66	0,988	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18694	chromosome (8)	1	47208	0	1	6	7	829	ST-828 complex	33	39	30	82	113	43	17	1.760.042	96,7	57	0,952	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18695	chromosome (3);plasmid (1)	1	56984	0	1	6	7	1213	ST-460 complex	7	30	2	2	89	59	6	1.793.168	97,1	40	0,995	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149

9 Appendix

BfR-CA-18717	chromosome (4)	1	2564	0	0	0	0	464	ST-464 complex	24	2	2	2	10	3	1	1750138	98,6	67	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	MiSeq	2 x 151
BfR-CA-18718	chromosome (4)	0	0	0	0	0	0	1121	ST-1150 complex	103	110	30	140	188	164	79	1702205	97,1	28	0,74	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18719	chromosome (4)	0	0	0	0	0	0	4108	ST-464 complex	24	2	2	2	11	3	1	1780627	97,7	82	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18728	chromosome (11);plasmid (1)	2	8966	0	1	0	1	860	ST-828 complex	33	39	30	79	113	47	17	1.722.356	96,9	50	0,941	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18729	chromosome (7)	2	5720	0	0	0	0	11865		8	2	2	212	2	253	147	1.790.286	96,6	146	0,976	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18731	chromosome (9);plasmid (1)	2	2543	0	0	0	0	11872		363	17	292	48	694	24	541	1.591.274	97	72	0,957	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18732	chromosome (6)	2	6407	0	0	0	0	2328		8	2	2	212	153	253	147	1.777.578	96,5	142	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18734	chromosome (8)	0	0	0	0	0	0	11877		37	476	4	28	682	3	23	1.675.715	97,1	65	0,941	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18735	chromosome (3);plasmid (1)	1	44060	0	1	6	7	5799	ST-443 complex	2	2	2	15	23	3	12	1.677.127	89,9	33	0,995	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18736	chromosome (10)	1	6724	1	0	0	1	1121	ST-1150 complex	103	110	30	140	188	164	79	1.723.959	57,2	20	0,771	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18737	chromosome (13)	0	0	0	0	0	0	10873		33	284	30	79	113	47	17	1721858	97,1	53	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18738	chromosome (14)	0	0	0	0	0	0	860	ST-828 complex	33	39	30	79	113	47	17	1714634	93,2	40	0,94	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18743	chromosome (6)	1	27948	0	1	10	11	7355	ST-353 complex	8	17	5	2	10	59	23	1806515	97,6	48	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18748	chromosome (5)	0	0	0	0	0	0	10183		114	110	30	140	104	625	79	1753005	97,6	43	0,75	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18820	chromosome (4)	3	11511	0	0	0	0	1919	ST-52 complex	9	2	2	10	10	3	5	1764653	96,5	152	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18821	chromosome (13)	0	0	0	0	0	0	10873		33	284	30	79	113	47	17	1720989	97,5	63	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18822	chromosome (4)	3	6829	0	0	0	0	2172	ST-828 complex	32	38	30	82	104	35	17	1786500	97,4	62	0,91	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18825	chromosome (4)	2	5774	0	0	0	0	4258		2	2	2	10	10	59	5	1.772.635	85,5	134	0,988	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18826	chromosome (8)	0	0	0	0	0	0	10873		33	284	30	79	113	47	17	1.694.057	44,2	42	0,957	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18834	chromosome (4)	2	12650	1	1	0	2	832	ST-828 complex	33	39	30	79	113	43	17	1.757.129	85,2	26	0,927	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18839	chromosome (3)	1	3160	0	0	0	0	354	ST-354 complex	8	10	2	2	11	12	6	1702392	98,1	39	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18840	chromosome (3)	0	0	0	0	0	0	354	ST-354 complex	8	10	2	2	11	12	6	1701781	88,6	33	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18841	chromosome (4)	1	2564	0	0	0	0	9649	ST-464 complex	24	2	2	2	10	3	629	1701625	103,6	92	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18842	chromosome (5)	0	0	0	0	0	0	829	ST-828 complex	33	39	30	82	113	43	17	1.701.380	96,7	49	0,962	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18843	chromosome (13)	0	0	0	0	0	0	10873		33	284	30	79	113	47	17	1.724.012	91,5	47	0,955	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18844	chromosome (4)	0	0	0	0	0	0	4108	ST-464 complex	24	2	2	2	11	3	1	1.781.769	70,8	61	0,992	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18869	chromosome (1)	0	0	0	0	0	0	50	ST-21 complex	2	1	12	3	2	1	5	1709930	97,8	59	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18879	chromosome (10)	1	3416	1	0	0	1	4360	ST-1150 complex	103	110	30	140	210	164	79	1.764.476	71,8	35	0,766	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18880	chromosome (4)	0	0	0	0	0	0	1121	ST-1150 complex	103	110	30	140	188	164	79	1706833	95	25	0,81	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18881	chromosome (4)	0	0	0	0	0	0	4108	ST-464 complex	24	2	2	2	11	3	1	1739745	99,6	75	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18883	chromosome (9)	1	2509	1	0	0	1	6267	ST-828 complex	33	42	30	82	189	35	17	1.691.304	76,7	48	0,954	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18884	chromosome (4)	0	0	0	0	0	0	4108	ST-464 complex	24	2	2	2	11	3	1	1.748.304	88,2	59	0,994	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18885	chromosome (9)	1	26971	0	1	10	11	1586	ST-828 complex	33	176	30	82	113	43	17	1.765.192	99,3	49	0,961	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18886	chromosome (1);plasmid (3)	4	40135	3	2	10	15	860	ST-828 complex	33	39	30	79	113	47	17	1.743.220	100,3	68	0,957	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18887	chromosome (5)	0	0	0	0	0	0	11992	ST-828 complex	33	176	30	82	1203	43	17	1.749.655	98,9	43	0,969	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18889	chromosome (3)	0	0	0	0	0	0	11861		166	1	1	10	151	3	1	1739273	98	46	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18891	chromosome (3);plasmid (1)	2	52410	2	1	6	9	6493		7	2	6	10	465	37	1	1.732.881	93	47	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18892	chromosome (2);plasmid (1)	1	43531	0	1	6	7	11878	ST-354 complex	8	3	2	2	11	12	6	1.638.627	56,4	25	0,987	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18894	chromosome (1)	0	0	0	0	0	0	4800		275	84	5	10	119	178	26	1729875	96,8	50	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-18901	chromosome (2)	0	0	0	0	0	0	658	ST-658 complex	2	4	2	4	19	3	6	1656440	96,6	121	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19025	chromosome (6)	0	0	0	0	0	0	829	ST-828 complex	33	39	30	82	113	43	17	1658725	97,7	58	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19026	chromosome (5)	0	0	0	0	0	0	3119	ST-828 complex	33	39	30	82	188	47	17	1726041	97,7	50	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19027	chromosome (9)	0	0	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1.691.222	63	32	0,983	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19028	chromosome (6)	0	0	0	0	0	0	829	ST-828 complex	33	39	30	82	113	43	17	1.658.011	57	64	0,973	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19029	chromosome (8);plasmid (1)	1	2126	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1.711.039	96,3	121	0,962	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19030	chromosome (8);plasmid (1)	1	2126	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1.711.903	96,5	120	0,961	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19031	chromosome (8);plasmid (1)	1	2126	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1.712.442	96,7	118	0,961	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19032	chromosome (9)	0	0	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1709973	97,2	128	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19033	chromosome (10)	0	0	0	0	0	0	1145	ST-828 complex	33	39	30	82	104	44	17	1667999	97	55	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19034	chromosome (8);plasmid (1)	1	2126	0	0	0	0	1586	ST-828 complex	33	176	30	82	113	43	17	1.711.834	96,4	109	0,961	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19035	chromosome (4)	0	0	0	0	0	0	9649	ST-464 complex	24	2	2	2	10	3	629	1741924	97,8	74	0,99	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19036	chromosome (3);plasmid (1)	6	47257	0	1	6	7	9131	ST-460 complex	24	30	2	2	11	716	6	1750782	98,3	57	1,00	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19037	chromosome (8)	0	0	0	0	0	0	1625	ST-828 complex	33	39	30	82	104	47	139	1.676.481	97,5	40	0,962	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19038	chromosome (7)	0	0	0	0	0	0	1625	ST-828 complex	33	39	30	82	104	47	139	1.699.348	80,7	30	0,962	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19039	chromosome (6)	1	27721	0	1	10	11	5507	ST-828 complex	33	39	30	79	112	64	17	1.759.591	66,3	31	0,967	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19040	chromosome (3);plasmid (3)	3	72311	2	2	16	20	860	ST-828 complex	33	39	30	79	113	47	17	1768224	59,8	78	0,95	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19044	chromosome (7)	2	32371	0	2	10	12	8053	ST-828 complex	33	39	30	79	113	625	17	1712060	95	24	0,94	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19052	chromosome (2)	0	0	0	0	0	0	2274		9	17	5	10	350	3	3	1839057	95,5	148	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19053	chromosome (2)	0	0	0	0	0	0	11879	ST-433 complex	2	15	4	3	154	12	35	1588795	96,6	29	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19055	chromosome (2)	0	0	0	0	0	0	11879	ST-433 complex	2	15	4	3	154	12	35	1588426	96,2	33	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19058	chromosome (5)	0	0	0	0	0	0	10183		114	110	30	140	104	625	79	1758880	97,7	39	0,76	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19082	chromosome (5)	1	43963	0	1	6	7	10025	ST-353 complex	2	17	5	2	23	59	6	1785670	104,5	47	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19085	chromosome (2)	3	16040	1	0	0	1	11880		2	28	12	405	527	25	40	1694129	97,7	116	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19086	chromosome (3)	1	2658	0	0	0	0	2274		9	17	5	10	350	3	3	1773048	96,6	45	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19087	chromosome (5)	3	7526	0	0	0	0	1096	ST-828 complex	33	38	30	82	104	35	17	1725371	82,9	43	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19088	chromosome (3)	1	24961	0	1	10	11	1595	ST-828 complex	33	38	30	79	104	43	17	1712211	96,2	30	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19089	chromosome (1)	0	0	0	0	0	0	50	ST-21 complex	2	1	12	3	2	1	5	1709200	92,6	39	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19092	chromosome (3)	1	8636	0	0	2	2	19	ST-21 complex	2	1	5	3	2	1	5	1762777	99	52	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19102	chromosome (3);plasmid (1)	6	44417	0	1	6	7	9131	ST-460 complex	24	30	2	2	11	716	6	1750008	87,9	62	1,00	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19104	chromosome (4)	2	71539	0	2	16	18	5123	ST-828 complex	33	39	30	140	113	47	17	1.774.230	59,8	43	0,939	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19106	chromosome (2);plasmid (1)	4	47124	0	1	6	7	11991	ST-460 complex	24	30	2	2	1197	59	6	1745115	97,7	60	1,00	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19107	chromosome (2);plasmid (1)	4	47124	0	1	6	7	11991	ST-460 complex	24	30	2	2	1197	59	6	1744406	97,8	63	1,00	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19108	chromosome (8);plasmid (1)	1	50464	0	1	6	7	11990		2	114	12	2	2	894	6	1683153	97,1	53	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19110	chromosome (2);plasmid (1)	4	47124	0	1	6	7	11991	ST-460 complex	24	30	2	2	1197	59	6	1744841	98,1	60	1,00	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19111	chromosome (3)	0	0	0	0	0	0	11855		166	1	1	10	22	3	1	1.862.802	97,1	39	0,962	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149

9 Appendix

BfR-CA-19112	chromosome (10)	0	0	0	0	0	0	1145	ST-828 complex	33	39	30	82	104	44	17	1.740.967	97,2	44	0,992	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19115	chromosome (8);plasmid (1)	1	50464	0	1	6	7	11990		2	114	12	2	2	894	6	1685148	96,9	41	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19116	chromosome (8);plasmid (1)	1	50464	0	1	6	7	11990		2	114	12	2	2	894	6	1685996	103	50	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19117	chromosome (8);plasmid (1)	1	50464	0	1	6	7	11990		2	114	12	2	2	894	6	1686117	97,6	38	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19118	chromosome (8);plasmid (1)	1	50464	0	1	6	7	11990		2	114	12	2	2	894	6	1686476	97,9	28	0,97	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19119	chromosome (10)	0	0	0	0	0	0	1145	ST-828 complex	33	39	30	82	104	44	17	1749840	107,3	47	0,96	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19120	chromosome (8);plasmid (1)	1	50464	0	1	6	7	11990		2	114	12	2	2	894	6	1685113	77,2	36	0,98	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19137	chromosome (5)	0	0	0	0	0	0	10183		114	110	30	140	104	625	79	1764492	97,4	19	0,75	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19154	chromosome (3);plasmid (1)	1	45578	0	1	6	7	7517	ST-443 complex	7	17	2	599	23	3	12	1721112	97,1	20	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19155	chromosome (2)	0	0	0	0	0	0	1595	ST-828 complex	33	38	30	79	104	43	17	1641163	102,2	33	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19156	chromosome (1)	5	85400	0	1	26	27	9890		33	39	30	79	113	47	650	1780947	95,5	67	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19164	chromosome (3)	0	0	0	0	0	0	400	ST-353 complex	8	17	5	2	10	59	6	1724632	97	54	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19165	chromosome (3)	0	0	0	0	0	0	400	ST-353 complex	8	17	5	2	10	59	6	1732466	96,2	49	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19166	chromosome (2)	1	3400	1	0	0	1	1445	ST-828 complex	33	39	30	82	104	85	17	1705300	97,8	28	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19171	chromosome (2)	1	24961	0	1	10	11	1595	ST-828 complex	33	38	30	79	104	43	17	1674543	96,6	45	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19180	chromosome (5)	1	43960	0	1	6	7	10025	ST-353 complex	2	17	5	2	23	59	6	1784132	96,8	53	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19181	chromosome (3)	0	0	0	0	0	0	50	ST-21 complex	2	1	12	3	2	1	5	1657848	93,1	26	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19192	chromosome (3)	0	0	0	0	0	0	2988	ST-354 complex	8	10	2	2	10	12	6	1743600	97	33	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19204	chromosome (3)	0	0	0	0	0	0	21	ST-21 complex	2	1	1	3	2	1	5	1667718	86,1	43	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19206	chromosome (5)	0	0	0	0	0	0	10025	ST-353 complex	2	17	5	2	23	59	6	1767436	76,2	33	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19207	chromosome (3);plasmid (1)	1	44636	0	1	6	7	7517	ST-443 complex	7	17	2	599	23	3	12	1717549	100,7	22	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19209	chromosome (3);plasmid (1)	1	45593	1	1	6	8	7517	ST-443 complex	7	17	2	599	23	3	12	1717288	83,2	17	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19211	chromosome (1)	3	14074	0	1	0	1	10030		7	61	5	3	154	25	23	1856324	91	77	0,95	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19213	chromosome (5)	0	0	0	0	0	0	11853	ST-828 complex	33	39	30	115	113	625	17	1698515	87,3	37	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19217	chromosome (5)	0	0	0	0	0	0	10628		37	61	12	64	363	24	23	1598956	74,2	22	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19218	chromosome (5)	0	0	0	0	0	0	10025	ST-353 complex	2	17	5	2	23	59	6	1775520	68,6	31	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19219	chromosome (2);plasmid (1)	1	41875	0	1	6	7	305	ST-574 complex	9	53	2	10	11	3	3	1752713	88,5	55	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19226	chromosome (5)	6	70349	0	2	16	18	11987		598	66	30	79	113	43	17	1806118	65,6	68	0,93	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19231	chromosome (3)	5	67139	0	3	16	19	832	ST-828 complex	33	39	30	79	113	43	17	1800990	89,3	44	0,89	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19235	chromosome (3)	0	0	0	0	0	0	51	ST-443 complex	7	17	2	15	23	3	12	1631731	75,2	34	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19239	chromosome (4)	1	5432	0	1	0	1	832	ST-828 complex	33	39	30	79	113	43	17	1735511	97,4	39	0,93	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19241	chromosome (3)	0	0	0	0	0	0	2254	ST-257 complex	8	2	4	62	4	5	6	1691675	79,6	17	0,96	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19250	chromosome (3)	0	0	0	0	0	0	50	ST-21 complex	2	1	12	3	2	1	5	1617083	94,6	21	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19254	chromosome (2);plasmid (1)	3	72551	0	3	16	19	828	ST-828 complex	33	39	30	82	104	43	17	1783757	73,9	58	0,94	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19256	chromosome (3)	1	20419	0	0	0	0	6175	ST-21 complex	2	1	5	10	608	1	5	1696110	86,5	44	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19257	chromosome (1)	0	0	0	0	0	0	1972		7	71	5	62	11	67	1	1718263	65,2	33	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19259	chromosome (3)	0	0	0	0	0	0	6148		33	38	30	79	113	47	17	1703694	64,1	23	0,95	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19269	chromosome (4)	0	0	0	0	0	0	464	ST-464 complex	24	2	2	2	10	3	1	1721360	91,4	48	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19273	chromosome (5)	0	0	0	0	0	0	10025	ST-353 complex	2	17	5	2	23	59	6	1730867	96,3	36	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19275	chromosome (1)	0	0	0	0	0	0	917	ST-21 complex	2	21	1	3	2	1	5	1708128	80,6	24	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19279	chromosome (7)	2	32371	0	2	10	12	8053	ST-828 complex	33	39	30	79	113	625	17	1.750.084	86,7	51	0,962	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19281	chromosome (7)	2	32431	1	2	10	13	8053	ST-828 complex	33	39	30	79	113	625	17	1.708.495	71	32	0,931	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19282	chromosome (2)	0	0	0	0	0	0	48	ST-48 complex	2	4	1	2	7	1	5	1693004	95,4	27	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19284	chromosome (7)	2	30437	1	2	10	13	8053	ST-828 complex	33	39	30	79	113	625	17	1.706.791	68,5	24	0,929	Illumina® DNA Prep, (M) Tagmentation	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19285	chromosome (3)	1	20419	0	0	0	0	6175	ST-21 complex	2	1	5	10	608	1	5	1695572	96,2	45	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19286	chromosome (6)	0	0	0	0	0	0	7355	ST-353 complex	8	17	5	2	10	59	23	1778341	96,2	51	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19287	<=0,12	0	0	0	0	0	0	45	ST-45 complex	4	7	10	4	1	7	1	1616477	96,3	29	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19288	chromosome (3)	1	6759	0	1	0	1	354	ST-354 complex	8	10	2	2	11	12	6	1750516	75,6	42	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19289	chromosome (2)	1	29262	0	1	10	11	855	ST-828 complex	33	39	30	79	104	35	17	1720840	65,1	29	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19290	chromosome (2)	0	0	0	0	0	0	855	ST-828 complex	33	39	30	79	104	35	17	1650848	76,6	32	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19295	chromosome (3)	1	20459	0	0	0	0	6175	ST-21 complex	2	1	5	10	608	1	5	1696208	75	41	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19298	chromosome (3)	0	0	0	0	0	0	51	ST-443 complex	7	17	2	15	23	3	12	1671701	96,5	86	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19301	chromosome (6)	0	0	0	0	0	0	7355	ST-353 complex	8	17	5	2	10	59	23	1778523	59,4	54	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19311	chromosome (3);plasmid (3)	1	48277	0	1	6	7	5973	ST-1034 complex	22	15	4	64	360	25	23	1800070	85,9	68	0,97	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19312	chromosome (3)	0	0	0	0	0	0	825	ST-828 complex	33	39	30	82	113	47	17	1690424	88,6	30	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19318	chromosome (3)	1	1600	0	0	0	0	11850		22	10	4	28	363	3	6	1620470	81,9	76	0,94	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19320	chromosome (3)	0	0	0	0	0	0	51	ST-443 complex	7	17	2	15	23	3	12	1670040	89,1	33	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19328	chromosome (2)	0	0	0	0	0	0	1595	ST-828 complex	33	38	30	79	104	43	17	1646306	82,3	35	0,98	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19329	chromosome (3);plasmid (1)	1	45125	0	1	6	7	7517	ST-443 complex	7	17	2	599	23	3	12	1725695	65,4	24	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19336	chromosome (3)	0	0	0	0	0	0	51	ST-443 complex	7	17	2	15	23	3	12	1627885	105,6	37	1,00	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19362	chromosome (4)	1	2718	0	0	0	0	464	ST-464 complex	24	2	2	2	10	3	1	1737514	101	70	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149
BfR-CA-19364	chromosome (4)	0	0	0	0	0	0	464	ST-464 complex	24	2	2	2	10	3	1	1738214	102,2	62	0,99	Nextera DNA Flex Library prep Kit	PureLink Genomic DNA Mini Kit	NextSeq 500	2 x 149

Sample overview Samples highlighted in blue were additionally sequenced with Oxford Nanopore Technology	**Unicycler hybrid assembly and BakCharak AMR prediction** Genes not found are highlighted in red Genes that were falsely annotated are struck through (e.g. ~~tet(O)~~) Genes found in close proximity to transposases are in **bold**. Partial genes correctly found are annotated as such (e.g. aadE2_Δ1-415) aad9 falsely annotated as truncated due to frame-shifting in the poly-C tract are shown in **bold and blue**							
isolate No.	**contigs**	**circular contigs**	**plasmid contigs**	**plasmids cumlength**	**largest contig size**	**Point mutations and AMR genes on chromosome** Bold highlighting indicates close proximity of AMR genes to AMR-associated transposase	**amr genes plasmid localization**	**AMR associated transposase (bakta annotation)**
BfR-CA-15687	2	2	1	44826	1657372	blaOXA-489;tet(O);GyrA_T86I	tet(O)	
BfR-CA-15991	1	1	0		1691542	**tet(O/M/O)$_{\text{Taiwanese variant}}$-catA9-tnp$_{\text{IS1216 family}}$-fexA-optrA-tnp$_{\text{IS1216 family}}$-tet(L)**;aac(6')-Ie/aph(2'')-Ia-aadE1-tet(O)x$_{\Delta\text{C-terminus}}$;blaOXA-193; 23S_A2075G; 23S_A2075G;23S_A2075G; GyrA_T86I		IS6-like element IS1216 family transposase (x2)
BfR-CA-16040	1	1	0		1760061	**tnp$_{\text{ISCco2 family}}$-catA13-aph(3')-IIIa-**aad9;tet(O/M/O)-aad9-erm(B)-aadE1;aac(6')-Ie/aph(2'')-Ia-aadE1-tet(O)x$_{\Delta\text{C-terminus}}$;blaOXA-489;GyrA_T86I		IS1595-like element ISCco2 family transposase
BfR-CA-16046	2	2	1	39212	1819504	**tnp$_{\text{ISCco2 family}}$-catA13-aph(3')-IIIa-aad9-aph(2'')-If-blaOXA-193**;tet(O/M/O)-aad9-erm(B)-aadE1;aadE-Cc;GyrA_T86I		IS1595-like element ISCco2 family transposase
BfR-CA-16077	1	1	0		1620666	**tnp$_{\text{ISCco2 family}}$-catA13-aph(3')-IIIa-aad9-aph(2'')-If**;tet(O/M/O)$_{\text{Henan variant}}$-aadE1-tet(O)x$_{\Delta\text{N-terminus}}$;**aph(3')-IIIa-tnp$_{\text{ISCaje6 family}}$**;blaOXA-184 family;**tnp$_{\text{ISCco2 family}}$-lnu(C)**;GyrA_T86I		IS1595-like element ISCco2 family transposase (x2); IS1595-like element ISCaje6 family transposase
BfR-CA-16088	1	1	0		1657686	**tnp$_{\text{ISCco2 family}}$-catA13-aph(3')-IIIa-aad9-aph(2'')-If**;tet(O/M/O)$_{\text{Henan variant}}$-aadE1-tet(O)x$_{\Delta\text{N-terminus}}$;**aph(3')-IIIa-tnp$_{\text{ISCaje6 family}}$**;blaOXA-184 family;**tnp$_{\text{ISCco2 family}}$-lnu(C)**; GyrA_T86I;23S_A2075G; 23S_A2075G;23S_A2075G		IS1595-like element ISCco2 family transposase (x2); IS1595-like element ISCaje6 family transposase
BfR-CA-16110	1	1	0		1673552	tet(O)-aad9-erm(B)-aadE1;blaOXA-193;GyrA_T86I		
BfR-CA-16201	2	2	1	3333	1734659	tet(O)-aad9-erm(B)-aadE1;**tnp$_{\text{ISCco2 family}}$-catA13-aph(3')-IIIa-aad9-aph(2'')-If-blaOXA-193**;tet(O);GyrA_T86I;50S_L22_A103V		IS1595-like element ISCco2 family transposase
BfR-CA-16258	2	2	1	3310	1724953	tet(O)-aad9-erm(B)-aadE1;tet(O);blaOXA-193;GyrA_T86I;50S_L22_A103V		
BfR-CA-16297	1	1	0		1703146	tet(O/M/O)-aad9-erm(B)-aadE1;**aph(2'')-If-aph(3')-IIIa-tnp$_{\text{ISCaje6 family}}$**;aac(6')-Ie/aph(2'')-Ia-aadE1-tet(O)x$_{\Delta\text{C-terminus}}$;**tet(O)-tnp$_{\text{IS607 family}}$**;blaOXA-193;GyrA_T86I		IS1595-like element ISCaje6 family transposase; IS607 Family transposase
BfR-CA-16737	2	2	1	52704	1817905	blaOXA-185 like;tet(O);GyrA_T86I	~~tet(O)~~tet(O/32/O)-aadE2_Δ1-415-sat4-aph(3')-IIIa	
BfR-CA-18842	1	1	0		1725012	aac(6')-Ie/aph(2'')-Ia-aadE1-tet(O)x$_{\Delta\text{C-terminus}}$;tet(O/M/O);blaOXA-193;GyrA_T86I		
BfR-CA-19087	2	2	1	4097	1733474	**tnp$_{\text{IS607 family}}$-~~tet(O)~~tet(O/32/O)-aph(2'')-Ii$_1$-aph(3')-IIIa-aad9-aadE1-tet(O)x$_{\Delta\text{N-terminus}}$**;tet(O/32/O);aadE-Cc;GyrA_T86I		IS607 Family transposase

BfR-CA-19301	1	1	0		1801855	**aadE3-sat4-aph(3')-IIIa-tnp$_{IS1216\ family}$;~~tet(O)~~**tet(O/32/O);blaOXA-193;GyrA_T86I;50S_L22_A103V		IS6-like element IS1216 family transposase

9 Appendix

Proof of principle comparison of AMR gene detection based on SKESA or shovill genome assemblies

Resistance determinants as reported by AMRFinderPlus

The coverage of the gene is expressed as a percentage of the full-length translated protein sequence

Genes not found are highlighted in red

differences in AMR detection based on SKESA vs. Shovill are highlighted with red shading

SAMPLE #	SAMPLE ID	Assembler	enhanced performance shovill vs. SKESA	blaOXA	blaOXA coverage	gyrA	tet(O)	tet(O) coverage	tet(O/M/O)	tet(O/M/O) coverage	aph(3')-IIIa	aph(3')-IIIa coverage	50S_L22	aad9	aad9 coverage	catA13	catA13 coverage	aadE1	aadE1 coverage	23S	aph(2'')-If	aph(2'')-If coverage	sat4	sat4 coverage
1	BfR-CA-15687	Shovill	no	blaOXA-489	100	gyrA_T86I	**tet(O)**	61,03		0		0			0		0		0			0		0
		SKESA		blaOXA-489	100	gyrA_T86I	**tet(O)**	59,94		0		0			0		0		0			0		0
2	BfR-CA-16062	Shovill	no	blaOXA-193	100	gyrA_T86I	**tet(O)**	70,27		0		0			0		0	aadE	100	23S_A2075G		0		0
		SKESA		blaOXA-193	100	gyrA_T86I	**tet(O)**	69,17		0		0			0		0	aadE	100	23S_A2075G		0		0
3	BfR-CA-16088	Shovill	no	blaOXA	100	gyrA_T86I		0	**tet(O/M/O)**	56,65	aph(3')-IIIa	100		aad9	83,72	catA13	100	aadE	100	23S_A2075G	aph(2'')-If	100		0
		SKESA		blaOXA	100	gyrA_T86I	tet(O)	54,77	**tet(O/M/O)**	51,8	aph(3')-IIIa			aad9	87,98	catA13	100	aadE	100	23S_A2075G	aph(2'')-If	100		0
4	BfR-CA-16220	Shovill	no	blaOXA-184	100	gyrA_T86I		0	**tet(O/M/O)**	56,65	aph(3')-IIIa	100			0		0	aadE	100			0	sat4	100
		SKESA		blaOXA-184	100	gyrA_T86I		0	**tet(O/M/O)**	51,8	aph(3')-IIIa	100			0		0	aadE	100			0	sat4	100
5	BfR-CA-16249	Shovill	no	blaOXA-489	100	gyrA_T86I	**tet(O)**	70,27		0		0			0		0	aadE	100	23S_A2075G		0		0
		SKESA		blaOXA-489	100	gyrA_T86I	**tet(O)**	69,17		0		0			0		0	aadE	100	23S_A2075G		0		0
6	BfR-CA-16258	Shovill	yes	blaOXA-193	100	gyrA_T86I	**tet(O)**	63,22		0		0	50S_L22_A103V	aad9	100		0	aadE	100			0		0
		SKESA		blaOXA-193	100	gyrA_T86I	**tet(O)**	62,13		0		0	50S_L22_A103V	aad9	83,72			aadE	100			0		0
7	BfR-CA-17105	Shovill	no	blaOXA-630	100		tet(O)	100		0		0			0		0		0			0		0
		SKESA		blaOXA-630	100		tet(O)	100		0		0			0		0		0			0		0
8	BfR-CA-18886	Shovill	no			gyrA_T86I	tet(O)	0	tet(O/M/O)	0		0		aad9	83,72		0	aadE	100			0		0
		SKESA				gyrA_T86I	tet(O)	0	tet(O/M/O)	0		0		aad9	81,4		0	aadE	100			0		0
9	BfR-CA-19033	Shovill	no	blaOXA-193	100	gyrA_T86I	tet(O)	0	**tet(O/M/O)**	69,17	aph(3')-IIIa	100		aad9	100		0	aadE	100			0	sat4	100
		SKESA		blaOXA-193	100	gyrA_T86I	tet(O)	0	**tet(O/M/O)**	64,32	aph(3')-IIIa	100		aad9	100		0	aadE	100			0	sat4	100
10	BfR-CA-19112	Shovill	no	blaOXA-193	100	gyrA_T86I	tet(O)	0	**tet(O/M/O)**	90,61	aph(3')-IIIa	100		aad9	84,5		0	**aadE**	88,89			0	sat4	100
		SKESA		blaOXA-193	100	gyrA_T86I	tet(O)	0	**tet(O/M/O)**	64,32	aph(3')-IIIa	100		aad9	81,4		0	**aadE**	86,46			0	sat4	100

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Proof of principle comparison of AMR gene detection based on SKESA or shovill genome assemblies
Resistance determinants as reported by AMRFinderPlus
The coverage of the gene is expressed as a percentage of the full-length translated protein sequence
Genes not found are highlighted in red
differences in AMR detection based on SKESA vs. Shovill are highlighted with red shading

SAMPLE #	SAMPLE ID	Assembler	enhanced performance shovill vs. SKESA	erm(B)	erm(B) coverage	aac(6')-Ie/aph(2'')-Ia	aac(6')-Ie/aph(2'')-Ia coverage	aadE-Cc	aadE-Cc coverage	tet(L)	tet(L) coverage	catA	catA coverage	optrA	optrA coverage	fexA	fexA coverage	rpsL_K43R	lnu(C)	lnu(C) coverage	ant(6)-Ia	ant(6)-Ia coverage	cat-TC	cat-TC coverage	rpsL_K88R	aph(2'')-Ii	aph(2'')-Ii coverage	tet(W)	tet(W) coverage
1	BfR-CA-15687	Shovill	no		0		0		0		0		0		0		0			0		0		0			0		0
		SKESA			0		0		0		0		0		0		0			0		0		0			0		0
2	BfR-CA-16062	Shovill	no		0	aac(6')-Ie/aph(2'')-Ia	100		0		0		0		0		0			0		0		0			0		0
		SKESA			0	aac(6')-Ie/aph(2'')-Ia	100		0		0		0		0		0			0		0		0			0		0
3	BfR-CA-16088	Shovill	no		0		0		0		0		0		0		0		lnu(C)	100		0		0			0		0
		SKESA			0		0		0		0		0		0		0		lnu(C)	100		0		0			0		0
4	BfR-CA-16220	Shovill	no		0		0		0		0		0		0		0			0	ant(6)-Ia	53,97		0			0		0
		SKESA			0		0		0		0		0		0		0			0	ant(6)-Ia	53,97		0			0		0
5	BfR-CA-16249	Shovill	no		0	aac(6')-Ie/aph(2'')-Ia	100	aadE-Cc	100		0		0		0		0			0		0		0			0		0
		SKESA			0	aac(6')-Ie/aph(2'')-Ia	100	aadE-Cc	100		0		0		0		0			0		0		0			0		0
6	BfR-CA-16258	Shovill	yes	erm(B)	100		0		0		0		0		0		0			0		0		0			0		0
		SKESA		erm(B)	100		0		0		0		0		0		0			0		0		0			0		0
7	BfR-CA-17105	Shovill	no		0		0		0		0		0		0		0			0		0		0			0		0
		SKESA			0		0		0		0		0		0		0			0		0		0			0		0
8	BfR-CA-18886	Shovill	no	erm(B)	100		0		0		0		0		0		0			0		0		0			0		0
		SKESA		erm(B)	100		0		0		0		0		0		0			0		0		0			0		0
9	BfR-CA-19033	Shovill	no	erm(B)	100	aac(6')-Ie/aph(2'')-Ia	100		0		0		0		0		0			0	ant(6)-Ia	87,75		0			0		0
		SKESA		erm(B)	100	aac(6')-Ie/aph(2'')-Ia	100		0		0		0		0		0			0	ant(6)-Ia	87,75		0			0		0
10	BfR-CA-19112	Shovill	no	erm(B)	100	aac(6')-Ie/aph(2'')-Ia	100		0		0		0		0		0			0	ant(6)-Ia	87,75		0			0		0
		SKESA		erm(B)	100	aac(6')-Ie/aph(2'')-Ia	100		0		0		0		0		0			0	ant(6)-Ia	87,75		0			0		0

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Antibiotic class	Resistance determinant	Accession of protein reference sequence(s)	Accession of nucleotide reference sequence(s)
Aminoglycoside	*aph(2'')-If*	WP_021424053.1	NG_047405.1
	aac(6')-Ie/aph(2'')-Ia	WP_001028144.1	NG_047055.1
	aph(2'')-Ii $_1$	WP_052776520.1	KX931104.1
	aadE 1	WP_001255868.1	NZ_CP109819.1:317969-318835
	aadE 2	WP_001255866.1	NG_047393.1
	aadE 3	WP_057035408.1 (missing in AMRFinder database)	NZ_RYYM01000001.1:c70287-69379
	aadE-Cc	WP_002785795.1	CP013733.1:c230242-229343
	RpsL_K43R; RpsL_K88R	n.a. - point mutation	n.a. - point mutation
	aph(3')-IIIa	WP_001096887.1	NG_047418.1
	aad9	WP_057031337.1	CP091310.1:1750066-1750845
Beta-lactam	*bla* $_{OXA-61}$ family	WP_002783228.1 (blaOXA-193 as example sequence); variants: blaOXA-61, blaOXA-450, blaOXA-460, blaOXA-461, blaOXA-489, blaOXA-577, blaOXA-579, blaOXA-584, blaOXA-591, blaOXA-594, blaOXA-595	NG_049489.1
	bla $_{OXA-184}$ family	WP_002872405.1 (blaOXA-184 as example sequence); variants: blaOXA-185, blaOXA-447, blaOXA-448, blaOXA-449, blaOXA-452, blaOXA-465, blaOXA-625, blaOXA-630, blaOXA-631, blaOXA-632, blaOXA-633	NG_049485.1
(Fluoro-)Quinolone	GyrA_T86I; GyrA_T86V	n.a. - point mutation	n.a. - point mutation
Lincosamide	*lnu* (C)	WP_002837187.1	NZ_CP114883.1:456702-457196
Macrolide	23S_A2075G	n.a. - point mutation	n.a. - point mutation
	50S_L22_A103V	n.a. - point mutation (to be deleted in AMRFinder database, since no macrolide resistance is conferred)	n.a. - point mutation (to be deleted in AMRFinder database, since no macrolide resistance is conferred)
	erm (B)	WP_002321849.1	NC_012926.1:1031089-1031826
Phenicol	*catA9*	WP_001010387.1	NG_047564.1
	catA13	WP_040564913.1	NG_047588.1
	optrA	WP_063854496.1	NZ_CP081833.1:c1246663-1244696
	fexA	WP_015585966.1	NG_047857.1
Tetracycline	*tet* (O)	WP_032490535.1	AY190525.1
	tet (O/32/O)	WP_215475009.1 (missing in AMRFinder database)	MT176412.1
	tet (O/M/O)	WP_002872163.1; WP_185886429.1 (Henan variant); WP_216170378.1 (Taiwanese variant); AVY51757.1 (Shanghai variant)	NG_048259.1; NZ_JACMID010000002.1:c171398-169479 (Henan variant); CP076508.1:43486-45405 (Taiwanese variant); MF037585.1:c18890-16971 (Shanghai variant)
	tet (L)	WP_002294500.1	NG_048206.1
	tet (W)	WP_000691721.1	NG_048291.1
	tet (M)	WP_002364936	EU182585.1
Streptothricin	*sat4*	WP_063854935.1, WP_000627290.1	NG_048073.1, NG_048072.1

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Odds ratio (OR) with 95 % confidence interval (CI)
Odds ratios with p-values of less than 0.05 are highlighted in bold

Comparison	Antimicrobial	Odds ratio (OR)	95% confidence interval (CI) lower bound	95% confidence interval (CI) upper bound	significance level (p)
***C. coli* vs. *C. jejuni* (VN)**	CIP	4,5672	0,2334	89,3794	0,3168
	ERY	**26,8235**	13,5002	53,2957	0,0001
	GEN	**13,2185**	7,154	24,4237	0,0001
	NAL	8,6522	0,482	155,3158	0,143
	STR	**40,9821**	19,6524	85,4621	0,0001
	TET	0,6364	0,0393	10,2925	0,7503
	3-4 fold resistance	**45,9556**	17,5241	120,5146	0,0001
***C. coli* vs. *C. jejuni* (DE)**	CIP	1,1647	0,62	2,1877	0,6356
	ERY	**27,7021**	3,6603	209,6546	0,0013
	GEN	5,5286	0,2626	116,391	0,2714
	NAL	1,4348	0,7829	2,6295	0,2428
	STR	0,6652	0,3282	1,3484	0,2581
	TET	1,2857	0,7495	2,2054	0,3613
	3-4 fold resistance	1,3757	0,7216	2,6224	0,3326
VN vs. DE (*C. coli*)	CIP	**47,8877**	2,8639	800,7344	0,0071
	ERY	**14,7909**	7,6114	28,7424	0,0001
	GEN	**209,8571**	47,8266	920,8264	0,0001
	NAL	**50,5568**	3,0272	844,3407	0,0063
	STR	**40,4762**	18,4868	88,6212	0,0001
	TET	**42,875**	5,7469	319,8688	0,0002
	3-4 fold resistance	**67,68**	24,8293	184,4826	0,0001
VN vs. DE (*C. jejuni*)	CIP	**13,9592**	4,1231	47,2608	0,0001
	ERY	**15,2754**	2,0035	116,4654	0,0085
	GEN	**71,2716**	4,3211	1175,5515	0,0029
	NAL	**8,9076**	3,5932	22,0822	0,0001
	STR	0,657	0,3423	1,2612	0,2067
	TET	**86,625**	11,7236	640,0665	0,0001
	3-4 fold resistance	**2,026**	1,1307	3,6302	0,0177
VN vs. DE (*C*. spp.)	3-4 fold resistance	**5,0975**	3,3985	7,6459	0,0001

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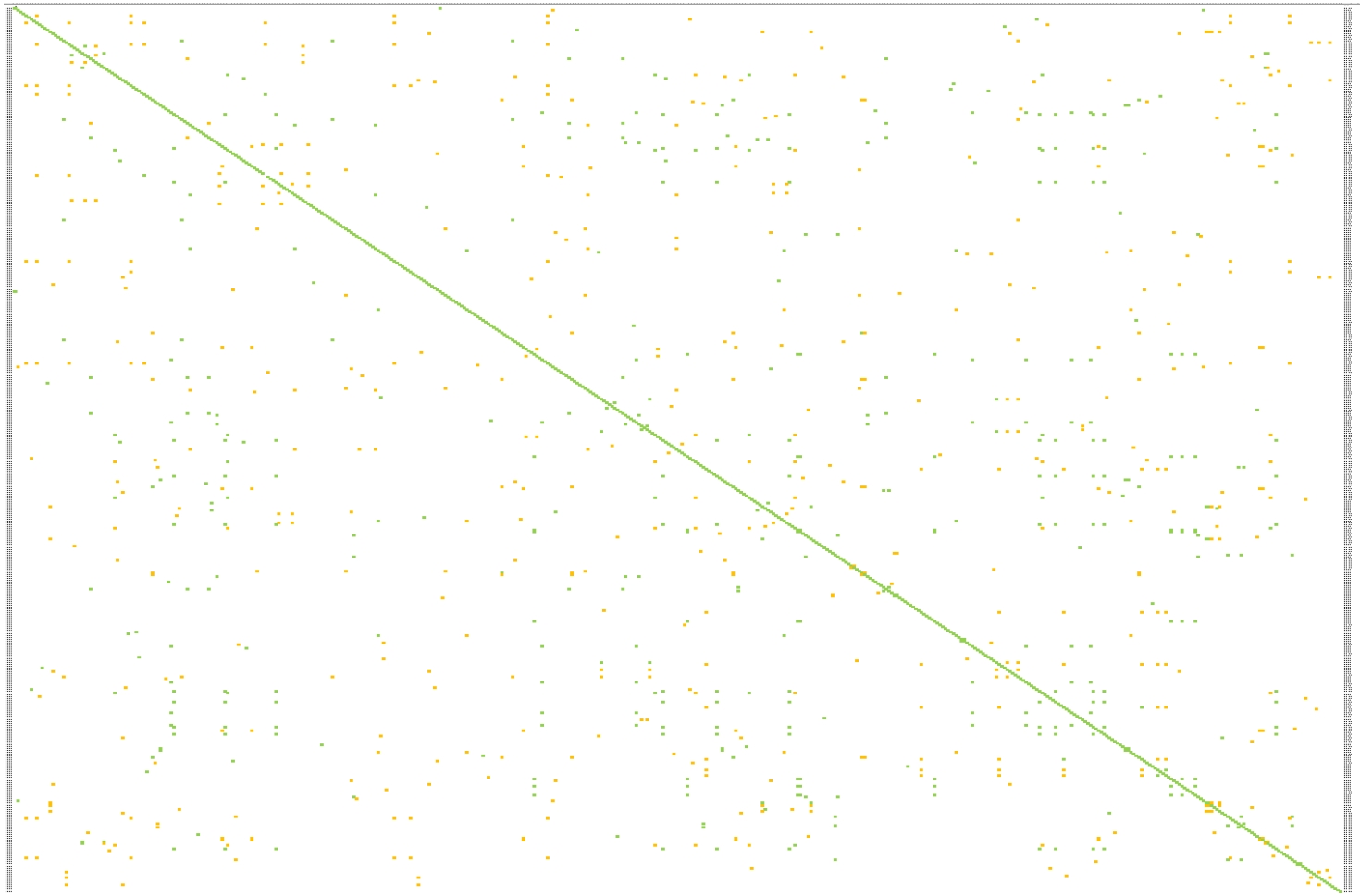


Distance matrix from cgMLST analysis using 1343 core genes and pairwise ignoring missing loci. Created with Ridom SeqSphere+ 8.4.2.

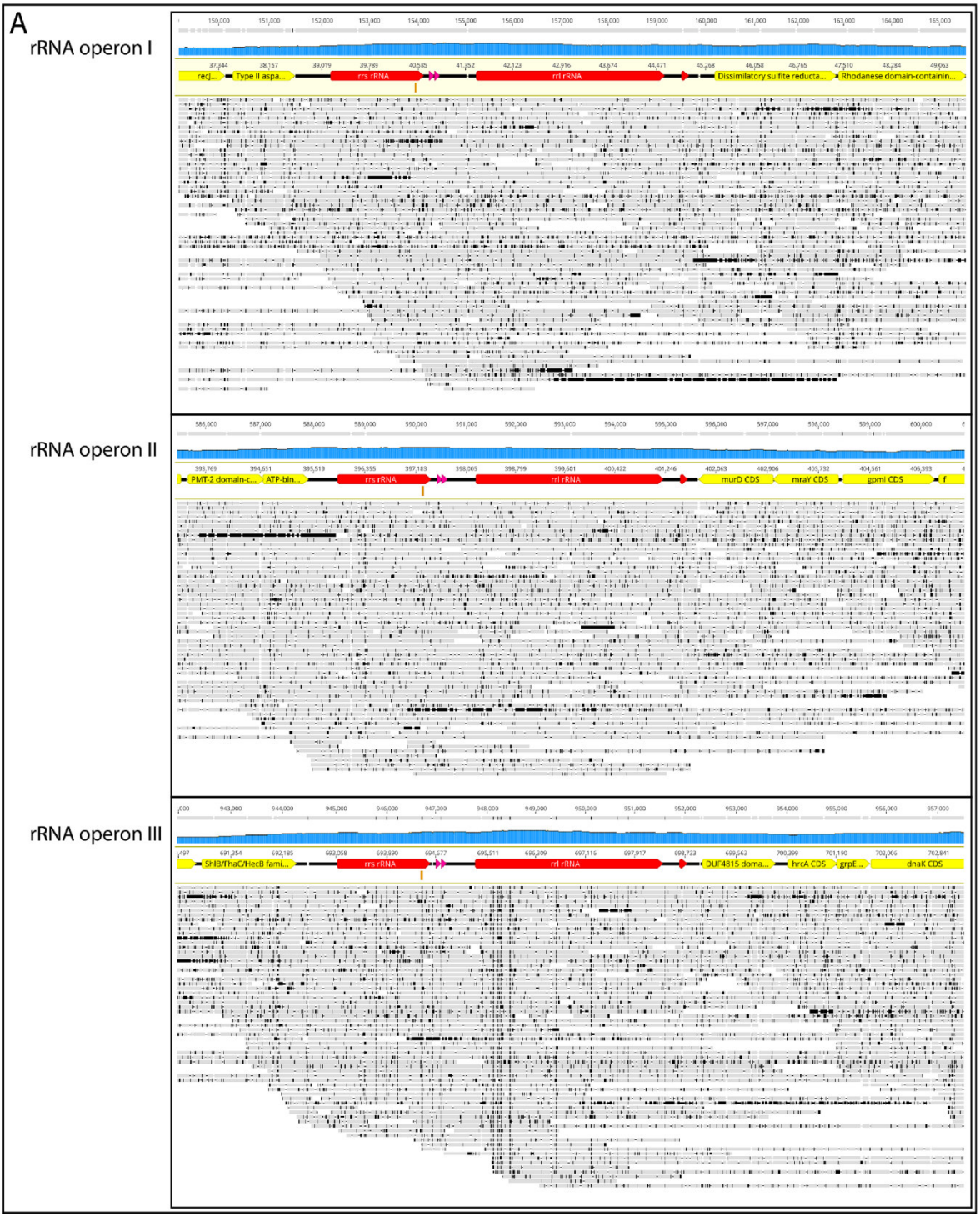
isolates with ≤ 10 allele distance are in green
isolates with 11-100 allele distance are in orange
isolates with >100 allele distance are in white

9.2.4 Publication 4: The point mutation A1387G in the 16S rRNA gene confers aminoglycoside resistance in C. jejuni and C. coli

Supplementary Figures

The point mutation A1387G in the 16S rRNA gene confers aminoglycoside resistance in *C. jejuni* and *C. coli*

Michael Zarske, Christiane Werckenthin, Julia Golz, Kerstin Stingl



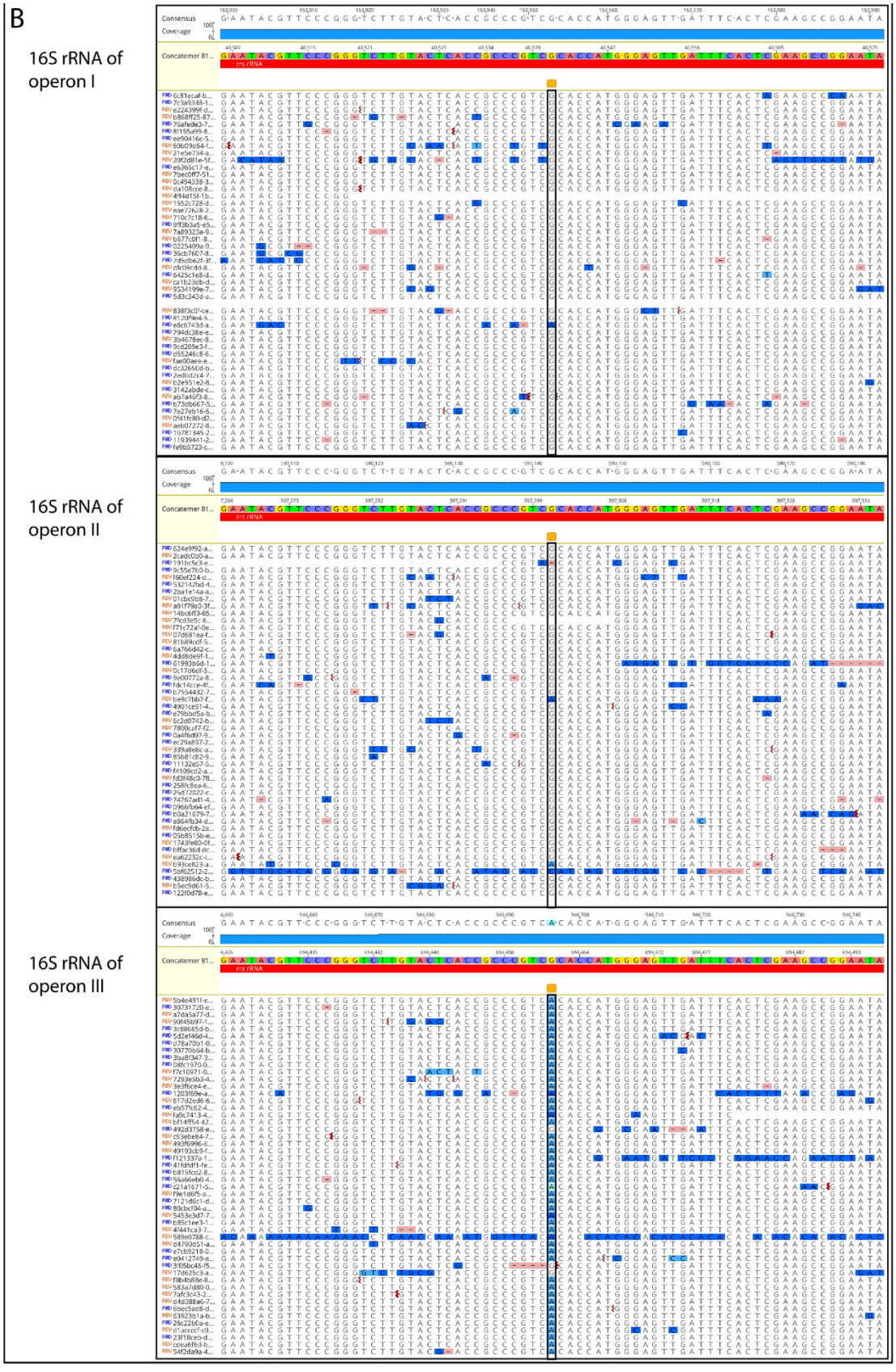


Figure S1. The transformant 81-176-TF15687-K8 harbored the A1387G point mutation in the rRNA operon I and II but remained wildtype A1387 in operon III. Trimmed ONT long reads of 81-176-TF15687-K8 were mapped to its unicycler hybrid assembly. Overview of the different gene contexts of rRNA operon I-III confirmed that long reads covered 5' and 3' regions specifically flanking the respective rRNA operon (A). The sequence sourrounding position 1387 (highlighed with a black frame) in the respective 16S rRNA genes is depicted in (B). Red arrows, rRNA genes; yellow arrows,

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Supplementary Tables

The point mutation A1387G in the 16S rRNA gene confers aminoglycoside resistance in *C. jejuni* and *C. coli*

Michael Zarske, Christiane Werckenthin, Julia C. Golz, Kerstin Stingl

Results from mapping of trimmed reads from nine APR-GEN-KAN-TOB resistant isolates to its isogenic sensitive recipient (BfR-CA-11057) after transformation of gDNA of BfR-CA-1568
and subsequent mapping of unused reads to the donor BfR-CA-15687

Table S1A SNP raw data: Sequence variants (raw data) exported from Geneious Prime Software identified between nine BfR-CA-11057-TF15687 transformants relative to the recipient strain (BfR-CA-11057
Table S1B SNP summary: Summary of number of sequence variants based on Table S1.
Table S2 Read coverage < 5 exported from Geneious Prime Software identified upon mapping of nine BfR-CA-11057-TF15687 transformants to the recipient strain (BfR-CA-11057
Table S3 Sequences with a coverage >=20 exported from Geneious Prime Software from unsued reads of each transformant after analysis in Table S1A mapped to the donor BfR-CA-1568

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Raw data export from Geneious Prime SNP analysis
variant frequency was set to 0.8 and minimum coverage was set to 40

Name	Minimum (bp)	Maximum (bp)	Length (bp)	Change	Polymorphism Type	Coverage	Variant Frequency	Variant P-Value (approximate)	Track Name	Sequence Name	Amino Acid Change	
G	3819	3819	1	A -> G	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	3825	3825	1	G -> A	SNP (transition)	120	97.5%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
A	4035	4035	1	T -> A	SNP (transversion)	135	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
T	4074	4074	1	G -> T	SNP (transversion)	121	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
A	4080	4080	1	T -> A	SNP (transversion)	121	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
A	4083	4083	1	T -> A	SNP (transversion)	124	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
T	4086	4086	1	C -> T	SNP (transition)	135	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
(CTT6)	4095	4098	3	TCTA -> CTT6	Substitution	126 -> 132	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
T	4821	4821	1	C -> T	SNP (transition)	154	98.7%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
C	5052	5052	1	G -> C	SNP (transversion)	148	98.6%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
T	5090	5089	0	(T)5 -> (T)6	Insertion (tandem repeat)	136	92.6%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
C	5101	5101	1	A -> C	SNP (transversion)	147	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
G	5129	5129	1	A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
T	5786	5786	1	C -> T	SNP (transition)	152	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	A -> V	Transcriptional initiation protein Tat CDS
A	5437	5437	1	G -> A	SNP (transition)	144	97.9%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Transcriptional initiation protein Tat CDS
A	5437	5437	1	G -> A	SNP (transition)	144	97.9%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		putative p-cresol methylhydroxylase subunit CDS
C	5444	5444	1	A -> C	SNP (transversion)	140	97.9%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	T -> P	putative p-cresol methylhydroxylase subunit CDS
T	5637	5637	1	C -> T	SNP (transition)	127	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	A -> V	putative p-cresol methylhydroxylase subunit CDS
T	6034	6034	1	A -> T	SNP (transversion)	64	100.0%	1,6E-140	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
(T)	6036	6037	2	AG -> T	Substitution	64	100.0%	4E-138	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	6048	6048	1	C -> A	SNP (transversion)	60	98.3%	4,8E-160	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
CAC	6051	6053	3	AGA -> CAC	Substitution	62 -> 74	94.4% -> 98.4%	1,2E-174	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	6399	6399	1	G -> A	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	G -> E	putative p-cresol methylhydroxylase subunit CDS
C	6704	6704	1	T -> C	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	P -> S	Chain B, Stru CDS
	6882	6882	1	(A)7 -> (A)6	Deletion (tandem repeat)	124	96.0%	1E-193	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Cytochrome c CDS
	7475	7475	1	(T)8 -> (T)7	Deletion (tandem repeat)	133	92.5%	4,2E-182	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
T	8868	8868	1	C -> T	SNP (transition)	158	98.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		actP CDS
C	9736	9736	1	T -> C	SNP (transition)	156	99.4%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	F -> L	Sodium:proton antiporter CDS
A	9882	9882	1	G -> A	SNP (transition)	141	97.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Sodium:proton antiporter CDS
G	10257	10257	1	A -> G	SNP (transition)	128	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Sodium:proton antiporter CDS
C	10376	10376	1	G -> C	SNP (transversion)	178	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	M -> I	Sodium:proton antiporter CDS
T	10353	10353	1	C -> T	SNP (transition)	136	98.5%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Sodium:proton antiporter CDS
T	11197	11197	1	C -> T	SNP (transition)	137	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	11386	11386	1	T -> G	SNP (transversion)	117	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	11560	11560	1	A -> G	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	11572	11572	1	C -> T	SNP (transition)	107	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
AAATA	11574	11578	4	CGCT -> AAATA	Substitution	108 -> 110	98.1% -> 98.2%	4E-307	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	TV -> KI	gltB3 CDS
G	11580	11580	1	A -> G	SNP (transition)	110	98.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	N -> S	gltB3 CDS
G	11593	11593	1	A -> G	SNP (transition)	116	98.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	11605	11605	1	A -> G	SNP (transition)	124	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
AG	11612	11613	2	GC -> AG	Substitution	128	97.7%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	A -> S	gltB3 CDS
ACG	11615	11617	3	TGT -> ACG	Substitution	112 -> 114	94.6% -> 94.7%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	C -> T	gltB3 CDS
A	11623	11623	1	T -> A	SNP (transversion)	112	96.4%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	11653	11653	1	T -> A	SNP (transversion)	113	97.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	11671	11671	1	C -> T	SNP (transition)	108	97.2%	2E-288	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11686	11686	1	T -> C	SNP (transition)	109	98.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	11713	11713	1	T -> A	SNP (transversion)	129	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11725	11725	1	T -> C	SNP (transition)	138	97.8%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11770	11770	1	T -> C	SNP (transition)	179	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11788	11788	1	T -> C	SNP (transition)	124	98.4%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	11812	11812	1	C -> T	SNP (transition)	117	98.3%	2,1E-283	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11824	11824	1	T -> C	SNP (transition)	120	98.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	11836	11836	1	C -> T	SNP (transition)	130	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	11863	11863	1	C -> T	SNP (transition)	135	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11866	11866	1	T -> C	SNP (transition)	170	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11872	11872	1	A -> C	SNP (transversion)	122	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	11881	11881	1	C -> T	SNP (transition)	126	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
CAA	11912	11914	2	GAG -> CAA	Substitution	127 -> 128	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	E -> Q	gltB3 CDS
T	11917	11917	1	C -> T	SNP (transition)	126	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	11920	11920	1	A -> G	SNP (transition)	125	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	11980	11980	1	T -> A	SNP (transversion)	131	98.5%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	12011	12011	1	T -> C	SNP (transition)	116	97.4%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	12349	12349	1	T -> C	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12607	12607	1	T -> A	SNP (transversion)	124	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12616	12616	1	G -> A	SNP (transition)	129	96.9%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	12751	12751	1	A -> T	SNP (transversion)	123	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	12760	12760	1	T -> C	SNP (transition)	137	97.8%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12769	12769	1	G -> A	SNP (transition)	139	98.6%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	12772	12772	1	T -> C	SNP (transition)	138	98.6%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12775	12775	1	T -> A	SNP (transversion)	138	97.8%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
AGCC	12781	12784	3	TTCT -> AGCC	Substitution	143 -> 145	96.5% -> 96.6%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	IS -> IA	gltB3 CDS
GTG	12791	12793	2	ATT -> GTG	Substitution	161	98.8%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	gltB3 CDS
A	12796	12796	1	T -> A	SNP (transversion)	161	99.4%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12808	12808	1	G -> A	SNP (transition)	154	98.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	12814	12814	1	C -> T	SNP (transition)	148	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12817	12817	1	G -> A	SNP (transition)	150	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	12823	12823	1	A -> G	SNP (transition)	142	97.9%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	12826	12826	1	C -> T	SNP (transition)	145	97.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	12832	12832	1	C -> T	SNP (transition)	142	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12835	12835	1	T -> A	SNP (transversion)	139	97.8%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	N -> K	gltB3 CDS
T	12838	12838	1	C -> T	SNP (transition)	139	98.6%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12965	12965	1	C -> A	SNP (transversion)	143	97.9%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	Q -> K	gltB3 CDS
C	13225	13225	1	T -> C	SNP (transition)	137	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	13231	13231	1	A -> G	SNP (transition)	140	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	13273	13273	1	A -> G	SNP (transition)	175	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	13282	13282	1	T -> C	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	13285	13285	1	A -> G	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	13300	13300	1	T -> C	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	13306	13306	1	T -> A	SNP (transversion)	110	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	13315	13315	1	G -> A	SNP (transition)	114	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	13319	13319	1	T -> C	SNP (transition)	117	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	13354	13354	1	T -> C	SNP (transition)	130	98.5%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	13365	13365	1	T -> C	SNP (transition)	143	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	I -> T	gltB3 CDS
C	13411	13411	1	T -> C	SNP (transition)	143	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	13501	13501	1	C -> T	SNP (transition)	127	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	13619	13619	1	C -> T	SNP (transition)	126	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	14023	14023	1	T -> G	SNP (transversion)	131	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	14029	14029	1	C -> T	SNP (transition)	140	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14032	14032	1	G -> A	SNP (transition)	143	95.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14035	14035	1	T -> A	SNP (transversion)	141	98.6%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14059	14059	1	T -> A	SNP (transversion)	141	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14062	14062	1	G -> A	SNP (transition)	144	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	14170	14170	1	A -> T	SNP (transversion)	130	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	14173	14173	1	A -> G	SNP (transition)	129	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	14179	14179	1	A -> C	SNP (transversion)	115	98.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	14431	14431	1	T -> C	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14662	14662	1	T -> A	SNP (transversion)	139	98.6%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
GCTA	14665	14668	3	AGTG -> GCTA	Substitution	137 -> 138	97.8%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	KV -> KL	gltB3 CDS
G	14674	14674	1	A -> G	SNP (transition)	131	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	15274	15274	1	G -> A	SNP (transition)	91	100.0%	2,5E-236	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	15526	15526	1	A -> G	SNP (transition)	112	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	15538	15538	1	C -> T	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
GAT	16211	16213	2	CAA -> GAT	Substitution	152 -> 160	99.3% -> 99.4%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	Q -> D	gltD CDS
C	16219	16219	1	G -> C	SNP (transversion)	138	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
T	16222	16222	1	G -> T	SNP (transversion)	137	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
A	16228	16228	1	G -> A	SNP (transition)	141	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
C	16231	16231	1	T -> C	SNP (transition)	141	98.6%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
G	16235	16235	1	A -> G	SNP (transition)	140	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	K -> E	gltD CDS
C	16240	16240	1	T -> C	SNP (transition)	140	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
T	16243	16243	1	C -> T	SNP (transition)	146	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
A	16246	16246	1	T -> A	SNP (transversion)	147	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
G	16255	16255	1	A -> G	SNP (transition)	132	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
A	16258	16258	1	G -> A	SNP (transition)	127	98.4%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
G	17240	17240	1	A -> G	SNP (transition)	165	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		rnhB CDS
C	17383	17383	1	T -> C	SNP (transition)	149	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	K -> E	rnhB CDS
G	17889	17889	1	A -> G	SNP (transition)	142	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Desulforredoxin Fe54 iron-binding domain-containing pro
T	18297	18297	1	C -> T	SNP (transition)	132	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Desulforredoxin Fe54 iron-binding domain-containing pro
T	18372	18372	1	C -> T	SNP (transition)	127	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	19670	19670	1	G -> A	SNP (transition)	106	98.1%	8,8E-177	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		ilvD CDS
A	20611	20611	1	G -> A	SNP (transition)	112	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20614	20614	1	T -> A	SNP (transversion)	115	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	20635	20635	1	T -> G	SNP (transversion)	132	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20638	20638	1	G -> A	SNP (transition)	129	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20644	20644	1	G -> A	SNP (transition)	122	97.5%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	20656	20656	1	T -> C	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20659	20659	1	A -> T	SNP (transversion)	105	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
CAA	20662	20664	2	TAG -> CAA	Substitution	107 -> 108	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	20674	20674	1	T -> C	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20680	20680	1	G -> A	SNP (transition)	111	98.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20692	20692	1	G -> A	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	20695	20695	1	T -> C	SNP (transition)	122	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	20709	20709	1	T -> C	SNP (transition)	122	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	N -> D	comGF CDS
C	20716	20716	1	T -> C	SNP (transition)	119	98.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20725	20725	1	A -> T	SNP (transversion)	117	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	20731	20731	1	A -> G	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	20735	20735	1	T -> C	SNP (transition)	124	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS

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C	20776	20776	1 A -> C	SNP (transversion)	123	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	20779	20779	1 A -> G	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20785	20785	1 A -> T	SNP (transversion)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20797	20797	1 G -> A	SNP (transition)	110	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20812	20812	1 C -> T	SNP (transition)	106	99.1%	3,3E-281	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	20821	20821	1 A -> G	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20830	20830	1 C -> T	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
AAG	20836	20838	2 TAA -> AAG	Substitution	109 -> 111	96.3% -> 96.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20842	20842	1 G -> A	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20845	20845	1 G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	20851	20851	1 T -> G	SNP (transversion)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20854	20854	1 G -> T	SNP (transversion)	106	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
TAA	20868	20868	2 AAG -> TAA	Substitution	110 -> 112	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20872	20872	1 G -> A	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20890	20890	1 G -> A	SNP (transition)	132	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	20893	20893	1 T -> C	SNP (transition)	136	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	20899	20899	1 A -> G	SNP (transition)	135	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20908	20908	1 C -> T	SNP (transition)	135	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20917	20917	1 A -> T	SNP (transversion)	130	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	D -> E	comGF CDS
A	20920	20920	1 G -> A	SNP (transition)	132	97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	20926	20926	1 A -> G	SNP (transition)	132	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20932	20932	1 G -> A	SNP (transition)	132	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20941	20941	1 G -> A	SNP (transition)	131	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21001	21001	1 G -> A	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21004	21004	1 G -> T	SNP (transversion)	135	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21007	21007	1 T -> A	SNP (transversion)	133	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21010	21010	1 A -> T	SNP (transversion)	127	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21034	21034	1 G -> A	SNP (transition)	125	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
AGC	21040	21042	2 GGT -> AGC	Substitution	140 -> 142	97.9%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	T -> A	comGF CDS
A	21046	21046	1 G -> A	SNP (transition)	134	97.8%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	21049	21049	1 A -> G	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21054	21054	1 G -> A	SNP (transition)	116	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21058	21058	1 T -> C	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	21075	21075	1 A -> G	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21079	21079	1 C -> T	SNP (transition)	107	98.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21082	21082	1 T -> C	SNP (transition)	108	98.1%	2,3E-303	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21106	21106	1 G -> A	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	21118	21118	1 A -> G	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21136	21136	1 C -> A	SNP (transversion)	112	97.3%	2,1E-288	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21139	21139	1 C -> T	SNP (transition)	109	95.4%	1,8E-272	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21142	21142	1 T -> A	SNP (transversion)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21154	21154	1 G -> A	SNP (transition)	106	97.2%	7,6E-283	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21157	21157	1 T -> C	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21172	21172	1 T -> C	SNP (transition)	104	99.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21193	21193	1 A -> T	SNP (transversion)	90	98.9%	2,8E-220	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21196	21196	1 T -> C	SNP (transition)	101	99.0%	1E-297	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21202	21202	1 G -> A	SNP (transition)	103	99.0%	1E-303	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21205	21205	1 G -> A	SNP (transition)	100	98.0%	4,9E-290	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21214	21214	1 T -> C	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21226	21226	1 A -> C	SNP (transversion)	104	98.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
CA	21238	21239	2 AG -> CA	Substitution	113 -> 115	97.3% -> 97.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> V	comGF CDS
T	21244	21244	1 C -> T	SNP (transition)	144	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	M -> I	comGF CDS
A	21268	21268	1 T -> A	SNP (transversion)	141	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	21271	21271	1 A -> G	SNP (transition)	141	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21274	21274	1 G -> A	SNP (transition)	142	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21280	21280	1 A -> T	SNP (transversion)	144	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	21283	21283	1 T -> G	SNP (transversion)	144	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21298	21298	1 C -> A	SNP (transversion)	145	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21313	21313	1 C -> T	SNP (transition)	145	96.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21316	21316	1 G -> A	SNP (transition)	147	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21319	21319	1 T -> C	SNP (transition)	149	98.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21418	21417	0 (T)6 -> (T)7	Insertion (tandem repeat)	186	88.2%	2,5E-303	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
T	21682	21682	1 C -> T	SNP (transition)	126	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		quaC CDS
A	22093	22093	1 G -> A	SNP (transition)	131	97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		quaC CDS
C	22173	22173	1 T -> C	SNP (transition)	139	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
A	22276	22276	1 G -> A	SNP (transition)	134	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
T	22282	22282	1 G -> T	SNP (transversion)	134	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
T	22291	22291	1 C -> T	SNP (transition)	128	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
C	22294	22294	1 T -> C	SNP (transition)	132	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
AG	27306	27307	2 GT -> AG	Substitution	141	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	D -> A	dsbI CDS
IG	22315	22315	1 A -> G	SNP (transition)	135	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
TA	22320	22321	2 CG -> TA	Substitution	139 -> 140	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	AV -> AI	dsbI CDS
G	22324	22324	1 A -> G	SNP (transition)	135	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
CT	22604	22605	2 TC -> CT	Substitution	137 -> 138	97.1% -> 98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	D -> S	dsbI CDS
CG	22608	22609	2 TT -> CG	Substitution	126 -> 128	96.0% -> 96.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	GK -> GE	dsbI CDS
C	22834	22834	1 T -> C	SNP (transition)	173	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
ATC	22864	22866	2 GTT -> ATC	Substitution	119 -> 121	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	N -> D	dsbI CDS
A	22870	22870	1 G -> A	SNP (transition)	126	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
T	22891	22891	1 G -> T	SNP (transversion)	149	98.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
A	22897	22897	1 G -> A	SNP (transition)	136	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
GA	22921	22922	2 TG -> GA	Substitution	108	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	T -> I	dsbI CDS
A	22924	22924	1 G -> A	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
GTCA	22939	22942	3 ATG -> GTCA	Substitution	129 -> 122	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	IN -> ID	dsbI CDS
C	22947	22947	1 T -> C	SNP (transition)	123	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	K -> E	dsbI CDS
A	22959	22959	1 C -> A	SNP (transversion)	127	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> S	dsbI CDS
A	22963	22963	1 G -> A	SNP (transition)	131	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
TG	22966	22967	2 GA -> TG	Substitution	128 -> 129	97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	I -> T	dsbI CDS
T	22971	22971	1 C -> T	SNP (transition)	130	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	D -> N	dsbI CDS
A	22987	22987	1 G -> A	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
CAA	22990	22992	2 AAG -> CAA	Substitution	130 -> 132	91.5% -> 91.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
C	23002	23002	1 T -> C	SNP (transition)	157	99.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
A	23038	23038	1 G -> A	SNP (transition)	120	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
C	23041	23041	1 T -> C	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
IG	24160	24160	1 T -> G	SNP (transversion)	143	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	K -> Q	ygjM CDS
T	24166	24166	1 G -> T	SNP (transversion)	127	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	H -> N	ygjM CDS
C	24170	24170	1 T -> C	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
G	24173	24173	1 A -> G	SNP (transition)	122	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
T	24185	24185	1 A -> T	SNP (transversion)	134	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
T	24212	24213	1 C -> T	SNP (transition)	129	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
T	24218	24218	1 G -> T	SNP (transversion)	141	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
IG	24224	24224	1 A -> G	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
A	24500	24500	1 G -> A	SNP (transition)	147	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
GC	24673	24674	2 AT -> GC	Substitution	146	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
C	24710	24710	1 T -> C	SNP (transition)	134	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
IG	25001	25001	1 A -> G	SNP (transition)	142	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	25286	25286	1 T -> C	SNP (transition)	165	98.8%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
T	25408	25408	1 C -> T	SNP (transition)	157	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	E -> K	RNA pseudouridylate synthase CDS
C	25469	25469	1 A -> C	SNP (transversion)	137	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
T	25474	25474	1 C -> T	SNP (transition)	144	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	E -> K	RNA pseudouridylate synthase CDS
A	25478	25478	1 T -> A	SNP (transversion)	144	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
A	25489	25489	1 G -> A	SNP (transition)	148	96.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	H -> Y	RNA pseudouridylate synthase CDS
A	25576	25576	1 G -> A	SNP (transition)	159	98.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
IG	25538	25538	1 A -> G	SNP (transition)	141	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
IG	25610	25610	1 A -> G	SNP (transition)	132	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	25691	25691	1 T -> C	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	26306	26306	1 T -> C	SNP (transition)	128	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
A	26321	26321	1 G -> A	SNP (transition)	138	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
ACTT	26342	26345	3 GTTA -> ACTT	Substitution	130 -> 132	96.9% -> 97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
G	26348	26349	1 T -> G	SNP (transversion)	129	97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
A	26369	26369	1 G -> A	SNP (transition)	135	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
T	27838	27838	1 C -> T	SNP (transition)	137	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	27892	27892	1 C -> T	SNP (transition)	117	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
C	27949	27949	1 T -> C	SNP (transition)	124	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
C	28003	28003	1 T -> C	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28015	28015	1 C -> T	SNP (transition)	108	98.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
C	28018	28018	1 T -> C	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
A	28024	28024	1 G -> A	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
GG	28135	28136	2 AA -> GG	Substitution	104	99.0%	1E-306	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	VS -> VG	mrdA CDS
C	28213	28213	1 T -> C	SNP (transition)	116	97.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28216	28216	1 C -> T	SNP (transition)	115	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28237	28237	1 G -> T	SNP (transversion)	125	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
G	28780	28780	1 T -> G	SNP (transversion)	134	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28816	28816	1 C -> T	SNP (transition)	135	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28822	28822	1 C -> T	SNP (transition)	132	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	32037	32037	1 C -> T	SNP (transition)	112	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pyrG CDS
A	33736	33736	1 G -> A	SNP (transition)	142	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33748	33748	1 T -> C	SNP (transition)	139	97.8%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33751	33751	1 T -> C	SNP (transition)	140	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
T	33757	33757	1 C -> T	SNP (transition)	150	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33769	33769	1 T -> C	SNP (transition)	159	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
A	36609	36609	1 G -> A	SNP (transition)	280	99.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
A	36610	36607	0 +A	Insertion	280	88.6%	9,5E-285	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
C	36624	36624	1 T -> C	SNP (transition)	322	99.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
	36651	36651	1 (A)3 -> (A)2	Deletion (tandem repeat)	340	93.5%	2E-97	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
A	36654	36654	1 T -> A	SNP (transversion)	331	97.6%	2,2E-275	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
AA	36660	36659	0 +AA	Insertion	327	94.8%	6,1E-256	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
C	36669	36669	1 T -> C	SNP (transition)	341	98.8%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
G	38113	38113	1 A -> G	SNP (transition)	312	99.0%	1,3E-86	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
	38420	38420	1 (T)3 -> (T)2	Deletion (tandem repeat)	333	99.7%	4,4E-31	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
G	74125	74125	1 A -> G	SNP (transition)	110	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mnmA CDS
C	74440	74440	1 T -> C	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mnmA CDS
G	75068	75069	1 A -> G	SNP (transition)	128	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Cytokinin riboside 5'-monophosphate phosphoribohydrolas

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C	75173	75173	1 T -> C	SNP (transition)	147	98.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	Cytokinin riboside 5'-monophosphate phosphoribohydrolas
G	75195	75195	1 A -> G	SNP (transition)	140	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Cytokinin riboside 5'-monophosphate phosphoribohydrolas
T	75279	75279	1 C -> T	SNP (transition)	122	96.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
TA	75302	75301	0 (TA)2 -> (TA)3	Insertion (tandem repeat)	131 -> 133	96.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
G	189257	189257	1 A -> G	SNP (transition)	108	97.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		rpsM CDS
C	189445	189445	1 T -> C	SNP (transition)	137	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	rpsM CDS
C	189538	189538	1 T -> C	SNP (transition)	158	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
C	189586	189586	1 T -> C	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
A	189981	189981	1 G -> A	SNP (transition)	81	97.5%	2,6E-225	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		infA CDS
CTG	195255	195257	3 TGT -> CTG	Substitution	40	100.0%	1E-123	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
TAA	195259	195261	3 GTT -> TAA	Substitution	40 -> 60	98.3% -> 100.0%	1E-115	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
A	195266	195266	1 T -> A	SNP (transversion)	61	100.0%	6,3E-195	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
C	195268	195268	1 G -> C	SNP (transversion)	61	96.7%	2,3E-179	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
T	195295	195295	1 C -> T	SNP (transition)	80	98.8%	6,3E-227	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
ATG	195297	195299	3 GAT -> ATG	Substitution	80 -> 84	96.3% -> 96.4%	1E-242	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
G	195307	195307	1 A -> G	SNP (transition)	87	100.0%	1E-260	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
G	195325	195325	1 A -> G	SNP (transition)	100	98.0%	7,8E-300	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
T	195344	195344	1 G -> T	SNP (transversion)	109	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
C	195431	195431	1 T -> C	SNP (transition)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
A	195464	195464	1 G -> A	SNP (transition)	106	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
C	196214	196214	1 A -> C	SNP (transversion)	144	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
AAA	196223	196225	3 GGG -> AAA	Substitution	138 -> 146	97.8% -> 97.9%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	LG -> LN	MFS transporter CDS
A	196279	196279	1 G -> A	SNP (transition)	134	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
G	196234	196234	1 C -> G	SNP (transversion)	136	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> G	MFS transporter CDS
G	196236	196236	1 A -> G	SNP (transition)	132	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	MFS transporter CDS
GATA	196256	196259	3 AGT -> GATA	Substitution	136 -> 138	97.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	QV -> QI	MFS transporter CDS
G	196271	196271	1 A -> G	SNP (transition)	129	97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
A	196274	196274	1 T -> A	SNP (transversion)	132	97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
GCTT	196278	196281	3 ACAC -> GCTT	Substitution	142 -> 145	96.6% -> 97.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	TL -> AL	MFS transporter CDS
C	196286	196286	1 T -> C	SNP (transition)	145	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
G	196289	196289	1 A -> G	SNP (transition)	141	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
T	196292	196292	1 G -> T	SNP (transversion)	135	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
T	196301	196301	1 C -> T	SNP (transition)	129	96.9%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
A	196310	196310	1 G -> A	SNP (transition)	121	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
T	196319	196319	1 A -> T	SNP (transversion)	143	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	I -> F	MFS transporter CDS
A	196325	196325	1 G -> A	SNP (transition)	126	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
C	196354	196354	1 T -> C	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> A	MFS transporter CDS
T	196360	196360	1 C -> T	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> V	MFS transporter CDS
TT	196372	196373	2 GC -> TT	Substitution	104 -> 105	98.1%	5,3E-302	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	C -> F	MFS transporter CDS
A	196376	196376	1 G -> A	SNP (transition)	105	98.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
G	196397	196397	1 T -> G	SNP (transversion)	95	98.9%	3,8E-285	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	D -> E	MFS transporter CDS
TTG	196407	196409	2 CTT -> TTG	Substitution	95 -> 96	100.0%	2,5E-297	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
T	196412	196412	1 C -> T	SNP (transition)	97	99.0%	1,5E-266	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
GGTG	196415	196418	4 AACC -> GGTG	Substitution	99 -> 102	96.0% -> 96.1%	5,1E-286	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	LT -> LV	MFS transporter CDS
G	196427	196427	1 A -> G	SNP (transition)	116	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
TCG	196431	196433	2 ACA -> TCG	Substitution	112	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	T -> S	MFS transporter CDS
T	196435	196435	1 G -> T	SNP (transversion)	112	98.4%	3,9E-308	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	S -> I	MFS transporter CDS
G	196463	196463	1 C -> G	SNP (transversion)	100	99.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
C	196466	196466	1 T -> C	SNP (transition)	97	99.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
A	196469	196469	1 T -> A	SNP (transversion)	97	99.0%	9,7E-285	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
T	196523	196523	1 C -> T	SNP (transition)	115	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
T	196529	196529	1 G -> T	SNP (transversion)	115	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
T	196538	196538	1 C -> T	SNP (transition)	109	97.2%	8,3E-302	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
A	196547	196547	1 T -> A	SNP (transversion)	112	98.4%	3,9E-308	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
TT	196550	196551	2 CG -> TT	Substitution	115	96.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	IA -> IS	MFS transporter CDS
C	196556	196556	1 A -> C	SNP (transition)	118	97.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
TA	196559	196560	2 GG -> TA	Substitution	144	97.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	GV -> GI	MFS transporter CDS
G	196568	196568	1 T -> G	SNP (transversion)	123	97.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
A	196571	196571	1 G -> A	SNP (transition)	120	96.7%	2E-294	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
CG	196574	196575	2 TA -> CG	Substitution	127	97.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	LI -> LV	MFS transporter CDS
T	196586	196586	1 C -> T	SNP (transition)	131	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
A	196592	196592	1 T -> A	SNP (transversion)	133	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
G	196598	196598	1 T -> G	SNP (transversion)	129	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
G	196600	196600	1 C -> G	SNP (transversion)	129	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	T -> S	MFS transporter CDS
A	196603	196603	1 G -> A	SNP (transition)	120	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	R -> K	MFS transporter CDS
AAT	196605	196607	3 GGC -> AAT	Substitution	118 -> 120	97.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	G -> N	MFS transporter CDS
T	196628	196628	1 A -> T	SNP (transversion)	129	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
T	196650	196650	1 C -> T	SNP (transition)	138	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
G	196655	196655	1 T -> G	SNP (transversion)	138	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
A	196661	196661	1 G -> A	SNP (transition)	138	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
C	196673	196673	1 T -> C	SNP (transition)	136	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
ATA	196680	196682	2 CTT -> ATA	Substitution	130 -> 132	96.9% -> 97.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	L -> I	MFS transporter CDS
A	196688	196688	1 G -> A	SNP (transition)	127	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
A	196700	196699	0 (A)3 -> (A)4	Insertion (tandem repeat)	130	83.8%	6,8E-292	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
A	196711	196711	1 G -> A	SNP (transition)	107	97.2%	2E-306	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	R -> H	MFS transporter CDS
G	196720	196720	1 A -> G	SNP (transition)	123	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
T	196723	196723	1 C -> T	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
A	196785	196785	1 G -> A	SNP (transition)	88	98.9%	1,4E-293	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
G	196791	196791	1 A -> G	SNP (transition)	88	100.0%	6,3E-299	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
A	196803	196803	1 T -> A	SNP (transversion)	91	100.0%	6,3E-291	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	F -> L	pvdE CDS
G	196806	196806	1 A -> G	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
G	196809	196809	1 C -> G	SNP (transversion)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	P -> L	pvdE CDS
T	196812	196812	1 C -> T	SNP (transition)	98	99.0%	2E-298	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
C	196822	196822	1 A -> C	SNP (transversion)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	I -> L	pvdE CDS
A	196837	196837	1 T -> A	SNP (transversion)	123	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	S -> T	pvdE CDS
C	196842	196842	1 T -> C	SNP (transition)	122	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
T	196848	196848	1 A -> T	SNP (transversion)	130	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
A	196851	196851	1 G -> A	SNP (transition)	132	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
T	196860	196860	1 C -> T	SNP (transition)	124	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
T	196863	196863	1 A -> T	SNP (transversion)	117	97.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
T	196866	196866	1 C -> T	SNP (transition)	122	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
G	196884	196884	1 A -> G	SNP (transition)	93	98.9%	5,8E-283	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
G	196894	196894	1 A -> G	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	T -> A	pvdE CDS
C	196902	196902	1 T -> C	SNP (transition)	115	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
T	196914	196914	1 A -> T	SNP (transversion)	113	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	L -> F	pvdE CDS
T	196917	196917	1 C -> T	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
T	196923	196923	1 C -> T	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
T	196925	196925	1 C -> T	SNP (transition)	120	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> V	pvdE CDS
TTGATT	196933	196938	4 ATAGTA -> TTGATT	Substitution	114 -> 115	96.5% -> 97.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	IV -> LI	pvdE CDS
ATA	196945	196947	2 CTT -> ATA	Substitution	114 -> 115	96.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	L -> I	pvdE CDS
T	196950	196950	1 C -> T	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
T	196962	196962	1 A -> T	SNP (transversion)	123	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
ACTT	196965	196968	3 GTTA -> ACTT	Substitution	121 -> 126	95.9% -> 96.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
CTT	196972	196974	2 TTA -> CTT	Substitution	113 -> 119	98.2% -> 98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
A	196978	196978	1 G -> A	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> I	pvdE CDS
A	196986	196986	1 T -> A	SNP (transversion)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
T	196995	196995	1 C -> T	SNP (transition)	100	100.0%	1E-299	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
A	197004	197004	1 G -> A	SNP (transition)	98	100.0%	1,6E-303	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
G	197013	197013	1 A -> G	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
A	197019	197019	1 G -> A	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
A	197130	197130	1 G -> A	SNP (transition)	125	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		pvdE CDS
T	197791	197791	1 C -> T	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	I -> F	pvdE CDS
C	199112	199112	1 T -> C	SNP (transition)	125	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	N -> D	cgb CDS
T	199238	199238	1 C -> T	SNP (transition)	111	98.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> I	cgb CDS
A	199242	199242	1 G -> A	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		cgb CDS
T	199248	199248	1 C -> T	SNP (transition)	114	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		cgb CDS
T	199263	199263	1 C -> T	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		cgb CDS
T	199266	199266	1 C -> T	SNP (transition)	173	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		cgb CDS
A	199269	199269	1 G -> A	SNP (transition)	123	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		cgb CDS
A	199284	199284	1 T -> A	SNP (transversion)	122	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		cgb CDS
C	199287	199287	1 T -> C	SNP (transition)	120	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		cgb CDS
A	199290	199290	1 G -> A	SNP (transition)	120	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		cgb CDS
T	200253	200253	1 C -> T	SNP (transition)	110	97.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		glcD CDS
C	200417	200417	1 A -> C	SNP (transversion)	135	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	N -> T	glcD CDS
C	200508	200508	1 G -> C	SNP (transversion)	158	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> L	glcD CDS
C	200967	200967	1 T -> C	SNP (transition)	134	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		glcD CDS
A	201208	201208	1 G -> A	SNP (transition)	143	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	D -> N	glcD CDS
G	201287	201287	1 A -> G	SNP (transition)	147	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	E -> G	glcD CDS
T	202059	202059	1 C -> T	SNP (transition)	149	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		glcD CDS
A	202570	202570	1 G -> A	SNP (transition)	129	97.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
T	202974	202974	1 C -> T	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	T -> I	ABC transporter substrate-binding protein CDS
G	203404	203404	1 C -> G	SNP (transversion)	98	98.0%	1,2E-259	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
A	203407	203407	1 G -> A	SNP (transition)	98	100.0%	4E-274	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
GCG	203429	203431	2 ACT -> GCG	Substitution	94 -> 95	98.9% -> 100.0%	2,4E-270	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	T -> A	ABC transporter substrate-binding protein CDS
C	203437	203437	1 T -> C	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
T	203447	203447	1 C -> T	SNP (transition)	109	98.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
A	203455	203455	1 G -> A	SNP (transition)	99	97.0%	1,6E-282	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
A	203461	203461	1 G -> A	SNP (transition)	98	95.9%	3,6E-275	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
T	203464	203464	1 A -> T	SNP (transversion)	98	100.0%	1E-293	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
A	203482	203482	1 G -> A	SNP (transition)	93	97.8%	5,4E-260	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
G	203487	203487	1 A -> G	SNP (transition)	94	98.9%	2,4E-295	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	K -> R	ABC transporter substrate-binding protein CDS
A	203497	203497	1 G -> A	SNP (transition)	96	96.9%	1,8E-303	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
G	203501	203501	1 A -> G	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	ABC transporter substrate-binding protein CDS
AGC	203504	203506	3 GCT -> AGC	Substitution	101 -> 105	98.0% -> 98.1%	1E-277	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> S	ABC transporter substrate-binding protein CDS
G	203512	203512	1 T -> G	SNP (transversion)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
G	203515	203515	1 A -> G	SNP (transition)	106	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
T	203518	203518	1 A -> T	SNP (transversion)	106	98.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
A	203521	203521	1 G -> A	SNP (transition)	103	100.0%	7,9E-278	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
T	203527	203527	1 G -> T	SNP (transversion)	101	98.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
A	203530	203530	1 C -> A	SNP (transversion)	101	97.0%	1,7E-288	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
ATA	203564	203566	2 GTG -> ATA	Substitution	110 -> 112	97.3% -> 98.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> I	ABC transporter substrate-binding protein CDS
C	203568	203568	1 T -> C	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS

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C	203599	203599	1 T -> C	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
T	203602	203602	1 C -> T	SNP (transition)	111	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
G	203608	203608	1 A -> G	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
A	203611	203611	1 G -> A	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
G	203642	203642	1 A -> G	SNP (transition)	121	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	N -> D	ABC transporter substrate-binding protein CDS
A	203662	203662	1 G -> A	SNP (transition)	122	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
A	203680	203680	1 G -> A	SNP (transition)	123	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
G	203683	203683	1 A -> G	SNP (transition)	129	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
G	203695	203695	1 A -> G	SNP (transition)	128	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
A	203704	203704	1 T -> A	SNP (transversion)	125	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
C	203715	203715	1 T -> C	SNP (transition)	131	97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	L -> S	ABC transporter substrate-binding protein CDS
A	203722	203722	1 G -> A	SNP (transition)	134	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
GAGA	203728	203731	3 ACGC -> GAGA	Substitution	120 -> 123	98.3% -> 98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
A	203737	203737	1 G -> A	SNP (transition)	124	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
T	203749	203749	1 A -> T	SNP (transversion)	135	97.8%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	E -> D	ABC transporter substrate-binding protein CDS
A	203755	203755	1 T -> A	SNP (transversion)	126	96.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
CTTGGCC	203788	203794	5 TCTAACT -> CTTGGCC	Substitution	132 -> 134	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	FLT -> FLA	ABC transporter substrate-binding protein CDS
T	203809	203809	1 C -> T	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
G	203812	203812	1 A -> G	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
AAAGATTTAAAA	203822	203833	9 GCTAAACTTGAG -> AAA	Substitution	111 -> 123	95.9% -> 96.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	AKLE -> KDLK	ABC transporter substrate-binding protein CDS
ATC	203837	203839	2 GTT -> ATC	Substitution	108 -> 110	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> I	ABC transporter substrate-binding protein CDS
A	203843	203843	1 G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> T	ABC transporter substrate-binding protein CDS
G	203848	203848	1 A -> G	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
C	203850	203850	1 A -> C	SNP (transversion)	136	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	N -> T	ABC transporter substrate-binding protein CDS
T	203857	203857	1 C -> T	SNP (transition)	133	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
C	203863	203863	1 T -> C	SNP (transition)	135	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
G	203869	203869	1 A -> G	SNP (transition)	130	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
G	203885	203885	1 A -> G	SNP (transition)	134	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	ABC transporter substrate-binding protein CDS
T	203901	203907	5 AAATA -> T	Deletion	178 -> 139	99.2% -> 99.3%	2,5E-264	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter substrate-binding protein CDS
C	203938	203938	1 T -> C	SNP (transition)	135	97.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
A	203941	203941	1 C -> A	SNP (transversion)	133	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
T	203965	203965	1 C -> T	SNP (transition)	140	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
A	203974	203974	1 G -> A	SNP (transition)	143	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
C	203992	203992	1 T -> C	SNP (transition)	145	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
A	203996	203996	1 G -> A	SNP (transition)	159	98.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> I	Peptide ABC-transport system permease protein CDS
T	204001	204001	1 G -> T	SNP (transversion)	156	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
T	204007	204007	1 A -> T	SNP (transversion)	142	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
GG	204011	204012	2 AA -> GG	Substitution	139 -> 140	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	K -> G	Peptide ABC-transport system permease protein CDS
T	204016	204016	1 C -> T	SNP (transition)	142	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
A	204022	204022	1 T -> A	SNP (transversion)	139	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
T	204028	204028	1 C -> T	SNP (transition)	143	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
A	204031	204031	1 G -> A	SNP (transition)	143	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
T	204037	204037	1 G -> T	SNP (transversion)	142	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	L -> F	Peptide ABC-transport system permease protein CDS
CAA	204053	204055	3 GCC -> CAA	Substitution	119 -> 120	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> Q	Peptide ABC-transport system permease protein CDS
T	204076	204076	1 C -> T	SNP (transition)	136	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
A	204092	204092	1 C -> A	SNP (transversion)	153	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	Q -> K	Peptide ABC-transport system permease protein CDS
A	204171	204171	1 G -> A	SNP (transition)	157	99.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
GGGA	204127	204130	3 AAGT -> GGGA	Substitution	159 -> 160	99.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	LS -> LG	Peptide ABC-transport system permease protein CDS
C	204145	204145	1 T -> C	SNP (transition)	129	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
A	204148	204148	1 G -> A	SNP (transition)	128	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
T	204166	204166	1 C -> T	SNP (transition)	137	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
A	204169	204169	1 T -> A	SNP (transversion)	137	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
A	204178	204178	1 G -> A	SNP (transition)	138	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
TTTT	204181	204184	4 GGCA -> TTTT	Substitution	138	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	MA -> IF	Peptide ABC-transport system permease protein CDS
T	204190	204190	1 C -> T	SNP (transition)	138	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
T	204193	204193	1 G -> T	SNP (transversion)	138	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	L -> F	Peptide ABC-transport system permease protein CDS
GG	204198	204200	2 AA -> GG	Substitution	137	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	LS -> LG	Peptide ABC-transport system permease protein CDS
TTT	204203	204205	2 CTA -> TTT	Substitution	136	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	L -> F	Peptide ABC-transport system permease protein CDS
A	204215	204215	1 G -> A	SNP (transition)	140	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> M	Peptide ABC-transport system permease protein CDS
A	204223	204223	1 G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
T	204427	204427	1 A -> T	SNP (transversion)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	L -> F	Peptide ABC-transport system permease protein CDS
C	204430	204430	1 T -> C	SNP (transition)	112	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
C	204433	204433	1 T -> C	SNP (transition)	112	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
AAA	204437	204439	2 GAG -> AAA	Substitution	113	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	E -> K	Peptide ABC-transport system permease protein CDS
CTT	204443	204445	2 TTG -> CTT	Substitution	95 -> 96	98.9% -> 99.0%	1,6E-300	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Peptide ABC-transport system permease protein CDS
C	207571	207571	1 T -> C	SNP (transition)	89	98.9%	1,4E-270	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	nusB CDS	
T	208094	208094	1 C -> T	SNP (transition)	154	98.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> V	nusC CDS
AGA	209123	209125	2 CGC -> AGA	Substitution	107 -> 109	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
GCTT	209140	209143	3 ATTA -> GCTT	Substitution	127 -> 129	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
T	209146	209146	1 C -> T	SNP (transition)	175	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
C	209149	209149	1 T -> C	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
G	209153	209153	1 A -> G	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	T -> A	nusD CDS
A	209176	209176	1 T -> A	SNP (transversion)	127	97.8%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
C	209182	209182	1 T -> C	SNP (transition)	126	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209185	209185	1 G -> A	SNP (transition)	126	97.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
G	209197	209197	1 T -> G	SNP (transversion)	127	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209209	209209	1 G -> A	SNP (transition)	128	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
G	209215	209215	1 A -> G	SNP (transition)	128	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
T	209218	209218	1 C -> T	SNP (transition)	126	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
C	209233	209233	1 A -> C	SNP (transversion)	127	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
G	209236	209236	1 A -> G	SNP (transition)	127	97.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209260	209260	1 G -> A	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209269	209269	1 T -> A	SNP (transversion)	112	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209275	209275	1 G -> A	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
T	209302	209302	1 C -> T	SNP (transition)	119	96.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209305	209305	1 G -> A	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209566	209566	1 G -> A	SNP (transition)	161	98.8%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209704	209704	1 G -> A	SNP (transition)	146	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
C	209710	209710	1 A -> C	SNP (transversion)	127	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
CAG	209713	209715	3 TGC -> CAG	Substitution	116 -> 124	99.1% -> 99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	SA -> SS	nusD CDS
A	209722	209722	1 G -> A	SNP (transition)	116	96.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
G	209725	209725	1 A -> G	SNP (transition)	118	97.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209740	209740	1 G -> A	SNP (transition)	126	97.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
GCTT	209767	209770	3 TTTA -> GCTT	Substitution	135 -> 136	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209773	209773	1 C -> A	SNP (transversion)	137	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
T	209791	209791	1 C -> T	SNP (transition)	139	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209794	209794	1 T -> A	SNP (transversion)	134	95.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
G	209797	209797	1 A -> G	SNP (transition)	135	97.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
T	209803	209803	1 C -> T	SNP (transition)	133	97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209815	209815	1 T -> A	SNP (transversion)	123	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
T	209827	209827	1 A -> T	SNP (transversion)	131	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
G	209830	209830	1 A -> G	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
G	209917	209917	1 A -> G	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209938	209938	1 G -> A	SNP (transition)	105	98.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
T	209941	209941	1 G -> T	SNP (transversion)	102	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209950	209950	1 G -> A	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	209962	209962	1 G -> A	SNP (transition)	108	97.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusD CDS
A	210266	210266	1 G -> A	SNP (transition)	118	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	M -> I	hypothetical protein CDS
C	211030	211030	1 T -> C	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
T	211186	211186	1 C -> T	SNP (transition)	137	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
G	211207	211207	1 A -> G	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
T	211213	211213	1 C -> T	SNP (transition)	123	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
T	211225	211225	1 C -> T	SNP (transition)	128	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
A	211228	211228	1 G -> A	SNP (transition)	125	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
C	211252	211252	1 T -> C	SNP (transition)	132	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
T	211291	211291	1 C -> T	SNP (transition)	127	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
G	211294	211294	1 A -> G	SNP (transition)	140	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
A	211351	211351	1 G -> A	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
C	211363	211363	1 T -> C	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
T	211366	211366	1 C -> T	SNP (transition)	121	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
T	211465	211465	1 C -> T	SNP (transition)	139	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
A	211495	211495	1 G -> A	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
C	211519	211519	1 A -> C	SNP (transversion)	113	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
C	211522	211522	1 T -> C	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
C	211524	211524	1 T -> C	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	M -> T	nusG CDS
A	211537	211537	1 T -> A	SNP (transversion)	127	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
A	211645	211645	1 G -> A	SNP (transition)	121	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
C	211654	211654	1 T -> C	SNP (transition)	124	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
TTG	211664	211666	2 CTT -> TTG	Substitution	133 -> 134	97.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
ATT	211679	211681	2 GTC -> ATT	Substitution	137 -> 140	98.5% -> 98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> I	nusG CDS
G	211684	211684	1 A -> G	SNP (transition)	141	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
C	211693	211693	1 T -> C	SNP (transition)	140	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
T	211699	211699	1 C -> T	SNP (transition)	129	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
AA	211710	211711	2 CT -> AA	Substitution	107 -> 108	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> E	nusG CDS
T	211723	211723	1 C -> T	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
G	211776	211776	1 A -> G	SNP (transition)	110	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
T	211729	211729	1 C -> T	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
C	211741	211741	1 T -> C	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
G	211768	211768	1 A -> G	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
GGA	211795	211797	3 AAG -> GGA	Substitution	118 -> 119	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	AS -> AD	nusG CDS
A	211801	211801	1 G -> A	SNP (transition)	118	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
C	211813	211813	1 T -> C	SNP (transition)	107	98.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
A	211822	211822	1 G -> A	SNP (transition)	95	98.9%	9,5E-233	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
G	211828	211828	1 A -> G	SNP (transition)	87	100.0%	2E-269	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
G	211831	211831	1 A -> G	SNP (transition)	85	100.0%	3,2E-280	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
G	211840	211840	1 A -> G	SNP (transition)	85	100.0%	1E-271	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
A	211849	211849	1 G -> A	SNP (transition)	88	100.0%	1,6E-272	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
A	211854	211854	1 G -> A	SNP (transition)	91	100.0%	1E-272	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	R -> K	nusG CDS
C	211838	211858	1 T -> C	SNP (transition)	99	100.0%	1,3E-308	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
T	211867	211867	1 C -> T	SNP (transition)	107	100.0%	2,5E-299	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
T	211873	211873	1 C -> T	SNP (transition)	110	100.0%	1E-307	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS
T	211879	211879	1 C -> T	SNP (transition)	125	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nusG CDS

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C	211882	211882	1 A -> C	SNP (transversion)	122	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
T	211885	211885	1 C -> T	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
A	211903	211903	1 G -> A	SNP (transition)	105	97.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
A	211912	211912	1 C -> A	SNP (transversion)	102	100.0%	1,6E-295	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	F -> L	nuoG CDS
T	211924	211924	1 C -> T	SNP (transition)	106	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
C	211987	211987	1 T -> C	SNP (transition)	139	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
T	211996	211996	1 C -> T	SNP (transition)	134	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
C	212035	212035	1 T -> C	SNP (transition)	128	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
C	212041	212041	1 T -> C	SNP (transition)	126	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
A	212077	212077	1 G -> A	SNP (transition)	144	98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
A	212156	212156	1 G -> A	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> T	nuoG CDS
T	212200	212200	1 C -> T	SNP (transition)	145	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
T	212206	212206	1 C -> T	SNP (transition)	145	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
G	212236	212236	1 A -> G	SNP (transition)	126	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
G	212278	212278	1 A -> G	SNP (transition)	108	98.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
A	212291	212291	1 G -> A	SNP (transition)	122	97.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> I	nuoG CDS
C	212322	212322	1 T -> C	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	I -> T	nuoG CDS
A	212432	212432	1 C -> A	SNP (transversion)	129	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	Q -> K	nuoG CDS
G	212440	212440	1 T -> G	SNP (transversion)	124	97.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
G	212659	212659	1 A -> G	SNP (transition)	110	98.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
AAA	212663	212665	2 GAG -> AAA	Substitution	108 -> 116	97.2% -> 97.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	E -> K	nuoG CDS
AC	212667	212668	2 GT -> AC	Substitution	107 -> 110	98.1% -> 98.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	S -> N	nuoG CDS
C	212670	212670	1 T -> C	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	M -> T	nuoG CDS
C	212680	212680	1 T -> C	SNP (transition)	115	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
A	212689	212689	1 G -> A	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
C	212692	212692	1 T -> C	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
C	212695	212695	1 T -> C	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
T	212698	212698	1 C -> T	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
A	212701	212701	1 G -> A	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	R -> K	nuoG CDS
T	212707	212707	1 A -> T	SNP (transversion)	110	98.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
T	212716	212716	1 C -> T	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
G	212731	212731	1 A -> G	SNP (transition)	128	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
A	212737	212737	1 T -> A	SNP (transversion)	136	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
A	212743	212743	1 G -> A	SNP (transition)	143	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
TGCG	212749	212752	3 CTCA -> TGCG	Substitution	141	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	SS -> SA	nuoG CDS
G	213008	213008	1 A -> G	SNP (transition)	117	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	Y -> C	nuoG CDS
C	213169	213169	1 T -> C	SNP (transition)	119	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
A	213346	213346	1 G -> A	SNP (transition)	137	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		nuoG CDS
A	215118	215118	1 C -> A	SNP (transversion)	116	97.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	T -> K	NADH-quinone oxidoreductase subunit J CDS
C	216776	216776	1 T -> C	SNP (transition)	90	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit L CDS
G	217573	217573	1 C -> G	SNP (transversion)	171	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	D -> E	NADH-ubiquinone oxidoreductase subunit L CDS
A	218646	218646	1 G -> A	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-ubiquinone oxidoreductase chain M CDS
A	218970	218970	1 G -> A	SNP (transition)	133	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-ubiquinone oxidoreductase chain M CDS
G	219316	219316	1 A -> G	SNP (transition)	136	97.8%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
T	219542	219542	1 C -> T	SNP (transition)	120	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
T	220004	220004	1 C -> T	SNP (transition)	109	98.2%	2,9E-308	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	H -> Y	NADH-quinone oxidoreductase subunit N CDS
T	220219	220219	1 C -> T	SNP (transition)	139	96.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
GTG	220228	220228	2 ATA -> GTG	Substitution	137 -> 140	97.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	NADH-quinone oxidoreductase subunit N CDS
G	220237	220237	1 A -> G	SNP (transition)	139	97.8%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
T	220249	220249	1 G -> T	SNP (transversion)	132	97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
T	220258	220258	1 A -> T	SNP (transversion)	126	96.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
C	220321	220321	1 T -> C	SNP (transition)	131	96.9%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
C	220345	220345	1 T -> C	SNP (transition)	117	97.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
T	220360	220360	1 G -> T	SNP (transversion)	122	96.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
C	220363	220363	1 T -> C	SNP (transition)	126	97.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
G	220366	220366	1 A -> G	SNP (transition)	127	96.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
T	220370	220370	1 C -> T	SNP (transition)	131	95.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
A	220373	220373	1 G -> A	SNP (transition)	132	94.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> I	NADH-quinone oxidoreductase subunit N CDS
G	220387	220387	1 A -> G	SNP (transition)	128	96.9%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
A	220391	220391	1 G -> A	SNP (transition)	127	95.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> I	NADH-quinone oxidoreductase subunit N CDS
C	220399	220399	1 T -> C	SNP (transition)	132	95.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
C	220410	220410	1 T -> C	SNP (transition)	145	96.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> A	NADH-quinone oxidoreductase subunit N CDS
A	220414	220414	1 G -> A	SNP (transition)	144	95.8%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
T	220451	220451	1 C -> T	SNP (transition)	132	93.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	L -> F	NADH-quinone oxidoreductase subunit N CDS
A	220462	220462	1 G -> A	SNP (transition)	175	96.8%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
G	220471	220471	1 A -> G	SNP (transition)	132	96.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
T	220492	220492	1 C -> T	SNP (transition)	142	96.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		NADH-quinone oxidoreductase subunit N CDS
A	220531	220531	1 G -> A	SNP (transition)	111	98.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
A	220537	220537	1 G -> A	SNP (transition)	118	97.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
A	220540	220540	1 G -> A	SNP (transition)	117	97.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
C	220549	220549	1 T -> C	SNP (transition)	126	97.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
A	220571	220571	1 G -> A	SNP (transition)	128	97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> T	Flagellar protein CDS
C	220579	220579	1 T -> C	SNP (transition)	137	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
C	220588	220588	1 T -> C	SNP (transition)	128	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
T	220594	220594	1 C -> T	SNP (transition)	130	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
T	220606	220606	1 C -> T	SNP (transition)	179	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
A	220651	220651	1 G -> A	SNP (transition)	118	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
AC	220655	220656	2 GT -> AC	Substitution	117	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> T	Flagellar protein CDS
C	220660	220660	1 T -> C	SNP (transition)	120	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
G	220669	220669	1 A -> G	SNP (transition)	124	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
A	220693	220693	1 G -> A	SNP (transition)	123	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	M -> I	Flagellar protein CDS
C	220696	220696	1 T -> C	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
A	220718	220718	1 G -> A	SNP (transition)	136	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	D -> N	Flagellar protein CDS
C	220726	220726	1 T -> C	SNP (transition)	131	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
T	220729	220729	1 C -> T	SNP (transition)	127	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
C	220742	220742	1 T -> C	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
C	220753	220753	1 T -> C	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
G	220759	220759	1 A -> G	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
T	220784	220784	1 C -> T	SNP (transition)	126	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
C	220798	220798	1 T -> C	SNP (transition)	122	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
A	220819	220819	1 G -> A	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
AT	220832	220833	2 GC -> AT	Substitution	127 -> 129	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> I	Flagellar protein CDS
A	220840	220840	1 G -> A	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
AC	220843	220844	2 GT -> AC	Substitution	177 -> 132	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
GAC	220847	220847	2 AAT -> GAC	Substitution	128 -> 133	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	N -> D	Flagellar protein CDS
GCA	220859	220861	3 ATG -> GCA	Substitution	121 -> 138	98.3% -> 98.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	M -> A	Flagellar protein CDS
T	220870	220870	1 C -> T	SNP (transition)	117	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
A	220873	220873	1 G -> A	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
T	220885	220885	1 C -> T	SNP (transition)	131	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
A	220888	220888	1 T -> A	SNP (transversion)	132	97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
T	220897	220897	1 A -> T	SNP (transversion)	134	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
CTT	220901	220903	2 TTA -> CTT	Substitution	134 -> 135	98.5%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
A	220906	220906	1 G -> A	SNP (transition)	132	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
GC	220908	220909	2 AT -> GC	Substitution	129 -> 131	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	H -> R	Flagellar protein CDS
C	220911	220911	1 T -> C	SNP (transition)	130	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> A	Flagellar protein CDS
C	220918	220918	1 T -> C	SNP (transition)	141	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
G	220927	220927	1 A -> G	SNP (transition)	130	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
C	222538	222538	1 T -> C	SNP (transition)	120	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Flagellar protein CDS
TTTGC	461516	461520	4 AGTTT -> TTTGC	Substitution	43 -> 45	86.4% -> 93.0%	8,6E-97	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	LNS -> LQT	DUF115 domain-containing protein CDS
TTT	461526	461528	2 ATC -> TTT	Substitution	41	90.2%	6,2E-92	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	D -> K	DUF115 domain-containing protein CDS
GGG	461532	461534	3 AAC -> GGG	Substitution	40 -> 41	87.5% -> 87.8%	2,1E-88	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> P	DUF115 domain-containing protein CDS
G	461540	461540	1 C -> G	SNP (transversion)	40	85.0%	2,4E-89	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	E -> Q	DUF115 domain-containing protein CDS
C	523110	523110	1 T -> C	SNP (transition)	87	98.9%	1,4E-281	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	pnp CDS
G	523841	523841	1 A -> G	SNP (transition)	70	100.0%	1E-230	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	V -> A	pnp CDS
T	526665	526665	1 C -> T	SNP (transition)	81	98.8%	8,1E-238	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		RDD family protein CDS
G	526683	526683	1 A -> G	SNP (transition)	79	98.7%	3,1E-255	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		RDD family protein CDS
A	526740	526740	1 G -> A	SNP (transition)	94	98.9%	2,4E-295	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		RDD family protein CDS
C	526992	526992	1 T -> C	SNP (transition)	130	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		RDD family protein CDS
A	527885	527885	1 G -> A	SNP (transition)	144	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		purD CDS
C	528344	528344	1 T -> C	SNP (transition)	112	97.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
T	528354	528354	1 C -> T	SNP (transition)	118	97.5%	8,3E-259	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
T	528615	528615	1 C -> T	SNP (transition)	88	100.0%	6,8E-298	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	R -> H	hypothetical protein CDS
A	528800	528800	1 T -> A	SNP (transversion)	118	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	528803	528803	1 A -> C	SNP (transversion)	116	97.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
TGC	528808	528808	2 GGA -> TGC	Substitution	106 -> 110	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	S -> A	hypothetical protein CDS
G	528812	528812	1 A -> G	SNP (transition)	111	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GA	528826	528827	2 AG -> GA	Substitution	132 -> 134	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	528833	528833	1 T -> C	SNP (transition)	122	98.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	528842	528842	1 A -> T	SNP (transversion)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	528854	528854	1 G -> A	SNP (transition)	100	98.0%	4,9E-290	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	528857	528857	1 A -> G	SNP (transition)	99	98.0%	9,7E-297	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	528872	528872	1 A -> G	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	528878	528878	1 A -> T	SNP (transversion)	92	98.9%	9,2E-271	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	528887	528887	1 A -> T	SNP (transversion)	92	100.0%	2,5E-303	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
TAA	528917	528919	2 CAG -> TAA	Substitution	107 -> 108	97.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	529675	529675	1 T -> C	SNP (transition)	117	99.1%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	N -> D	hypothetical protein CDS
G	530578	530578	1 A -> G	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	T -> A	SAM-dependent methyltransferase CDS
G	530614	530614	1 C -> G	SNP (transversion)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	F -> L	SAM-dependent methyltransferase CDS
T	530815	530815	1 C -> T	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Class I SAM-dependent methyltransferase CDS
C	530893	530893	1 T -> C	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Class I SAM-dependent methyltransferase CDS
C	530897	530897	1 T -> C	SNP (transition)	131	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	D -> G	Class I SAM-dependent methyltransferase CDS
G	531367	531367	1 A -> G	SNP (transition)	131	97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Class I SAM-dependent methyltransferase CDS
	531427	531427	1 -A	Deletion	135	98.5%	1,8E-248	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
C	531673	531673	1 T -> C	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
C	531807	531807	1 T -> C	SNP (transition)	89	98.9%	2,2E-279	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	N -> D	guaA CDS
C	531817	531817	1 T -> C	SNP (transition)	99	98.0%	2,4E-277	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	531985	531985	1 G -> A	SNP (transition)	95	100.0%	1E-284	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532006	532006	1 T -> A	SNP (transversion)	85	98.8%	5,4E-253	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
TATG	532012	532015	3 AACA -> TATG	Substitution	88 -> 89	98.6%	2,2E-264	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	LV -> LI	guaA CDS
T	532030	532030	1 C -> T	SNP (transition)	80	100.0%	1E-231	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
T	532039	532039	1 C -> T	SNP (transition)	80	98.8%	8E-235	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
G	532042	532042	1 T -> G	SNP (transversion)	84	100.0%	2,5E-285	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS

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C	532045	532045	1 A -> C	SNP (transversion)	90	100.0%	1E-278	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532054	532054	1 G -> A	SNP (transition)	89	100.0%	1,8E-275	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532057	532057	1 G -> A	SNP (transition)	87	100.0%	2E-268	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532066	532066	1 G -> A	SNP (transition)	78	98.7%	3,8E-221	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
G	532069	532069	1 A -> G	SNP (transition)	79	97.5%	3,1E-227	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
C	532088	532088	1 T -> C	SNP (transition)	85	100.0%	3,2E-263	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	guaA CDS
A	532090	532090	1 C -> A	SNP (transversion)	83	100.0%	5E-257	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
G	532126	532126	1 A -> G	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
AAG	532129	532131	2 TAA -> AAG	Substitution	105 -> 106	100.0%	3,2E-304	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
T	532133	532133	1 A -> T	SNP (transversion)	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	F -> Y	guaA CDS
T	532138	532138	1 C -> T	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532147	532147	1 G -> A	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532156	532156	1 A -> T	SNP (transversion)	110	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
C	532173	532173	1 T -> C	SNP (transition)	112	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	guaA CDS
TCT	532201	532203	2 GCG -> TCT	Substitution	107 -> 108	100.0%	2,5E-299	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
T	532210	532210	1 C -> T	SNP (transition)	112	97.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
T	532219	532219	1 A -> T	SNP (transversion)	113	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
G	532222	532222	1 A -> G	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
ATTA	532225	532228	4 TCCT -> ATTA	Substitution	114	98.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	AG -> AN	guaA CDS
CT	532238	532239	2 TC -> CT	Substitution	112 -> 113	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	D -> S	guaA CDS
A	532242	532242	1 G -> A	SNP (transition)	117	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
TTCA	532249	532252	3 CTTG -> TTCA	Substitution	117	98.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	SK -> SE	guaA CDS
G	532267	532267	1 T -> G	SNP (transversion)	117	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
G	532270	532270	1 A -> G	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
CG	532275	532276	2 TA -> CG	Substitution	109 -> 112	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	IN -> ID	guaA CDS
G	532279	532279	1 C -> G	SNP (transversion)	108	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
TC	532321	532322	2 GT -> TC	Substitution	119 -> 120	97.5%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	D -> G	guaA CDS
T	532362	532362	1 C -> T	SNP (transition)	117	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	V -> I	guaA CDS
C	532366	532366	1 A -> C	SNP (transversion)	111	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	D -> E	guaA CDS
T	532372	532372	1 G -> T	SNP (transversion)	118	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532375	532375	1 T -> A	SNP (transversion)	117	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
C	532379	532379	1 T -> C	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	N -> S	guaA CDS
A	532381	532381	1 T -> A	SNP (transversion)	114	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
AAAGT	532386	532390	4 GTAAG -> AAAGT	Substitution	109 -> 114	97.2% -> 97.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532393	532393	1 T -> A	SNP (transversion)	110	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532396	532396	1 T -> A	SNP (transversion)	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
T	532399	532399	1 G -> T	SNP (transversion)	107	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
G	532402	532402	1 A -> G	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532405	532405	1 G -> A	SNP (transition)	123	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
T	532414	532414	1 C -> T	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532420	532420	1 G -> A	SNP (transition)	98	100.0%	1E-293	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
C	532435	532435	1 A -> C	SNP (transversion)	120	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532444	532444	1 T -> A	SNP (transversion)	118	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	K -> N	guaA CDS
T	532450	532450	1 C -> T	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
G	532462	532462	1 A -> G	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
T	532471	532471	1 A -> T	SNP (transversion)	112	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532492	532492	1 T -> A	SNP (transversion)	116	98.3%	4,2E-258	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
A	532513	532513	1 G -> A	SNP (transition)	119	97.5%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
T	532531	532531	1 T -> A	SNP (transversion)	115	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
T	532543	532543	1 C -> T	SNP (transition)	117	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		guaA CDS
AT	532549	532550	2 GC -> AT	Substitution	121	98.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	S -> N	guaA CDS
A	533903	533903	1 T -> A	SNP (transversion)	105	99.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
GCG	533910	533917	2 ACA -> GCG	Substitution	98 -> 105	95.9% -> 96.2%	2,3E-248	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	T -> A	uvrC CDS
T	533930	533930	1 C -> T	SNP (transition)	98	100.0%	2,5E-264	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	533933	533933	1 T -> A	SNP (transversion)	98	100.0%	6,3E-284	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	533936	533936	1 T -> A	SNP (transversion)	101	99.0%	1E-277	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	533945	533945	1 G -> A	SNP (transition)	92	96.7%	7,9E-244	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
G	533981	533981	1 A -> G	SNP (transition)	78	98.7%	3,1E-244	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
T	533987	533987	1 G -> T	SNP (transversion)	79	98.7%	1,3E-239	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
C	533999	533999	1 T -> C	SNP (transition)	84	98.8%	4,2E-255	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
G	534023	534023	1 A -> G	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	534044	534044	1 G -> A	SNP (transition)	103	98.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
AAT	534053	534053	2 GAA -> AAT	Substitution	103 -> 104	99.0%	2,6E-283	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	E -> N	uvrC CDS
G	534065	534065	1 A -> G	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
T	534068	534068	1 C -> T	SNP (transition)	97	97.9%	1,5E-233	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	534074	534074	1 G -> A	SNP (transition)	97	97.9%	4,7E-300	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
T	534092	534092	1 A -> T	SNP (transversion)	99	99.0%	3,9E-272	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
T	534101	534101	1 C -> T	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
C	534107	534107	1 T -> C	SNP (transition)	98	99.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
C	534122	534122	1 T -> C	SNP (transition)	102	99.0%	1E-303	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	534134	534134	1 C -> A	SNP (transversion)	103	99.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
T	534200	534200	1 C -> T	SNP (transition)	81	98.8%	8,1E-270	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
G	535091	535091	1 A -> G	SNP (transition)	76	98.7%	2,4E-230	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	535179	535179	1 G -> A	SNP (transition)	76	100.0%	1,6E-212	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	D -> N	uvrC CDS
C	535746	535746	1 T -> C	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		Putative membrane protein CDS
C	536172	536172	1 T -> C	SNP (transition)	96	97.9%	7,2E-297	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		Putative membrane protein CDS
C	538264	538264	1 T -> C	SNP (transition)	127	98.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	N -> D	hemE CDS
T	538297	538297	1 G -> T	SNP (transversion)	119	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	Q -> K	hemE CDS
G	539033	539033	1 A -> G	SNP (transition)	96	100.0%	1E-287	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
	539103	539103	1 (T)8 -> (T)7	Deletion (tandem repeat)	118	94.1%	5,1E-189	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	539153	539153	1 C -> A	SNP (transversion)	97	97.9%	4,6E-262	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
	539158	539157	0 +TTAGAAAATTTTT	Insertion	95 -> 99	86.3% -> 86.9%	1,1E-245	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
GATCATTT	539158	539157	0 +GATCATTT	Insertion	85 -> 90	94.1% -> 94.4%	2,8E-220	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
T	539211	539211	1 C -> T	SNP (transition)	81	96.3%	2,1E-244	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
C	539300	539300	1 T -> C	SNP (transition)	116	96.6%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
T	539555	539555	1 A -> T	SNP (transversion)	124	98.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	N -> I	hypothetical protein CDS
A	539628	539628	1 G -> A	SNP (transition)	115	97.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
	539667	539669	3 -TTT	Deletion	105	100.0%	3,2E-199	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	FF -> F	hypothetical protein CDS
A	546536	546536	1 G -> A	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	T -> I	glyS CDS
T	546863	546863	1 C -> T	SNP (transition)	117	97.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	A -> T	glyS CDS
A	546876	546876	1 G -> A	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		glyS CDS
C	547139	547139	1 T -> C	SNP (transition)	99	98.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	K -> E	glyS CDS
C	547308	547308	1 T -> C	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
C	547477	547477	1 T -> C	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	Q -> R	HAD family hydrolase CDS
T	547701	547701	1 C -> T	SNP (transition)	126	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	E -> K	HAD family hydrolase CDS
C	548420	548420	1 T -> C	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	I -> M	kch CDS
C	549972	549972	1 T -> C	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	K -> R	hspR CDS
A	551886	551886	1 G -> A	SNP (transition)	87	100.0%	4E-278	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		Periplasmic serine endoprotease DegP-like CDS
T	550013	550013	1 C -> T	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
G	555271	555271	1 A -> G	SNP (transition)	91	97.8%	5,1E-277	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	555334	555334	1 G -> A	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
T	555375	555374	0 (T)7 -> (T)8	Insertion (tandem repeat)	85	94.1%	3,3E-218	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
G	555565	555565	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	Filamentous hemagglutinin CDS
C	555932	555932	1 T -> C	SNP (transition)	131	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	I -> T	Filamentous hemagglutinin CDS
A	555977	555977	1 G -> A	SNP (transition)	136	99.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	G -> D	Filamentous hemagglutinin CDS
T	688815	688815	1 C -> T	SNP (transition)	90	100.0%	1E-278	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	R -> Q	ispE CDS
C	690474	690474	1 T -> C	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		truB CDS
G	690584	690584	1 A -> G	SNP (transition)	98	99.0%	3,9E-308	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
A	690974	690974	1 G -> A	SNP (transition)	132	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
A	692722	692722	1 G -> A	SNP (transition)	96	99.0%	9,6E-264	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	692820	692820	1 C -> T	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	A -> T	hypothetical protein CDS
G	692827	692827	1 A -> G	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	692857	692857	1 C -> T	SNP (transition)	114	98.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	M -> I	hypothetical protein CDS
G	692999	692999	1 A -> G	SNP (transition)	133	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		M3 family oligoendopeptidase CDS
C	694539	694539	1 T -> C	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		M3 family oligoendopeptidase CDS
G	695208	695208	1 T -> G	SNP (transversion)	93	97.8%	6,8E-251	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		pyrB CDS
C	695252	695252	1 T -> C	SNP (transition)	108	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	pyrB CDS
A	695436	695436	1 G -> A	SNP (transition)	115	97.4%	6,2E-308	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		pyrB CDS
T	695807	695807	1 C -> T	SNP (transition)	129	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		Serine/threonine transporter SstT CDS
G	695825	695825	1 A -> G	SNP (transition)	128	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		Serine/threonine transporter SstT CDS
A	695900	695900	1 G -> A	SNP (transition)	113	98.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		Serine/threonine transporter SstT CDS
T	696072	696072	1 C -> T	SNP (transition)	122	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	R -> H	Serine/threonine transporter SstT CDS
C	696212	696212	1 T -> C	SNP (transition)	97	100.0%	2E-303	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		Serine/threonine transporter SstT CDS
C	697013	697013	1 T -> C	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
C	697241	697241	1 T -> C	SNP (transition)	93	100.0%	2,5E-297	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
C	697253	697253	1 T -> C	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
C	697262	697262	1 T -> C	SNP (transition)	100	100.0%	1E-299	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
C	697322	697322	1 A -> C	SNP (transversion)	94	100.0%	1,6E-302	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
C	697337	697337	1 T -> C	SNP (transition)	91	100.0%	5E-305	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
A	697346	697346	1 T -> A	SNP (transversion)	98	99.0%	2E-298	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
G	697349	697349	1 T -> G	SNP (transversion)	96	100.0%	2,5E-297	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
C	697352	697352	1 A -> C	SNP (transversion)	98	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
A	697469	697469	1 G -> A	SNP (transition)	111	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
G	697523	697523	1 A -> G	SNP (transition)	114	98.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
G	697526	697526	1 T -> G	SNP (transversion)	113	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
G	697577	697577	1 A -> G	SNP (transition)	103	98.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
T	697583	697583	1 C -> T	SNP (transition)	100	97.0%	1,6E-285	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
G	697665	697665	1 A -> G	SNP (transition)	110	96.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	N -> D	metK CDS
AAT	697671	697673	2 GAA -> AAT	Substitution	109	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	E -> N	metK CDS
A	697688	697688	1 G -> A	SNP (transition)	125	97.6%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
T	697718	697718	1 C -> T	SNP (transition)	103	100.0%	4E-288	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
G	697775	697775	1 A -> G	SNP (transition)	86	100.0%	2,5E-266	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
G	697898	697898	1 A -> G	SNP (transition)	93	100.0%	1,3E-308	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
T	697919	697919	1 C -> T	SNP (transition)	94	98.9%	4,7E-286	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
T	697922	697922	1 C -> T	SNP (transition)	100	98.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
A	698078	698078	1 T -> A	SNP (transversion)	101	100.0%	1,3E-292	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	D -> E	metK CDS
T	698147	698147	1 C -> T	SNP (transition)	84	98.8%	2,1E-263	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		metK CDS
CC	698177	698178	2 TA -> CC	Substitution	130	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	IK -> IQ	metK CDS
T	698254	698254	1 C -> T	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
G	698296	698296	1 A -> G	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
T	698305	698305	1 C -> T	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
C	698340	698340	1 T -> C	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		

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G	698344	698344	1 A -> G	SNP (transition)	120	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
T	698358	698358	1 C -> T	SNP (transition)	118	97.5%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	698370	698370	1 C -> A	SNP (transversion)	124	98.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
G	698373	698373	1 A -> G	SNP (transition)	124	98.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
G	698376	698376	1 A -> G	SNP (transition)	124	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
GA	698383	698384	2 AC -> GA	Substitution	136	99.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
T	698388	698388	1 C -> T	SNP (transition)	137	99.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
C	698411	698411	1 T -> C	SNP (transition)	132	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	698460	698460	1 G -> A	SNP (transition)	99	100.0%	1E-296	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
C	698481	698481	1 T -> C	SNP (transition)	106	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	698487	698487	1 G -> A	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	698494	698494	1 G -> A	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	698511	698511	1 G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	698532	698532	1 G -> A	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
T	698535	698535	1 A -> T	SNP (transversion)	115	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
G	698539	698539	1 A -> G	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
G	1038237	1038237	1 A -> G	SNP (transition)	139	99.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	I -> T	MBL fold metallo-hydrolase CDS
G	1038273	1038273	1 A -> G	SNP (transition)	111	98.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1040325	1040325	1 G -> A	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		dnaK CDS
T	1042179	1042179	1 C -> T	SNP (transition)	107	99.1%	4,3E-305	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042182	1042182	1 G -> A	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
AC	1042187	1042188	2 GT -> AC	Substitution	111 -> 112	98.2%	6,2E-304	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
T	1042191	1042191	1 C -> T	SNP (transition)	108	98.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
C	1042194	1042194	1 T -> C	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042206	1042206	1 A -> G	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042218	1042218	1 A -> G	SNP (transition)	108	98.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042221	1042221	1 G -> A	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
T	1042233	1042233	1 C -> T	SNP (transition)	124	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
C	1042249	1042249	1 T -> C	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	N -> S	hrcA CDS
A	1042293	1042293	1 G -> A	SNP (transition)	110	97.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042371	1042371	1 G -> A	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042431	1042431	1 A -> G	SNP (transition)	114	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042479	1042479	1 A -> G	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
T	1042488	1042488	1 C -> T	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1042490	1042490	1 T -> A	SNP (transversion)	114	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
G	1042492	1042492	1 T -> G	SNP (transversion)	114	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
AG	1042520	1042521	2 TA -> AG	Substitution	125 -> 137	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
T	1042591	1042591	1 A -> T	SNP (transversion)	143	99.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1042596	1042596	1 G -> A	SNP (transition)	144	99.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1042608	1042608	1 G -> A	SNP (transition)	146	99.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
G	1042632	1042632	1 A -> G	SNP (transition)	147	98.6%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1042634	1042634	1 C -> A	SNP (transversion)	140	99.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1042638	1042638	1 C -> A	SNP (transversion)	131	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1042642	1042642	1 T -> C	SNP (transition)	123	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
GT	1042650	1042651	2 AA -> GT	Substitution	112 -> 113	95.5% -> 95.6%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
ACAG	1042654	1042657	4 TGCA -> ACAG	Substitution	107 -> 112	94.4% -> 94.6%	1,7E-280	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
G	1042659	1042658	0 +G	Insertion	103	91.0%	1,2E-278	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1042687	1042687	1 T -> A	SNP (transversion)	80	98.8%	1E-242	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
T	1042690	1042690	1 A -> T	SNP (transversion)	82	87.8%	3,3E-196	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1042692	1042692	1 T -> C	SNP (transition)	83	88.0%	6,1E-221	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
AA	1042696	1042697	2 TG -> AA	Substitution	86 -> 87	83.7% -> 83.9%	1,1E-185	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
T	1042699	1042699	1 C -> T	SNP (transition)	87	81.6%	9,8E-203	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1042702	1042702	1 G -> A	SNP (transition)	90	80.0%	1,5E-175	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1042729	1042729	1 T -> C	SNP (transition)	92	91.3%	1,5E-257	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
AC	1042750	1042751	2 GA -> AC	Substitution	86	97.7%	5,8E-265	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1042763	1042763	1 T -> C	SNP (transition)	86	97.7%	2,3E-273	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
T	1042765	1042765	1 C -> T	SNP (transition)	82	98.8%	1E-232	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
AC	1042784	1042785	2 GT -> AC	Substitution	99	98.0%	2,4E-277	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	N -> S	cfrA CDS
A	1042793	1042793	1 G -> A	SNP (transition)	105	98.1%	1,1E-294	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042796	1042796	1 A -> G	SNP (transition)	105	99.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1042805	1042805	1 C -> T	SNP (transition)	109	98.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	M -> I	cfrA CDS
A	1042829	1042829	1 G -> A	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042832	1042832	1 A -> G	SNP (transition)	111	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042835	1042835	1 G -> A	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042841	1042841	1 T -> G	SNP (transversion)	111	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
AG	1042850	1042851	2 GC -> AG	Substitution	118 -> 120	97.5%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	S -> T	cfrA CDS
GT	1042854	1042855	2 CC -> GT	Substitution	111 -> 119	97.3% -> 97.5%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	G -> T	cfrA CDS
CGCT	1042858	1042861	3 TCCC -> CGCT	Substitution	106 -> 107	97.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	GS -> SG	cfrA CDS
T	1042863	1042863	1 C -> T	SNP (transition)	107	99.1%	4,3E-305	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	S -> N	cfrA CDS
TG	1042866	1042867	2 GC -> TG	Substitution	108	98.1%	5,4E-308	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	A -> Q	cfrA CDS
A	1042880	1042880	1 G -> A	SNP (transition)	126	98.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042885	1042885	1 T -> C	SNP (transition)	123	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	N -> D	cfrA CDS
A	1042892	1042892	1 G -> A	SNP (transition)	124	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1042900	1042900	1 C -> T	SNP (transition)	118	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	D -> N	cfrA CDS
G	1042922	1042922	1 A -> G	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042937	1042937	1 T -> C	SNP (transition)	119	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042940	1042940	1 G -> A	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042964	1042964	1 G -> A	SNP (transition)	128	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042985	1042985	1 G -> A	SNP (transition)	123	98.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042994	1042994	1 T -> C	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043000	1043000	1 G -> T	SNP (transversion)	115	98.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043087	1043087	1 T -> C	SNP (transition)	114	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043093	1043093	1 G -> A	SNP (transition)	117	98.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043099	1043099	1 G -> A	SNP (transition)	118	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043258	1043258	1 G -> A	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
TC	1043267	1043268	2 CT -> TC	Substitution	113 -> 114	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	K -> R	cfrA CDS
G	1043271	1043271	1 A -> G	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	F -> S	cfrA CDS
C	1043584	1043584	1 G -> C	SNP (transversion)	133	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	L -> V	cfrA CDS
CAA	1043648	1043650	2 AAG -> CAA	Substitution	112 -> 114	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GTT	1043657	1043659	2 ATC -> GTT	Substitution	109 -> 115	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	D -> N	cfrA CDS
G	1043669	1043669	1 A -> G	SNP (transition)	126	98.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043672	1043672	1 A -> G	SNP (transition)	135	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043690	1043690	1 A -> T	SNP (transversion)	110	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043717	1043717	1 A -> G	SNP (transition)	108	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043720	1043720	1 A -> C	SNP (transversion)	107	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043724	1043724	1 C -> T	SNP (transition)	107	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	S -> N	cfrA CDS
A	1043765	1043765	1 G -> A	SNP (transition)	125	98.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043769	1043769	1 A -> G	SNP (transition)	120	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	V -> A	cfrA CDS
C	1043774	1043774	1 T -> C	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
CAA	1043792	1043794	2 TAC -> CAA	Substitution	113	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043801	1043801	1 A -> G	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043861	1043861	1 C -> T	SNP (transition)	99	99.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043867	1043867	1 T -> C	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
TGC	1043870	1043872	2 AGA -> TGC	Substitution	103 -> 104	99.0%	1,6E-265	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	S -> A	cfrA CDS
T	1043876	1043876	1 C -> T	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043882	1043882	1 G -> A	SNP (transition)	127	99.2%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043891	1043891	1 G -> A	SNP (transition)	128	96.9%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043896	1043896	1 C -> T	SNP (transition)	148	98.6%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	D -> N	cfrA CDS
T	1043903	1043903	1 C -> T	SNP (transition)	141	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043912	1043912	1 A -> G	SNP (transition)	159	99.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GTC	1043922	1043924	3 CCA -> GTC	Substitution	144 -> 145	95.8% -> 95.9%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	SG -> ST	cfrA CDS
G	1043927	1043927	1 A -> G	SNP (transition)	146	99.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043930	1043930	1 G -> A	SNP (transition)	146	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043966	1043966	1 A -> G	SNP (transition)	149	99.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043999	1043999	1 T -> C	SNP (transition)	142	99.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044005	1044005	1 A -> G	SNP (transition)	140	98.6%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044024	1044024	1 G -> T	SNP (transversion)	139	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	P -> Q	cfrA CDS
A	1044029	1044029	1 T -> A	SNP (transversion)	138	97.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	R -> S	cfrA CDS
G	1044044	1044044	1 A -> G	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044047	1044047	1 A -> G	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044074	1044074	1 G -> A	SNP (transition)	115	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044110	1044110	1 A -> G	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1044128	1044128	1 T -> C	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044155	1044155	1 G -> A	SNP (transition)	125	98.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044191	1044191	1 C -> T	SNP (transition)	136	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044314	1044314	1 C -> T	SNP (transition)	151	99.3%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044662	1044662	1 A -> G	SNP (transition)	100	100.0%	1E-299	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044720	1044720	1 C -> G	SNP (transversion)	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	S -> T	cfrA CDS
G	1044722	1044722	1 A -> G	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GGT	1044761	1044763	2 AGC -> GGT	Substitution	96	99.0%	3,2E-294	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	A -> T	cfrA CDS
G	1044767	1044767	1 T -> G	SNP (transversion)	103	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1044781	1044781	1 T -> C	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	cfrA CDS
T	1044785	1044785	1 C -> T	SNP (transition)	99	99.0%	3,9E-272	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044788	1044788	1 A -> G	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044791	1044791	1 G -> A	SNP (transition)	108	99.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044797	1044797	1 C -> T	SNP (transition)	111	96.4%	3E-303	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044815	1044815	1 A -> G	SNP (transition)	102	98.0%	5,1E-298	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044821	1044821	1 A -> G	SNP (transition)	103	96.1%	4,4E-290	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GCTT	1044824	1044827	4 AGCC -> GCTT	Substitution	110 -> 114	90.9% -> 91.8%	1,6E-263	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	LA -> LS	cfrA CDS
G	1044830	1044830	1 A -> G	SNP (transition)	110	94.5%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044833	1044833	1 G -> A	SNP (transition)	109	93.6%	7,4E-275	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044842	1044842	1 A -> G	SNP (transition)	98	98.0%	3E-303	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044848	1044848	1 C -> T	SNP (transition)	104	98.1%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044859	1044859	1 A -> T	SNP (transversion)	109	94.5%	4E-289	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	L -> I	cfrA CDS
T	1044863	1044863	1 C -> T	SNP (transition)	108	96.3%	5,3E-300	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044903	1044903	1 G -> A	SNP (transition)	117	97.4%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
	1052542	1052543	1 (A)3 -> (A)2	Deletion (tandem repeat)	133	99.7%	4,4E-31	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1052849	1052849	1 T -> C	SNP (transition)	112	99.0%	1,3E-86	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		
T	1056828	1056828	1 T -> C	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	E -> G	ccmA CDS
C	1058557	1058557	1 T -> C	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	Putative ABC transport system permease CDS
T	1058795	1058795	1 G -> T	SNP (transversion)	105	100.0%	0	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss		Putative ABC transport system permease CDS
T	1058819	1058819	1 C -> T	SNP (transition)	103	98.1%	5,2E-298	Variants: BfR-CA-11057-TF156B7-11_R	Concatemer BfR-CA-11057 - UniAss	R -> K	ataC CDS

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T	1058880	1058880	1 C -> T	SNP (transition)	96	100.0%	6,3E-307	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	V -> I	ataC CDS
G	1058884	1058884	1 A -> G	SNP (transition)	96	100.0%	6,3E-307	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1058971	1058971	1 G -> A	SNP (transition)	115	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059022	1059022	1 A -> G	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059106	1059106	1 G -> A	SNP (transition)	157	98.7%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059154	1059154	1 G -> A	SNP (transition)	138	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059162	1059162	1 A -> G	SNP (transition)	143	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	F -> L	ataC CDS
T	1059259	1059259	1 C -> T	SNP (transition)	118	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059283	1059283	1 A -> G	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059487	1059487	1 A -> G	SNP (transition)	151	98.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
C	1059541	1059541	1 T -> C	SNP (transition)	116	98.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
CA	1059570	1059571	2 TG -> CA	Substitution	115	98.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	ST -> SA	ataC CDS
G	1059624	1059624	1 A -> G	SNP (transition)	120	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1059660	1059660	1 C -> T	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1059675	1059675	1 C -> T	SNP (transition)	115	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1059897	1059897	1 A -> G	SNP (transition)	127	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1059915	1059915	1 A -> G	SNP (transition)	179	98.4%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1059961	1059961	1 G -> A	SNP (transition)	127	98.4%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	A -> V	Phytase-like domain-containing protein CDS
G	1059973	1059973	1 A -> G	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	I -> T	Phytase-like domain-containing protein CDS
C	1060048	1060048	1 T -> C	SNP (transition)	123	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	N -> S	Phytase-like domain-containing protein CDS
G	1060134	1060134	1 A -> G	SNP (transition)	118	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1060458	1060458	1 G -> A	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1060491	1060491	1 G -> T	SNP (transversion)	107	99.1%	2,7E-273	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1060503	1060503	1 A -> G	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1060557	1060557	1 G -> A	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1060596	1060596	1 A -> G	SNP (transition)	95	100.0%	3,2E-275	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1060641	1060641	1 C -> T	SNP (transition)	71	100.0%	5E-234	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
C	1061191	1061191	1 T -> C	SNP (transition)	119	98.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
A	1061194	1061194	1 G -> A	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
A	1061399	1061399	1 G -> A	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	A -> V	afuA CDS
A	1061809	1061809	1 G -> A	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
A	1061821	1061821	1 G -> A	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
C	1062232	1062232	1 T -> C	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	V -> A	corA CDS
G	1062305	1062305	1 A -> G	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		corA CDS
G	1063367	1063367	1 A -> G	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	mraW CDS
AGC	1065015	1065017	3 GCT -> AGC	Substitution	128 -> 129	96.9%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	A -> S	Peptidase, M48 family protein CDS
C	1065021	1065021	1 G -> C	SNP (transversion)	127	98.4%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	V -> L	Peptidase, M48 family protein CDS
G	1065032	1065032	1 A -> G	SNP (transition)	127	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Peptidase, M48 family protein CDS
G	1066684	1066684	1 A -> G	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	I -> V	ftsC CDS
T	1066860	1066860	1 C -> T	SNP (transition)	106	99.1%	1,1E-293	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		ftsC CDS
A	1067475	1067475	1 G -> A	SNP (transition)	113	96.5%	2E-285	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	A -> T	Pyridoxal phosphate homeostasis protein CDS
T	1068252	1068252	1 C -> T	SNP (transition)	110	97.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	G -> E	dnaE CDS
A	1068284	1068284	1 G -> A	SNP (transition)	100	97.0%	8,1E-276	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1068497	1068497	1 G -> A	SNP (transition)	96	96.9%	1,8E-301	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1069352	1069352	1 G -> A	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1070006	1070006	1 G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
G	1070291	1070291	1 A -> G	SNP (transition)	93	97.8%	4,3E-269	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1072148	1072148	1 G -> A	SNP (transition)	108	97.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
G	1072658	1072658	1 A -> G	SNP (transition)	101	97.0%	2,6E-298	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
T	1072835	1072835	1 C -> T	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
G	1072943	1072943	1 A -> G	SNP (transition)	121	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
G	1073017	1073017	1 A -> G	SNP (transition)	177	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
A	1073509	1073509	1 G -> A	SNP (transition)	171	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	H -> Y	uraH CDS
A	1073632	1073632	1 G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		uraH CDS
A	1073645	1073645	1 G -> A	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	A -> V	uraH CDS
C	1073813	1073813	1 T -> C	SNP (transition)	151	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	N -> S	uraH CDS
C	1074956	1074956	1 T -> C	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	N -> D	trmD CDS
G	1075095	1075095	1 A -> G	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	V -> A	rimM CDS
G	1075504	1075504	1 T -> G	SNP (transversion)	173	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	K -> Q	rimM CDS
G	1075743	1075743	1 A -> G	SNP (transition)	152	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		RNA-binding protein CDS
C	1076616	1076616	1 T -> C	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	I -> M	ffh CDS
T	1078818	1078818	1 C -> T	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	R -> Q	3-deoxy-D-manno-octulosonic acid transferase CDS
T	1080585	1080585	1 G -> T	SNP (transversion)	116	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	L -> I	NrfB-like dinuclear metal center hexameric protein CDS
T	1081250	1081250	1 C -> T	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		glyQ1 CDS
T	1081253	1081253	1 C -> T	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		glyQ1 CDS
C	1081259	1081259	1 T -> C	SNP (transition)	115	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		glyQ1 CDS
C	1081469	1081469	1 T -> C	SNP (transition)	100	95.0%	2,4E-286	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
A	1081520	1081520	1 G -> A	SNP (transition)	83	98.8%	3,3E-219	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
C	1081523	1081523	1 T -> C	SNP (transition)	99	98.0%	1,2E-267	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		glyQ1 CDS
A	1081526	1081526	1 T -> A	SNP (transversion)	96	96.9%	2,2E-236	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		glyQ1 CDS
A	1081571	1081571	1 C -> A	SNP (transversion)	80	97.8%	2E-248	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		glyQ1 CDS
C	1081580	1081580	1 T -> C	SNP (transition)	91	97.8%	3,2E-254	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		glyQ1 CDS
T	1081589	1081589	1 A -> T	SNP (transversion)	97	95.9%	1,7E-281	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
T	1081971	1081971	1 C -> T	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		DUF3972 domain-containing protein CDS
C	1083619	1083619	1 T -> C	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	S -> G	putative protease from collagenase family CDS
C	1084688	1084688	1 T -> C	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	N -> S	Chemotaxis protein CDS
C	1084756	1084756	1 T -> C	SNP (transition)	106	95.3%	3,2E-244	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1085392	1085392	1 G -> A	SNP (transition)	93	100.0%	2E-269	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	V -> I	glmA CDS
G	1087996	1087996	1 A -> G	SNP (transition)	106	98.1%	5,6E-308	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		flgG2 CDS
A	1088029	1088029	1 G -> A	SNP (transition)	96	97.9%	1,8E-287	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		flgG2 CDS
T	1088125	1088125	1 C -> T	SNP (transition)	83	98.8%	8,3E-244	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		flgG2 CDS
A	1088419	1088419	0 (A)6 -> (A)7	Insertion (tandem repeat)	108	96.3%	2,1E-263	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
G	1088948	1088948	1 A -> G	SNP (transition)	88	97.7%	1,5E-249	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		ftsZ CDS
A	1089178	1089178	1 G -> A	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		ftsZ CDS
G	1311022	1311022	1 T -> G	SNP (transversion)	110	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
C	1311340	1311340	1 T -> C	SNP (transition)	120	98.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
T	1312069	1312069	1 C -> T	SNP (transition)	126	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
A	1312081	1312081	1 G -> A	SNP (transition)	135	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
C	1312087	1312087	1 T -> C	SNP (transition)	131	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
A	1312095	1312095	1 G -> A	SNP (transition)	135	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	L -> F	MatC-N domain-containing protein CDS
A	1312289	1312289	1 T -> A	SNP (transversion)	154	99.4%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1312291	1312291	1 T -> C	SNP (transition)	144	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
AA	1312296	1312298	3 TTT -> AA	Deletion	140 -> 144	96.4% -> 96.5%	2,3E-237	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
TTT	1312313	1312315	3 AAG -> TTT	Substitution	133	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
GT	1312330	1312331	2 TC -> GT	Substitution	126	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
AG	1312333	1312334	2 TA -> AG	Substitution	123 -> 124	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1312340	1312340	1 A -> C	SNP (transversion)	135	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1312342	1312342	1 T -> C	SNP (transition)	134	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1312352	1312352	1 T -> C	SNP (transition)	151	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
G	1312383	1312383	1 A -> G	SNP (transition)	126	99.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
G	1312394	1312394	1 A -> G	SNP (transition)	126	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
T	1312407	1312407	1 C -> T	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1312413	1312413	1 G -> A	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
T	1312415	1312415	1 C -> T	SNP (transition)	95	100.0%	3,2E-294	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
	1312427	1312427	1 (T)6 -> (T)5	Deletion (tandem repeat)	81	93.8%	9,6E-137	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1312433	1312433	1 T -> C	SNP (transition)	77	94.8%	4,3E-249	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
AG	1312440	1312441	2 GT -> AG	Substitution	76 -> 77	93.4% -> 93.5%	2E-208	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1312448	1312448	1 G -> A	SNP (transition)	74	100.0%	6,3E-244	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
TGTG	1312456	1312459	4 GCAT -> TGTG	Substitution	70 -> 72	98.6%	1,1E-218	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
GC	1312461	1312460	0 +GC	Insertion	78	83.3%	6,9E-300	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
G	1312465	1312465	1 A -> G	SNP (transition)	80	96.3%	6,5E-249	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1312470	1312470	1 G -> A	SNP (transition)	85	96.5%	3,9E-252	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1312481	1312481	1 G -> A	SNP (transition)	90	98.9%	7,1E-258	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1312485	1312485	1 T -> C	SNP (transition)	94	100.0%	4E-291	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1312487	1312487	1 A -> C	SNP (transversion)	95	92.6%	2,8E-271	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1312489	1312489	1 G -> A	SNP (transition)	88	93.2%	3,4E-245	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1312505	1312505	1 T -> C	SNP (transition)	76	98.7%	2,4E-245	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1312507	1312507	1 A -> C	SNP (transversion)	76	98.7%	2,4E-245	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
	1312512	1312512	1 -T	Deletion	76	90.8%	4,2E-149	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
GG	1312516	1312517	2 TT -> GG	Substitution	72 -> 77	98.6% -> 98.7%	6,3E-223	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
AT	1312519	1312520	2 TA -> AT	Substitution	77	97.4%	9,2E-229	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
TA	1312529	1312530	2 AC -> TA	Substitution	81 -> 82	98.8%	4,1E-265	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1312538	1312538	1 T -> C	SNP (transition)	85	95.3%	1E-260	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
ATG	1312540	1312542	3 TGT -> ATG	Substitution	86	90.7%	8,5E-243	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1312544	1312545	2 GG -> A	Deletion	86 -> 87	89.7% -> 90.7%	5,1E-128	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
	1312551	1312551	1 -C	Deletion	89	97.8%	3,8E-170	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1312558	1312558	1 G -> A	SNP (transition)	91	100.0%	7,9E-282	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
T	1312560	1312560	1 C -> T	SNP (transition)	91	100.0%	1E-272	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1312565	1312565	1 T -> A	SNP (transversion)	93	98.9%	2,3E-253	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
G	1312568	1312568	1 T -> G	SNP (transversion)	95	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
G	1312570	1312570	1 A -> G	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
G	1312577	1312577	1 A -> G	SNP (transition)	98	99.0%	2E-298	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
T	1312580	1312580	1 A -> T	SNP (transition)	100	100.0%	1E-289	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1312591	1312590	0 (A)3 -> (A)4	Insertion (tandem repeat)	109	88.1%	2,8E-271	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
GGG	1312610	1312612	3 TAA -> GGG	Substitution	115 -> 116	97.4%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		
A	1312664	1312664	1 G -> A	SNP (transition)	95	100.0%	3,2E-275	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
A	1312674	1312674	1 G -> A	SNP (transition)	95	97.9%	7E-238	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	A -> V	accA CDS
C	1312676	1312676	1 A -> C	SNP (transversion)	94	100.0%	2,5E-272	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
T	1312685	1312685	1 C -> T	SNP (transition)	95	95.8%	7,9E-230	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
T	1313231	1313231	1 C -> T	SNP (transition)	105	96.2%	7,5E-276	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
G	1314216	1314216	1 A -> G	SNP (transition)	113	98.2%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		fabF CDS
A	1314306	1314306	1 G -> A	SNP (transition)	120	98.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		fabF CDS
C	1314653	1314653	1 T -> C	SNP (transition)	156	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	T -> A	fabF CDS
A	1316808	1316808	1 G -> A	SNP (transition)	144	99.3%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
G	1316877	1316877	1 A -> G	SNP (transition)	139	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
C	1316976	1316976	1 T -> C	SNP (transition)	123	100.0%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
A	1317402	1317402	1 G -> A	SNP (transition)	98	100.0%	1,6E-303	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	L -> F	gpmI CDS
A	1317449	1317449	1 G -> A	SNP (transition)	98	98.0%	4,7E-284	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss	A -> V	gpmI CDS
A	1317460	1317460	1 G -> A	SNP (transition)	112	98.4%	3,3E-308	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317562	1317562	1 G -> A	SNP (transition)	107	98.1%	1,8E-300	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317946	1317946	1 G -> A	SNP (transition)	108	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317949	1317949	1 T -> C	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF156871-11_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS

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C	1317958	1317958	1 A -> C	SNP (transversion)	117	98.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	D -> E	gpmI CDS
T	1317970	1317970	1 C -> T	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317973	1317973	1 A -> C	SNP (transversion)	126	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317976	1317976	1 T -> C	SNP (transition)	132	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317979	1317979	1 T -> A	SNP (transversion)	134	97.8%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	E -> D	gpmI CDS
G	1318008	1318008	1 A -> G	SNP (transition)	127	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1318015	1318015	1 G -> C	SNP (transversion)	126	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318018	1318018	1 A -> G	SNP (transition)	128	97.7%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318207	1318207	1 A -> G	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318468	1318468	1 A -> G	SNP (transition)	116	97.4%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
T	1319026	1319026	1 C -> T	SNP (transition)	125	97.6%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mraY CDS
C	1319170	1319170	1 T -> C	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		mraY CDS
T	1320129	1320129	1 C -> T	SNP (transition)	150	99.3%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		murD CDS
G	1320495	1320495	1 A -> G	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		murD CDS
A	1321003	1321002	0 (A)5 -> (A)6	Insertion (tandem repeat)	88	94.3%	3,9E-241	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
	1321003	1321100	1 (A)3 -> (A)2	Deletion (tandem repeat)	133	99.7%	4,4E-31	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
C	1326407	1326407	1 T -> C	SNP (transition)	112	99.0%	1,3E-88	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
G	1327896	1327896	1 A -> G	SNP (transition)	117	100.0%	3,2E-58	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
T	1327911	1327911	1 C -> T	SNP (transition)	85	100.0%	3,2E-42	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
T	1327924	1327913	0 (T)2 -> (T)3	Insertion (tandem repeat)	82	92.7%	3,7E-30	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		
T	1329416	1329416	1 G -> T	SNP (transversion)	136	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	A -> D	Methyl-accepting chemotaxis protein CDS
A	1329562	1329562	1 G -> A	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		Methyl-accepting chemotaxis protein CDS
T	1329774	1329774	1 C -> T	SNP (transition)	122	99.2%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	E -> K	Methyl-accepting chemotaxis protein CDS
A	1330823	1330823	1 G -> A	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss		PMT-2 domain-containing protein CDS
G	1330927	1330927	1 A -> G	SNP (transition)	99	100.0%	1,3E-306	Variants: BfR-CA-11057-TF15687-11_R	Concatemer BfR-CA-11057 - UniAss	F -> L	PMT-2 domain-containing protein CDS
G	38113	38113	1 A -> G	SNP (transition)	112	99.0%	1,3E-88	Variants: BfR-CA-11057-TF15687-11_R & Variant	Concatemer BfR-CA-11057 - UniAss		
C	1052849	1052849	1 T -> C	SNP (transition)	112	99.0%	1,3E-88	Variants: BfR-CA-11057-TF15687-11_R & Variant	Concatemer BfR-CA-11057 - UniAss		
C	1326407	1326407	1 T -> C	SNP (transition)	112	99.0%	1,3E-88	Variants: BfR-CA-11057-TF15687-11_R & Variant	Concatemer BfR-CA-11057 - UniAss		
C	26306	26306	1 T -> C	SNP (transition)	134	99.3%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
A	26321	26321	1 G -> A	SNP (transition)	141	99.3%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
ACTT	26342	26345	3 GTTA -> ACTT	Substitution	108 -> 114	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
G	26348	26348	1 T -> G	SNP (transversion)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
A	26369	26369	1 G -> A	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
T	27838	27838	1 C -> T	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	27892	27892	1 C -> T	SNP (transition)	105	99.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
C	27949	27949	1 T -> C	SNP (transition)	112	98.2%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
C	28003	28003	1 T -> C	SNP (transition)	121	98.3%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28015	28015	1 C -> T	SNP (transition)	113	97.3%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
C	28018	28018	1 T -> C	SNP (transition)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
A	28024	28024	1 G -> A	SNP (transition)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
GG	28135	28136	2 AA -> GG	Substitution	96	99.0%	9,8E-283	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	VS -> VG	nrdA CDS
C	28213	28213	1 T -> C	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28216	28216	1 C -> T	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28237	28237	1 G -> T	SNP (transversion)	102	99.0%	1E-300	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
G	28780	28780	1 T -> G	SNP (transversion)	122	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28816	28816	1 C -> T	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28827	28827	1 C -> T	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	32037	32037	1 C -> T	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		pyrG CDS
A	33736	33736	1 G -> A	SNP (transition)	123	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33748	33748	1 T -> C	SNP (transition)	127	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33751	33751	1 T -> C	SNP (transition)	127	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
T	33757	33757	1 C -> T	SNP (transition)	127	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33769	33769	1 T -> C	SNP (transition)	139	99.3%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
AA	36609	36609	1 G -> AA	Insertion	245 -> 246	92.2% -> 92.3%	6,4E-291	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		
C	36624	36624	1 T -> C	SNP (transition)	287	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		
	36651	36651	1 (A)3 -> (A)2	Deletion (tandem repeat)	277	96.8%	1,6E-92	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		
A	36654	36654	1 T -> A	SNP (transversion)	274	98.2%	5E-232	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		
AA	36660	36659	0 +AA	Insertion	271	96.7%	9E-220	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		
C	36669	36669	1 T -> C	SNP (transition)	274	99.6%	4,8E-243	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		
G	38113	38113	1 A -> G	SNP (transition)	273	100.0%	1,3E-81	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		
	38420	38420	1 (T)3 -> (T)2	Deletion (tandem repeat)	273	98.5%	5,4E-21	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		
T	263407	263407	1 C -> T	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		purM CDS
TTTG	461516	461519	3 AGTT -> TTTG	Substitution	58 -> 61	77.0% -> 82.8%	1,4E-114	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	NS -> QT	DUF115 domain-containing protein CDS
T	461526	461526	1 A -> T	SNP (transversion)	57	86.0%	5,1E-111	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	D -> E	DUF115 domain-containing protein CDS
C	461537	461537	1 T -> C	SNP (transition)	57	93.0%	1,2E-126	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	N -> D	DUF115 domain-containing protein CDS
	1052544	1052544	1 (A)3 -> (A)2	Deletion (tandem repeat)	278	96.4%	1,6E-19	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		
C	1052849	1052849	1 T -> C	SNP (transition)	273	100.0%	1,3E-81	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		
C	1056828	1056828	1 T -> C	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	E -> G	ccmA CDS
C	1058557	1058557	1 T -> C	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	I -> V	Putative ABC transport system permease CDS
T	1058795	1058795	1 G -> T	SNP (transversion)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Putative ABC transport system permease CDS
T	1058819	1058819	1 C -> T	SNP (transition)	86	100.0%	6,3E-275	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	R -> K	ataC CDS
T	1058880	1058880	1 C -> T	SNP (transition)	89	100.0%	2,5E-302	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	V -> I	ataC CDS
G	1058884	1058884	1 A -> G	SNP (transition)	86	100.0%	6,3E-275	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1058971	1058971	1 G -> A	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059022	1059022	1 A -> G	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059108	1059108	1 G -> A	SNP (transition)	130	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059154	1059154	1 G -> A	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059162	1059162	1 A -> G	SNP (transition)	137	98.5%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	F -> L	ataC CDS
T	1059259	1059259	1 C -> T	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059283	1059283	1 A -> G	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059487	1059487	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
C	1059541	1059541	1 T -> C	SNP (transition)	91	100.0%	6,3E-295	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
CA	1059570	1059571	2 TG -> CA	Substitution	99	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	ST -> SA	ataC CDS
G	1059624	1059624	1 A -> G	SNP (transition)	129	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1059660	1059660	1 C -> T	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1059675	1059675	1 C -> T	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1059897	1059897	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1059915	1059915	1 A -> G	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1059961	1059961	1 G -> A	SNP (transition)	93	100.0%	5E-288	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	A -> V	Phytase-like domain-containing protein CDS
G	1059973	1059973	1 A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	I -> T	Phytase-like domain-containing protein CDS
C	1060048	1060048	1 T -> C	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	N -> S	Phytase-like domain-containing protein CDS
G	1060134	1060134	1 A -> G	SNP (transition)	80	100.0%	1E-263	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1060458	1060458	1 G -> A	SNP (transition)	109	97.2%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1060491	1060491	1 G -> T	SNP (transversion)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1060503	1060503	1 A -> G	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1060557	1060557	1 G -> A	SNP (transition)	117	99.1%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1060596	1060596	1 A -> G	SNP (transition)	99	99.0%	1,6E-301	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1060641	1060641	1 C -> T	SNP (transition)	92	100.0%	2,5E-303	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
C	1061191	1061191	1 T -> C	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
A	1061194	1061194	1 G -> A	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
A	1061399	1061399	1 G -> A	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	A -> V	afuA CDS
A	1061809	1061809	1 G -> A	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
A	1061821	1061821	1 G -> A	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
C	1062232	1062232	1 T -> C	SNP (transition)	126	96.8%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	V -> A	corA CDS
G	1062305	1062305	1 A -> G	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		corA CDS
G	1063367	1063367	1 A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	I -> V	mcaR CDS
AGC	1065015	1065017	3 GCT -> AGC	Substitution	112 -> 114	99.1%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	A -> S	Peptidase, M48 family protein CDS
C	1065021	1065021	1 G -> C	SNP (transversion)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	V -> L	Peptidase, M48 family protein CDS
G	1065032	1065032	1 A -> G	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Peptidase, M48 family protein CDS
G	1066684	1066684	1 A -> G	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	I -> V	ftsC CDS
T	1066860	1066860	1 C -> T	SNP (transition)	92	100.0%	6,3E-285	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		ftsC CDS
A	1067475	1067475	1 G -> A	SNP (transition)	103	98.1%	5,2E-299	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	A -> T	Pyridoxal phosphate homeostasis protein CDS
T	1068252	1068252	1 C -> T	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	G -> E	dnaE CDS
A	1068284	1068284	1 G -> A	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1068497	1068497	1 G -> A	SNP (transition)	80	98.8%	2E-266	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1069152	1069152	1 G -> A	SNP (transition)	88	100.0%	6,3E-299	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1070006	1070006	1 G -> A	SNP (transition)	85	100.0%	1E-288	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
G	1070291	1070291	1 A -> G	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1072148	1072148	1 G -> A	SNP (transition)	96	97.9%	5,8E-303	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
G	1072658	1072658	1 A -> G	SNP (transition)	87	100.0%	4E-278	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
T	1072835	1072835	1 C -> T	SNP (transition)	84	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
G	1072943	1072943	1 A -> G	SNP (transition)	87	100.0%	2E-268	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
G	1073012	1073012	1 A -> G	SNP (transition)	87	100.0%	1,6E-295	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
A	1073559	1073559	1 G -> A	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	H -> Y	uraH CDS
A	1073632	1073632	1 G -> A	SNP (transition)	88	97.7%	5,6E-283	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		uraH CDS
A	1073645	1073645	1 G -> A	SNP (transition)	87	100.0%	4E-278	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	A -> V	uraH CDS
C	1073813	1073813	1 T -> C	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	N -> S	uraH CDS
C	1074956	1074956	1 T -> C	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	N -> D	trmD CDS
G	1075095	1075095	1 A -> G	SNP (transition)	85	100.0%	1E-288	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	V -> A	rimM CDS
G	1075504	1075504	1 T -> G	SNP (transversion)	82	100.0%	2,5E-270	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	K -> Q	rimM CDS
G	1075743	1075743	1 A -> G	SNP (transition)	84	100.0%	2,5E-285	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		RNA-binding protein CDS
C	1076616	1076616	1 T -> C	SNP (transition)	83	100.0%	5E-257	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	I -> M	ffh CDS
T	1078818	1078818	1 C -> T	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	R -> Q	3-deoxy-D-manno-octulosonic acid transferase CDS
T	1080585	1080585	1 G -> T	SNP (transversion)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	L -> I	NrfB-like dinuclear metal center hexameric protein CDS
T	1081250	1081250	1 C -> T	SNP (transition)	88	100.0%	2,5E-285	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
T	1081253	1081253	1 C -> T	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
C	1081259	1081259	1 T -> C	SNP (transition)	98	99.0%	5,8E-289	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
C	1081469	1081469	1 T -> C	SNP (transition)	84	100.0%	1,6E-268	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
A	1081520	1081520	1 G -> A	SNP (transition)	67	98.5%	1,7E-202	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
C	1081523	1081523	1 T -> C	SNP (transition)	95	98.9%	9,5E-280	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
A	1081526	1081526	1 T -> A	SNP (transversion)	94	98.9%	9,4E-277	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
A	1081571	1081571	1 C -> A	SNP (transversion)	100	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
C	1081580	1081580	1 T -> C	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
T	1081589	1081589	1 A -> T	SNP (transversion)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
T	1081971	1081971	1 C -> T	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		DUF3972 domain-containing protein CDS
C	1083619	1083619	1 T -> C	SNP (transition)	94	100.0%	1,6E-300	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	S -> G	putative protease from collagenase family CDS
C	1084688	1084688	1 T -> C	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	N -> S	Chemotaxis protein CDS
C	1084756	1084756	1 T -> C	SNP (transition)	96	97.9%	7,2E-250	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		
A	1085392	1085392	1 G -> A	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	V -> I	glnA CDS
G	1087996	1087996	1 A -> G	SNP (transition)	82	100.0%	6,3E-254	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		flgG2 CDS
A	1088029	1088029	1 G -> A	SNP (transition)	90	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		flgG2 CDS
T	1088125	1088125	1 C -> T	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss		flgG2 CDS

9 Appendix

A	1088420	1088415	0 (A)6 -> (A)7	Insertion (tandem repeat)	78	94.9%	1,4E-215	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	
G	1088948	1088948	1 A -> G	SNP (transition)	66	100.0%	2,5E-204	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	ftsZ CDS
A	1089176	1089176	1 G -> A	SNP (transition)	84	100.0%	2,5E-285	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	ftsZ CDS
G	1089353	1089353	1 A -> G	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	ftsZ CDS
T	1090158	1090158	1 C -> T	SNP (transition)	80	100.0%	1E-271	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	ftsA CDS
G	1091208	1091208	1 A -> G	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	I -> T
T	1091270	1091270	1 C -> T	SNP (transition)	141	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	M -> I
C	1091511	1091511	1 T -> C	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	K -> R
T	1091521	1091521	1 C -> T	SNP (transition)	85	100.0%	3,2E-263	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	D -> N
G	1091616	1091616	1 A -> G	SNP (transition)	88	100.0%	4E-290	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	V -> A
A	1093146	1093146	1 G -> A	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	mraW;ruvX CDS
A	1093703	1093703	1 G -> A	SNP (transition)	68	100.0%	2,5E-217	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	Membrane protein CDS
T	1093840	1093840	1 C -> T	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	T -> I
G	1093863	1093863	1 A -> G	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	K -> E
C	1093992	1093992	1 T -> C	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	S -> P
T	1094028	1094028	1 C -> T	SNP (transition)	94	100.0%	2,5E-272	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	Membrane protein CDS
T	1096444	1096444	1 C -> T	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	gta CDS
T	1096752	1096752	1 C -> T	SNP (transition)	92	100.0%	2,5E-303	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	A -> T
A	1098210	1098210	1 G -> A	SNP (transition)	80	98.9%	2,2E-273	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	D -> N
A	1099469	1099469	1 T -> A	SNP (transversion)	77	100.0%	7,8E-254	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	flgH CDS
A	1099993	1099993	1 G -> A	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	lspA CDS
A	1100197	1100197	1 G -> A	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
C	1100203	1100203	1 T -> C	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
C	1100209	1100209	1 T -> C	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
C	1100212	1100212	1 T -> C	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
C	1100218	1100218	1 T -> C	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
A	1100221	1100221	1 G -> A	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
T	1100230	1100230	1 C -> T	SNP (transition)	106	99.1%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
C	1100245	1100245	1 T -> C	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
C	1100263	1100263	1 T -> C	SNP (transition)	95	100.0%	1E-303	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
G	1100275	1100275	1 A -> G	SNP (transition)	95	100.0%	1E-303	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
C	1100281	1100281	1 T -> C	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
G	1100290	1100290	1 A -> G	SNP (transition)	101	100.0%	1E-302	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
C	1100487	1100487	1 T -> C	SNP (transition)	82	100.0%	2,5E-270	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	T -> A
C	1100504	1100504	1 T -> C	SNP (transition)	90	100.0%	1E-296	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	Q -> R
A	1100551	1100551	1 G -> A	SNP (transition)	91	100.0%	5E-300	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
T	1100934	1100934	1 C -> T	SNP (transition)	90	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	A -> T
A	1100947	1100947	1 G -> A	SNP (transition)	88	100.0%	6,3E-299	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
C	1100998	1100998	1 T -> C	SNP (transition)	79	98.7%	2E-247	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
AAC	1101006	1101006	2 GAT -> AAC	Substitution	86	100.0%	2,5E-266	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	I -> V
C	1101010	1101010	1 T -> C	SNP (transition)	72	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
T	1101220	1101220	1 G -> T	SNP (transversion)	62	100.0%	6,3E-192	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	prlA CDS
A	1101396	1101396	1 G -> A	SNP (transition)	83	100.0%	1,2E-273	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	H -> Y
T	1103468	1103468	1 C -> T	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	uvrB CDS
A	1103471	1103471	1 G -> A	SNP (transition)	104	99.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	uvrB CDS
A	1104573	1104573	1 T -> A	SNP (transversion)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	uvrB CDS
A	1104599	1104599	1 G -> A	SNP (transition)	93	100.0%	1,3E-308	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	uvrB CDS
T	1104865	1104865	1 C -> T	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	Anaerobic C4-dicarboxylate transporter CDS
G	1105435	1105435	1 A -> G	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	Anaerobic C4-dicarboxylate transporter CDS
G	1106155	1106155	1 C -> G	SNP (transition)	118	99.2%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	Anaerobic C4-dicarboxylate transporter CDS
G	1107577	1107577	1 A -> G	SNP (transition)	92	100.0%	4E-294	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	rpoN CDS
C	1107840	1107840	1 T -> C	SNP (transition)	89	100.0%	1,3E-275	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	lptA CDS
A	1107971	1107971	1 G -> A	SNP (transition)	94	100.0%	1,6E-300	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	lptA CDS
A	1109102	1109102	1 G -> A	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	
A	1317946	1317946	1 G -> A	SNP (transition)	123	99.2%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	gpmI CDS
C	1317949	1317949	1 T -> C	SNP (transition)	125	99.2%	0	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	gpmI CDS
	1326102	1326102	1 (A)3 -> (A)2	Deletion (tandem repeat)	278	96.4%	1,6E-15	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	
C	1326407	1326407	1 T -> C	SNP (transition)	273	100.0%	1,3E-81	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	
G	1327851	1327851	1 A -> G	SNP (transition)	134	99.3%	2,9E-64	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	
TT	1327864	1327863	0 >TT	Insertion	127	94.5%	2,7E-38	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	
T	1327866	1327866	1 A -> T	SNP (transversion)	123	98.4%	1,1E-44	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	
	1327871	1327871	1 (T)3 -> (T)2	Deletion (tandem repeat)	121	100.0%	6,3E-24	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	
G	1327896	1327896	1 A -> G	SNP (transition)	98	100.0%	1E-48	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	
T	1327911	1327911	1 C -> T	SNP (transition)	74	100.0%	4E-44	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	
T	1327914	1327913	0 (T)2 -> (T)3	Insertion (tandem repeat)	74	91.9%	5,3E-33	Variants: BfR-CA-11057-TF15687-12_R	Concatemer BfR-CA-11057 - UniAss	
A	1461975	1461975	1 G -> A	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	cheY CDS
C	6704	6704	1 T -> C	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	F -> S
C	13282	13282	1 T -> C	SNP (transition)	84	98.8%	4,2E-255	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	Chain B, Stru
G	13285	13285	1 A -> G	SNP (transition)	76	100.0%	6,3E-243	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	gltB3 CDS
G	17889	17889	1 A -> G	SNP (transition)	95	100.0%	1E-303	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	gltB3 CDS
T	18297	18297	1 C -> T	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	Desulfoferrodoxin FeS4 iron-binding domain-containing pro
A	19670	19670	1 G -> A	SNP (transition)	83	97.6%	6,8E-215	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	Desulfoferrodoxin FeS4 iron-binding domain-containing pro
C	20709	20709	1 T -> C	SNP (transition)	86	98.8%	8,6E-270	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	ilvD CDS
C	20716	20716	1 T -> C	SNP (transition)	85	98.8%	8,5E-250	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	N -> D
T	20725	20725	1 A -> T	SNP (transversion)	84	98.8%	3,3E-230	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
G	20731	20731	1 A -> G	SNP (transition)	80	100.0%	1E-263	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
C	20755	20755	1 T -> C	SNP (transition)	85	98.8%	2,1E-241	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
C	20776	20776	1 A -> C	SNP (transversion)	89	98.9%	5,6E-253	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
G	20779	20779	1 A -> G	SNP (transition)	86	100.0%	4E-249	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
T	20785	20785	1 A -> T	SNP (transversion)	80	98.8%	1,3E-250	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	20797	20797	1 G -> A	SNP (transition)	88	95.5%	3,7E-262	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
T	20812	20812	1 C -> T	SNP (transition)	87	98.9%	5,5E-230	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
G	20821	20821	1 A -> G	SNP (transition)	86	100.0%	1,8E-283	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
T	20830	20830	1 C -> T	SNP (transition)	94	100.0%	6,3E-263	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
AAG	20836	20838	2 TAA -> AAG	Substitution	109	94.0%	7,1E-274	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	20842	20842	2 GGT -> AGC	Substitution	105	98.1%	1,1E-294	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	20845	20845	1 G -> A	SNP (transition)	106	99.1%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
G	20851	20851	1 T -> G	SNP (transversion)	102	98.0%	5,1E-276	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
T	20854	20854	1 G -> T	SNP (transversion)	102	99.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
TAA	20866	20868	2 AAG -> TAA	Substitution	103 -> 106	98.1%	1E-300	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	20872	20872	1 G -> A	SNP (transition)	102	99.0%	1E-300	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	20890	20890	1 G -> A	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
C	20893	20893	1 T -> C	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
G	20899	20899	1 A -> G	SNP (transition)	111	99.1%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
T	20908	20908	1 C -> T	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
T	20917	20917	1 A -> T	SNP (transversion)	96	100.0%	4E-278	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	D -> E
A	20920	20920	1 G -> A	SNP (transition)	103	99.0%	6,5E-263	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
G	20926	20926	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	20932	20932	1 G -> A	SNP (transition)	105	100.0%	3,2E-304	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	20941	20941	1 G -> A	SNP (transition)	103	98.0%	4,9E-290	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	21001	21001	1 G -> A	SNP (transition)	93	100.0%	2E-269	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
T	21004	21004	1 G -> T	SNP (transversion)	93	98.9%	2,8E-301	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	21007	21007	1 T -> A	SNP (transversion)	92	96.7%	9,9E-253	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
T	21010	21010	1 A -> T	SNP (transition)	89	98.9%	1,4E-270	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	21034	21034	1 G -> A	SNP (transition)	87	97.7%	1,2E-275	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
AGC	21040	21042	2 GCT -> AGC	Substitution	95 -> 107	98.9% -> 99.0%	9,5E-280	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	T -> A
A	21046	21046	1 G -> A	SNP (transition)	96	97.9%	7,2E-297	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
G	21049	21049	1 A -> G	SNP (transition)	94	100.0%	1,6E-300	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	21054	21054	1 G -> A	SNP (transition)	86	98.8%	2,7E-261	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
C	21058	21058	1 T -> C	SNP (transition)	88	100.0%	2,5E-281	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
G	21075	21075	1 A -> G	SNP (transition)	82	100.0%	4E-262	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
T	21079	21079	1 C -> T	SNP (transition)	79	98.7%	7,9E-232	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
C	21082	21082	1 T -> C	SNP (transition)	79	100.0%	6,3E-221	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	21108	21106	1 G -> A	SNP (transition)	85	96.5%	6,2E-249	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
G	21118	21118	1 A -> G	SNP (transition)	85	98.8%	1,3E-266	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	21136	21136	1 C -> A	SNP (transversion)	82	96.3%	4,4E-208	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
T	21139	21139	1 C -> T	SNP (transition)	78	98.7%	3,9E-221	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	21142	21142	1 T -> A	SNP (transversion)	75	100.0%	3,2E-247	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	21154	21154	1 G -> A	SNP (transition)	75	96.0%	1,7E-196	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
C	21157	21157	1 T -> C	SNP (transition)	75	100.0%	3,2E-247	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
C	21172	21172	1 T -> C	SNP (transition)	86	100.0%	1,6E-283	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
T	21193	21193	1 A -> T	SNP (transversion)	86	98.8%	8,6E-236	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
C	21196	21196	1 T -> C	SNP (transition)	95	98.9%	9,5E-280	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	21202	21202	1 G -> A	SNP (transition)	93	100.0%	1E-278	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	21205	21205	1 G -> A	SNP (transition)	89	100.0%	1E-266	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	21298	21298	1 C -> A	SNP (transversion)	133	99.2%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
T	21313	21313	1 C -> T	SNP (transition)	133	97.7%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
A	21316	21316	1 G -> A	SNP (transition)	131	97.7%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
C	21319	21319	1 T -> C	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	comGF CDS
T	21418	21417	0 (T)6 -> (T)7	Insertion (tandem repeat)	118	90.7%	4,7E-295	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	
A	22093	22093	1 G -> A	SNP (transition)	72	98.6%	2,9E-230	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	queC CDS
C	22173	22173	1 T -> C	SNP (transition)	90	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	
A	22276	22276	1 G -> A	SNP (transition)	98	100.0%	4E-274	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	dsbI CDS
T	22282	22282	1 G -> T	SNP (transversion)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	dsbI CDS
T	22291	22291	1 C -> T	SNP (transition)	96	99.0%	9,6E-283	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	dsbI CDS
C	22294	22294	1 T -> C	SNP (transition)	95	100.0%	3,2E-275	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	dsbI CDS
AG	22306	22307	2 GT -> AG	Substitution	94 -> 95	100.0%	1E-303	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	D -> A
G	22315	22315	1 A -> G	SNP (transition)	93	100.0%	1,3E-308	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	dsbI CDS
TA	22320	22321	2 CG -> TA	Substitution	95 -> 96	97.9%	3E-292	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	AV -> AI
G	22324	22324	1 A -> G	SNP (transition)	85	100.0%	1E-271	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	dsbI CDS
CT	22604	22605	2 TC -> CT	Substitution	91	95.6%	3E-276	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	D -> S
CG	22608	22607	2 TT -> CG	Substitution	82 -> 83	96.3% -> 96.4%	2,2E-263	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	QK -> GE
C	22834	22834	1 T -> C	SNP (transition)	104	99.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	dsbI CDS
ATC	22864	22866	2 GTT -> ATC	Substitution	92 -> 94	100.0%	4E-294	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	N -> D
A	22870	22870	1 G -> A	SNP (transition)	96	99.0%	3E-273	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	dsbI CDS
T	22891	22891	1 G -> T	SNP (transversion)	97	100.0%	5E-283	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	dsbI CDS
A	22897	22897	1 G -> A	SNP (transition)	86	100.0%	1E-257	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	dsbI CDS
GA	22921	22922	2 TG -> GA	Substitution	68	98.5%	1,4E-205	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	T -> I
A	22924	22924	1 G -> A	SNP (transition)	70	98.6%	5,8E-198	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	dsbI CDS
GTCA	22939	22942	3 ATTG -> GTCA	Substitution	62 -> 64	98.4%	1,6E-179	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	IN -> ID
C	22947	22947	1 T -> C	SNP (transition)	63	100.0%	1,3E-207	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	K -> E
A	22958	22959	1 C -> A	SNP (transversion)	63	100.0%	1E-188	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	A -> S

A	22963	22963	1	G -> A	SNP (transition)	63	100.0%	1,3E-207	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
TG	22966	22967	2	GA -> TG	Substitution	65 -> 66	96.9% -> 97.0%	4,1E-179	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	I -> T	dsbI CDS
T	22971	22971	1	C -> T	SNP (transition)	66	100.0%	2,5E-204	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	D -> N	dsbI CDS
A	22987	22987	1	G -> A	SNP (transition)	71	100.0%	1E-212	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
CAA	22990	22992	2	AAG -> CAA	Substitution	66 -> 67	95.5% -> 97.0%	2,1E-188	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
C	23002	23002	1	T -> C	SNP (transition)	76	100.0%	1,6E-250	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
A	23038	23038	1	G -> A	SNP (transition)	72	100.0%	1E-215	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
C	23041	23041	1	T -> C	SNP (transition)	72	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
G	24160	24160	1	T -> G	SNP (transversion)	94	98.9%	1,2E-304	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	K -> Q	ycgM CDS
T	24166	24166	1	G -> T	SNP (transversion)	82	98.8%	8,2E-241	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	H -> N	ycgM CDS
C	24170	24170	1	T -> C	SNP (transition)	79	100.0%	1,6E-252	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		ycgM CDS
G	24173	24173	1	A -> G	SNP (transition)	78	97.4%	3E-224	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		ycgM CDS
T	24185	24185	1	A -> T	SNP (transversion)	89	98.9%	2,2E-279	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		ycgM CDS
T	24212	24212	1	C -> T	SNP (transition)	91	96.7%	7,6E-250	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		ycgM CDS
T	24218	24218	1	G -> T	SNP (transversion)	102	100.0%	2,5E-285	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		ycgM CDS
G	24224	24224	1	A -> G	SNP (transition)	85	100.0%	1E-288	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		ycgM CDS
A	24500	24500	1	G -> A	SNP (transition)	86	100.0%	1E-257	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		ycgM CDS
GC	24673	24674	2	AT -> GC	Substitution	105	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		ycgM CDS
C	24710	24710	1	T -> C	SNP (transition)	99	99.0%	1,6E-301	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		ycgM CDS
G	25001	25001	1	A -> G	SNP (transition)	109	98.2%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	25286	25286	1	T -> C	SNP (transition)	111	99.1%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	25469	25469	1	A -> C	SNP (transversion)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
T	25474	25474	1	C -> T	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	E -> K	RNA pseudouridylate synthase CDS
A	25478	25478	1	T -> A	SNP (transversion)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
A	25489	25489	1	G -> A	SNP (transition)	106	99.1%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	H -> Y	RNA pseudouridylate synthase CDS
A	25526	25526	1	G -> A	SNP (transition)	112	99.1%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
G	25538	25538	1	A -> G	SNP (transition)	110	98.2%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
G	25610	25610	1	A -> G	SNP (transition)	125	99.2%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	25691	25691	1	T -> C	SNP (transition)	115	99.1%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	26306	26306	1	T -> C	SNP (transition)	101	98.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
A	26321	26321	1	G -> A	SNP (transition)	109	98.2%	3,7E-274	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
ACTT	26342	26345	3	GTTA -> ACTT	Substitution	92 -> 93	98.9%	7,3E-280	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
G	26348	26348	1	T -> G	SNP (transversion)	92	97.8%	4,2E-293	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
A	26369	26369	1	G -> A	SNP (transition)	101	99.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
T	27838	27838	1	C -> T	SNP (transition)	105	97.1%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	27892	27892	1	C -> T	SNP (transition)	73	100.0%	2,5E-233	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
C	27949	27949	1	T -> C	SNP (transition)	91	100.0%	7,9E-282	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
C	28003	28003	1	T -> C	SNP (transition)	92	100.0%	2,5E-303	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28015	28015	1	C -> T	SNP (transition)	85	97.6%	4,5E-270	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
C	28018	28018	1	T -> C	SNP (transition)	83	98.8%	2,1E-268	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
A	28024	28024	1	G -> A	SNP (transition)	87	100.0%	7,9E-287	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
GG	28135	28136	2	AA -> GG	Substitution	86	100.0%	4E-249	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	VS -> VG	nrdA CDS
C	28213	28213	1	T -> C	SNP (transition)	66	100.0%	6,3E-211	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28216	28216	1	C -> T	SNP (transition)	66	98.5%	6,6E-206	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28237	28237	1	G -> T	SNP (transversion)	80	98.8%	5E-219	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
G	28780	28780	1	T -> G	SNP (transversion)	87	98.9%	5,5E-273	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28816	28816	1	C -> T	SNP (transition)	83	98.8%	1,3E-235	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28822	28822	1	C -> T	SNP (transition)	83	98.8%	1,3E-276	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	32037	32037	1	C -> T	SNP (transition)	90	98.9%	5,7E-247	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		pyrG CDS
A	33736	33736	1	G -> A	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33748	33748	1	T -> C	SNP (transition)	105	98.1%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33751	33751	1	T -> C	SNP (transition)	105	99.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
T	33757	33757	1	C -> T	SNP (transition)	105	99.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33769	33769	1	T -> C	SNP (transition)	105	99.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
AA	36609	36609	1	G -> AA	Insertion	141 -> 145	87.9% -> 88.3%	9,4E-140	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	36624	36624	1	T -> C	SNP (transition)	162	98.1%	6,8E-169	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
	36651	36651	1	(A)3 -> (A)2	Deletion (tandem repeat)	184	91.3%	2,7E-32	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	36654	36654	1	T -> A	SNP (transversion)	181	92.8%	2,6E-132	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
AA	36660	36659	0	+AA	Insertion	178	91.6%	2E-113	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	36669	36669	1	T -> C	SNP (transition)	182	99.5%	2E-160	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
G	38113	38113	1	A -> G	SNP (transition)	219	99.5%	4,4E-63	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
	38420	38420	1	(T)3 -> (T)2	Deletion (tandem repeat)	217	100.0%	2E-21	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
G	41815	41815	1	T -> G	SNP (transversion)	206	99.0%	3,3E-57	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
T	42200	42200	1	G -> T	SNP (transversion)	361	99.2%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
AG	42203	42204	2	GA -> AG	Substitution	357 -> 367	98.6%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
	42428	42428	1	(A)7 -> (A)6	Deletion (tandem repeat)	325	100.0%	3,2E-292	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
	42797	42802	6	(TTTATG)3 -> (TTTATG)2	Deletion (tandem repeat)	272	100.0%	4E-54	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	43128	43128	1	G -> A	SNP (transition)	100	99.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	T -> I	hypothetical protein CDS
A	48711	48711	1	G -> A	SNP (transition)	73	97.3%	1,7E-223	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		Class I SAM-dependent DNA methyltransferase CDS
A	48795	48795	1	G -> A	SNP (transition)	82	95.1%	1,1E-219	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		Class I SAM-dependent DNA methyltransferase CDS
C	48804	48804	1	T -> C	SNP (transition)	84	97.6%	5,5E-275	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		Class I SAM-dependent DNA methyltransferase CDS
C	48819	48819	1	T -> C	SNP (transition)	79	98.7%	3,1E-255	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		Class I SAM-dependent DNA methyltransferase CDS
A	48822	48822	1	G -> A	SNP (transition)	78	98.7%	1,2E-259	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		Class I SAM-dependent DNA methyltransferase CDS
T	48825	48825	1	C -> T	SNP (transition)	78	98.7%	1,2E-259	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		Class I SAM-dependent DNA methyltransferase CDS
C	48858	48858	1	T -> C	SNP (transition)	82	98.8%	4,1E-265	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		Class I SAM-dependent DNA methyltransferase CDS
A	48882	48882	1	C -> A	SNP (transversion)	91	97.8%	2,6E-245	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		Class I SAM-dependent DNA methyltransferase CDS
C	49144	49144	1	T -> C	SNP (transition)	81	100.0%	5E-267	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		Class I SAM-dependent DNA methyltransferase CDS
C	49873	49873	1	T -> C	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	S -> P	Class I SAM-dependent DNA methyltransferase CDS
C	1015338	1015338	1	T -> C	SNP (transition)	75	100.0%	3,2E-247	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	N -> S	napA CDS
G	1017555	1017555	1	A -> G	SNP (transition)	72	98.6%	5,7E-218	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1019956	1019956	1	A -> G	SNP (transition)	71	100.0%	6,3E-227	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
C	1019962	1019962	1	T -> C	SNP (transition)	69	100.0%	7,9E-200	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
G	1019974	1019974	1	A -> G	SNP (transition)	69	100.0%	1E-206	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
C	1020030	1020030	1	T -> C	SNP (transition)	68	98.5%	3,4E-192	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	K -> E	DNA helicase CDS
G	1020034	1020034	1	A -> G	SNP (transition)	70	98.6%	8,8E-212	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
G	1020043	1020043	1	A -> G	SNP (transition)	66	100.0%	2,5E-204	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
G	1020340	1020340	1	A -> G	SNP (transition)	89	98.9%	3,5E-288	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
T	1020478	1020478	1	C -> T	SNP (transition)	81	95.1%	1,7E-224	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
T	1020753	1020753	1	C -> T	SNP (transition)	74	98.6%	7,4E-217	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	G -> S	DNA helicase CDS
AA	1020795	1020796	2	GG -> AA	Substitution	49	98.0%	7,8E-147	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
A	1020811	1020811	1	G -> A	SNP (transition)	53	100.0%	2,5E-169	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
G	1020817	1020817	1	A -> G	SNP (transition)	54	100.0%	6,3E-178	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
C	1020952	1020952	1	T -> C	SNP (transition)	51	100.0%	6,3E-163	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
A	1021000	1021000	1	G -> A	SNP (transition)	78	98.7%	1,6E-236	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
TAA	1021003	1021005	2	AAG -> TAA	Substitution	97 -> 99	100.0%	1E-296	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
C	1021009	1021009	1	T -> C	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
C	1021012	1021012	1	T -> C	SNP (transition)	97	99.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
TTC	1021015	1021017	2	ATT -> TTC	Substitution	94	100.0%	1E-281	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	N -> E	DNA helicase CDS
C	1021025	1021025	1	T -> C	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	K -> R	DNA helicase CDS
A	1021027	1021027	1	T -> A	SNP (transversion)	97	99.0%	6,1E-305	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
T	1021040	1021040	1	A -> T	SNP (transversion)	93	100.0%	2E-269	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
	1021050	1021050	1	-T	Deletion	84	95.2%	1,8E-137	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
CACG	1021056	1021059	4	TTAA -> CACG	Substitution	80 -> 81	97.5%	5E-238	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1021067	1021067	1	A -> G	SNP (transition)	81	97.5%	8,1E-265	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1021075	1021075	1	T -> A	SNP (transversion)	81	100.0%	1,3E-234	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1021077	1021077	1	A -> G	SNP (transition)	81	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1021099	1021099	1	A -> C	SNP (transversion)	88	98.9%	1,8E-267	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
TA	1021103	1021104	2	AC -> TA	Substitution	89 -> 90	97.8%	5,6E-253	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
ATA	1021114	1021116	3	GAT -> ATA	Substitution	104 -> 108	96.3% -> 97.2%	9,1E-293	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1021147	1021147	1	C -> T	SNP (transition)	90	82.2%	1,3E-189	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1021159	1021159	1	G -> A	SNP (transition)	67	92.5%	9,6E-179	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
TAA	1021162	1021164	3	AGC -> TAA	Substitution	65 -> 66	86.4% -> 87.7%	1,3E-149	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1021166	1021166	1	A -> G	SNP (transition)	65	89.2%	2,8E-182	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1021175	1021175	1	G -> T	SNP (transversion)	67	100.0%	5E-194	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	L -> F	hypothetical protein CDS
T	1021179	1021179	1	A -> T	SNP (transversion)	67	100.0%	2E-207	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	I -> F	hypothetical protein CDS
A	1021196	1021196	1	T -> A	SNP (transversion)	75	100.0%	3,2E-232	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1021199	1021199	1	C -> G	SNP (transversion)	75	100.0%	3,2E-232	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021202	1021202	1	A -> T	SNP (transversion)	74	100.0%	2,5E-214	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GTC	1021206	1021208	2	ATT -> GTC	Substitution	74	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	I -> V	hypothetical protein CDS
T	1021210	1021210	1	C -> T	SNP (transition)	74	100.0%	1E-184	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	A -> V	hypothetical protein CDS
G	1021214	1021214	1	T -> G	SNP (transversion)	73	100.0%	6,3E-248	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021218	1021218	1	G -> T	SNP (transversion)	73	100.0%	2,5E-233	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	V -> L	hypothetical protein CDS
CTTAGC	1021224	1021229	4	TTAGGT -> CTTAGC	Substitution	72 -> 73	100.0%	4E-230	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	LG -> LS	hypothetical protein CDS
T	1021235	1021235	1	C -> T	SNP (transition)	71	100.0%	5E-234	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1021241	1021241	1	T -> C	SNP (transition)	68	100.0%	4E-224	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1021253	1021253	1	A -> G	SNP (transition)	62	100.0%	2,5E-204	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021259	1021259	1	A -> T	SNP (transversion)	60	100.0%	1E-191	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021265	1021265	1	A -> T	SNP (transversion)	46	100.0%	2,5E-142	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GCT	1021267	1021269	3	AGA -> GCT	Substitution	42 -> 46	100.0%	1,6E-142	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	KN -> SY	hypothetical protein CDS
A	1021715	1021715	1	G -> A	SNP (transition)	42	97.6%	6,6E-113	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021719	1021719	1	C -> T	SNP (transition)	44	100.0%	1,6E-140	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1021723	1021723	1	A -> G	SNP (transition)	44	100.0%	1,6E-140	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	N -> S	hypothetical protein CDS
TTG	1021725	1021727	2	ATA -> TTG	Substitution	45	97.8%	4E-114	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	I -> L	hypothetical protein CDS
T	1021736	1021736	1	C -> T	SNP (transition)	47	97.9%	3E-145	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
CCTT	1021742	1021745	3	TTTA -> CCTT	Substitution	56 -> 58	100.0%	2,5E-156	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
CAA	1021752	1021754	2	GAG -> CAA	Substitution	67	97.0%	6,6E-180	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	E -> Q	hypothetical protein CDS
A	1021757	1021757	1	T -> A	SNP (transversion)	73	98.6%	7,3E-214	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021760	1021760	1	C -> T	SNP (transition)	78	97.4%	1,9E-239	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GTGCTT	1021782	1021787	4	ATTTTA -> GTGCTT	Substitution	86 -> 88	98.8% -> 98.9%	2,5E-243	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	IL -> VL	hypothetical protein CDS
T	1021793	1021793	1	A -> T	SNP (transversion)	92	100.0%	1E-275	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1021799	1021799	1	T -> C	SNP (transition)	96	100.0%	6,3E-307	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GAT	1021806	1021808	2	CAA -> GAT	Substitution	94 -> 97	97.9%	9,6E-264	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	Q -> D	hypothetical protein CDS
T	1021811	1021811	1	C -> T	SNP (transition)	97	99.0%	2,4E-295	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	1021814	1021814	1	G -> A	SNP (transition)	99	99.0%	9,9E-292	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1021820	1021820	1	T -> G	SNP (transversion)	95	98.9%	1,5E-298	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	N -> K	hypothetical protein CDS
T	1021823	1021823	1	G -> T	SNP (transversion)	95	100.0%	3,2E-275	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021836	1021836	1	C -> T	SNP (transition)	100	99.0%	6,3E-275	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GCGA	1021839	1021842	4	AGCG -> GCGA	Substitution	99	89.9%	1,1E-279	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	SV -> AI	hypothetical protein CDS
G	1021848	1021848	1	C -> G	SNP (transversion)	97	99.0%	6,1E-305	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	Q -> E	hypothetical protein CDS
TCT	1021857	1021859	2	GCA -> TCT	Substitution	89 -> 91	97.8%	7,1E-256	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	A -> S	hypothetical protein CDS
C	1021865	1021865	1	T -> C	SNP (transition)	78	100.0%	2,5E-249	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021868	1021868	1	C -> T	SNP (transition)	78	100.0%	1E-233	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS

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T	1021870	1021870	1	A -> T	SNP (transversion)	82	100.0%	6,3E-254	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	Y -> F	hypothetical protein CDS
T	1021874	1021874	1	A -> T	SNP (transversion)	82	100.0%	6,3E-254	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1021895	1021895	1	A -> G	SNP (transition)	80	100.0%	1E-255	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021898	1021898	1	A -> T	SNP (transversion)	79	100.0%	1,3E-244	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1021901	1021901	1	A -> G	SNP (transition)	75	98.7%	3E-227	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GT	1021912	1021913	2	AA -> GT	Substitution	66	100.0%	2,5E-171	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	K -> S	hypothetical protein CDS
T	1021922	1021922	1	C -> T	SNP (transition)	65	100.0%	3,2E-214	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1021925	1021925	1	T -> C	SNP (transition)	60	100.0%	1E-185	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021928	1021928	1	C -> T	SNP (transition)	60	100.0%	1E-191	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021934	1021934	1	A -> T	SNP (transversion)	54	100.0%	6,3E-178	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	E -> D	hypothetical protein CDS
T	1021940	1021940	1	C -> T	SNP (transition)	50	98.0%	5E-145	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1021943	1021943	1	T -> C	SNP (transition)	48	97.9%	3,8E-153	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021946	1021946	1	A -> T	SNP (transversion)	47	100.0%	7,9E-155	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021959	1021959	1	G -> T	SNP (transversion)	41	97.6%	4,1E-126	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	A -> S	hypothetical protein CDS
TCA	1021989	1021991	3	AGC -> TCA	Substitution	41 -> 43	93.0% -> 95.1%	1,2E-115	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021994	1021994	1	A -> T	SNP (transversion)	42	92.9%	1,4E-116	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
ATT	1021998	1022000	2	TTA -> ATT	Substitution	45 -> 47	80.0% -> 80.9%	1,4E-91	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	L -> I	hypothetical protein CDS
A	1022003	1022003	1	C -> A	SNP (transversion)	43	93.0%	1,2E-107	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	N -> K	hypothetical protein CDS
CC	1022005	1022006	2	AT -> CC	Substitution	47 -> 48	93.6% -> 93.8%	1,6E-127	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	N -> T	hypothetical protein CDS
TG	1022009	1022010	2	AA -> TG	Substitution	48	97.9%	1,9E-148	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	PK -> PE	hypothetical protein CDS
TGCTT	1022014	1022018	4	AATTA -> TGCTT	Substitution	45	97.8%	1,1E-125	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	EL -> VL	hypothetical protein CDS
C	1022022	1022022	1	G -> C	SNP (transversion)	42	97.6%	2,1E-133	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	E -> Q	hypothetical protein CDS
T	1022025	1022025	1	C -> T	SNP (transition)	48	97.9%	3,8E-153	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	H -> Y	hypothetical protein CDS
C	1022036	1022036	1	T -> C	SNP (transition)	46	97.8%	4,6E-142	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	1022046	1022046	1	T -> A	SNP (transversion)	50	98.0%	7,9E-155	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	L -> I	hypothetical protein CDS
T	1022055	1022055	1	C -> T	SNP (transition)	53	98.1%	3,3E-159	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	L -> F	hypothetical protein CDS
G	1022060	1022060	1	A -> G	SNP (transition)	53	98.1%	8,4E-175	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1022068	1022068	1	T -> C	SNP (transition)	57	96.5%	1,6E-183	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	I -> T	hypothetical protein CDS
A	1022078	1022078	1	T -> A	SNP (transversion)	59	98.3%	9,3E-178	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	D -> E	hypothetical protein CDS
A	1022081	1022081	1	C -> A	SNP (transversion)	63	98.4%	2,5E-196	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	1022093	1022093	1	T -> A	SNP (transversion)	64	98.4%	1,6E-199	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	D -> E	hypothetical protein CDS
G	1022102	1022102	1	A -> G	SNP (transition)	67	98.5%	1,1E-215	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	1022108	1022108	1	C -> A	SNP (transversion)	75	97.3%	1,4E-222	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1022111	1022111	1	A -> T	SNP (transversion)	78	97.4%	1,2E-254	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	K -> N	hypothetical protein CDS
C	1022114	1022114	1	T -> C	SNP (transition)	80	98.8%	1,6E-258	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	1022117	1022117	1	G -> A	SNP (transition)	80	98.8%	5E-219	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1022132	1022132	1	T -> C	SNP (transition)	88	98.9%	7E-285	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
AG	1022134	1022135	2	CA -> AG	Substitution	81 -> 83	97.5% -> 97.6%	4,3E-231	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	T -> K	hypothetical protein CDS
T	1022138	1022138	1	A -> T	SNP (transversion)	76	98.7%	7,6E-223	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1022144	1022144	1	T -> C	SNP (transition)	73	87.7%	6,1E-200	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1022147	1022147	1	C -> T	SNP (transition)	74	100.0%	6,3E-207	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1022150	1022150	1	C -> T	SNP (transition)	75	88.0%	3,1E-193	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	1022153	1022153	1	G -> A	SNP (transition)	67	100.0%	4E-214	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1022165	1022165	1	T -> C	SNP (transition)	66	100.0%	6,3E-211	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
CT	1022176	1022177	2	GC -> CT	Substitution	60	96.7%	2,8E-176	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	S -> T	hypothetical protein CDS
CGTA	1022180	1022183	3	TATT -> CGTA	Substitution	59 -> 60	96.6% -> 96.7%	1,2E-174	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	SI -> SV	hypothetical protein CDS
CGCGTA	1022192	1022197	6	TAAAAC -> CGCGTA	Substitution	58 -> 61	85.2% -> 89.7%	1,5E-154	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1022206	1022206	1	C -> T	SNP (transition)	61	95.1%	5,7E-175	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
AAA	1022210	1022209	0	+AAA	Insertion	62	85.5%	8,4E-147	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
GCA	1022225	1022227	3	ATT -> GCA	Substitution	65 -> 69	96.9% -> 97.1%	5,2E-198	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	NL -> SI	valS CDS
ACA	1022236	1022238	3	GAG -> ACA	Substitution	75	97.3%	4,7E-205	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	E -> T	valS CDS
G	1022259	1022259	1	A -> G	SNP (transition)	66	100.0%	1,6E-217	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
T	1022262	1022262	1	C -> T	SNP (transition)	66	98.5%	6,6E-167	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
G	1022265	1022265	1	A -> G	SNP (transition)	83	98.8%	1,3E-235	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
A	1022283	1022283	1	C -> A	SNP (transversion)	79	97.5%	7,7E-212	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
G	1022290	1022290	1	A -> G	SNP (transition)	80	97.5%	3,2E-230	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	T -> A	valS CDS
C	1022451	1022451	1	T -> C	SNP (transition)	74	100.0%	4E-229	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
T	1022454	1022454	1	C -> T	SNP (transition)	72	98.6%	5,7E-218	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
A	1022460	1022460	1	T -> A	SNP (transversion)	77	100.0%	5E-223	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
T	1022529	1022529	1	C -> T	SNP (transition)	78	97.4%	4,7E-209	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
A	1028995	1028995	1	G -> A	SNP (transition)	73	97.3%	8,3E-174	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	S -> N	DL-methionine ABC transporter MetINQ, substrate-binding
G	1029015	1029015	1	A -> G	SNP (transition)	67	100.0%	2E-207	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	N -> D	DL-methionine ABC transporter MetINQ, substrate-binding
T	1029122	1029122	1	C -> T	SNP (transition)	64	98.4%	3,2E-193	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		DL-methionine ABC transporter MetINQ, substrate-binding
A	1029394	1029394	1	G -> A	SNP (transition)	83	100.0%	2,5E-265	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1029442	1029442	1	C -> T	SNP (transition)	98	96.9%	1,5E-260	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1029517	1029517	1	T -> C	SNP (transition)	93	98.9%	3,7E-292	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
CC	1029544	1029545	2	TT -> CC	Substitution	88	100.0%	2,5E-281	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1029550	1029550	1	T -> C	SNP (transition)	86	100.0%	2,5E-266	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1029556	1029556	1	T -> C	SNP (transition)	79	100.0%	2,5E-268	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029559	1029559	1	C -> T	SNP (transition)	78	100.0%	1,6E-241	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
A	1029622	1029622	1	G -> A	SNP (transition)	74	100.0%	4E-229	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029748	1029748	1	C -> T	SNP (transition)	71	98.6%	7,1E-215	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029757	1029757	1	C -> T	SNP (transition)	72	98.6%	5,7E-218	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
G	1029760	1029760	1	A -> G	SNP (transition)	70	100.0%	1E-223	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029769	1029769	1	C -> T	SNP (transition)	81	98.8%	8,1E-222	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
GG	1029777	1029778	2	AA -> GG	Substitution	82 -> 83	98.8%	1,6E-237	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	K -> R	flgA CDS
T	1029790	1029790	1	C -> T	SNP (transition)	84	98.8%	4,2E-255	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029901	1029901	1	C -> T	SNP (transition)	85	100.0%	1E-271	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
ATC	1029914	1029916	2	GTT -> ATC	Substitution	85 -> 86	100.0%	3,2E-263	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	V -> I	flgA CDS
C	1029922	1029922	1	T -> C	SNP (transition)	82	98.8%	5,2E-257	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
G	1029943	1029943	1	A -> G	SNP (transition)	73	100.0%	2,5E-233	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1030030	1030030	1	T -> C	SNP (transition)	105	99.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1030264	1030264	1	G -> T	SNP (transversion)	92	98.9%	7,3E-280	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	A -> S	3-octaprenyl-4-hydroxybenzoate carboxy-lyase CDS
A	1030581	1030581	1	G -> A	SNP (transition)	100	98.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		3-octaprenyl-4-hydroxybenzoate carboxy-lyase CDS
G	1030821	1030821	1	A -> G	SNP (transition)	74	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		coaD CDS
G	1032161	1032161	1	A -> G	SNP (transition)	89	100.0%	1E-266	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	S -> G	hisS CDS
T	1032172	1032172	1	C -> T	SNP (transition)	83	100.0%	5E-257	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
AG	1032227	1032228	2	GA -> AG	Substitution	91	97.8%	5,1E-272	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	E -> R	hisS CDS
G	1032244	1032244	1	A -> G	SNP (transition)	88	100.0%	1E-263	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032250	1032250	1	T -> C	SNP (transition)	81	97.5%	3,2E-233	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032265	1032265	1	C -> T	SNP (transition)	83	98.8%	2,1E-268	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032304	1032304	1	C -> T	SNP (transition)	88	100.0%	1,6E-272	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032307	1032307	1	T -> C	SNP (transition)	84	100.0%	1,6E-268	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
A	1032310	1032310	1	G -> A	SNP (transition)	84	100.0%	1,6E-268	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
GC	1032325	1032326	2	AT -> GC	Substitution	77 -> 81	96.3% -> 97.4%	9,2E-229	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	EY -> EH	hisS CDS
G	1032355	1032355	1	A -> G	SNP (transition)	69	98.6%	1,1E-208	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1032361	1032361	1	A -> G	SNP (transition)	67	100.0%	7,9E-221	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032376	1032376	1	T -> C	SNP (transition)	70	98.6%	1,1E-218	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1032406	1032406	1	A -> G	SNP (transition)	80	100.0%	1E-255	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032466	1032466	1	C -> T	SNP (transition)	87	96.6%	1,6E-179	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1032523	1032523	1	A -> G	SNP (transition)	75	100.0%	1E-224	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032526	1032526	1	C -> T	SNP (transition)	71	100.0%	1E-212	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032529	1032529	1	C -> T	SNP (transition)	75	97.3%	7E-230	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032532	1032532	1	T -> C	SNP (transition)	74	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1038237	1038237	1	A -> G	SNP (transition)	86	100.0%	2,5E-266	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	I -> T	MBL fold metallo-hydrolase CDS
G	1038273	1038273	1	A -> G	SNP (transition)	84	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1040325	1040325	1	G -> A	SNP (transition)	67	98.5%	4,2E-209	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		dnaK CDS
T	1042179	1042179	1	C -> T	SNP (transition)	109	98.2%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042182	1042182	1	G -> A	SNP (transition)	114	96.5%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
AC	1042187	1042188	2	GT -> AC	Substitution	117	97.4%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
T	1042191	1042191	1	C -> T	SNP (transition)	109	98.2%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
C	1042194	1042194	1	T -> C	SNP (transition)	109	98.2%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042206	1042206	1	A -> G	SNP (transition)	109	98.2%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042218	1042218	1	A -> G	SNP (transition)	113	98.2%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042221	1042221	1	G -> A	SNP (transition)	113	97.3%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
T	1042233	1042233	1	C -> T	SNP (transition)	115	97.4%	6,2E-308	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
C	1042249	1042249	1	T -> C	SNP (transition)	106	97.2%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	N -> S	hrcA CDS
A	1042293	1042293	1	G -> A	SNP (transition)	84	96.4%	7,6E-246	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042371	1042371	1	G -> A	SNP (transition)	95	98.9%	6E-308	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042431	1042431	1	A -> G	SNP (transition)	91	98.9%	9,1E-268	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042479	1042479	1	A -> G	SNP (transition)	82	97.6%	3,3E-252	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1042488	1042488	1	C -> T	SNP (transition)	87	100.0%	5E-252	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1042490	1042490	1	T -> A	SNP (transversion)	87	98.9%	8,7E-256	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1042492	1042492	1	T -> G	SNP (transversion)	86	100.0%	1,6E-283	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
AG	1042520	1042521	2	TA -> AG	Substitution	62 -> 70	98.4% -> 98.6%	6,3E-192	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1042591	1042591	1	A -> T	SNP (transversion)	87	100.0%	7,9E-287	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1042596	1042596	1	G -> A	SNP (transition)	89	100.0%	1,3E-275	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1042608	1042608	1	G -> A	SNP (transition)	88	98.9%	3,5E-276	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1042632	1042632	1	A -> G	SNP (transition)	88	100.0%	1E-263	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1042634	1042634	1	C -> A	SNP (transversion)	86	100.0%	1,6E-283	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1042638	1042638	1	C -> A	SNP (transversion)	83	100.0%	1,3E-273	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1042642	1042642	1	T -> C	SNP (transition)	80	100.0%	1E-255	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
GT	1042650	1042651	2	AA -> GT	Substitution	79	96.2%	3,1E-227	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
ACAG	1042654	1042657	4	TGCA -> ACAG	Substitution	75 -> 79	96.0% -> 96.2%	7,7E-212	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1042659	1042658	0	+G	Insertion	69	94.2%	2,7E-195	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1042687	1042687	1	T -> A	SNP (transversion)	56	96.4%	6,1E-164	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1042690	1042690	1	A -> T	SNP (transversion)	55	87.3%	8E-126	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1042692	1042692	1	T -> C	SNP (transition)	59	83.1%	9,9E-146	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1042729	1042729	1	T -> C	SNP (transition)	76	96.1%	1,8E-228	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
AC	1042750	1042751	2	GA -> AC	Substitution	69	98.6%	1,6E-220	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1042763	1042763	1	T -> C	SNP (transition)	73	100.0%	2,5E-233	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1042765	1042765	1	C -> T	SNP (transition)	68	100.0%	1E-203	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
AC	1042784	1042785	2	GT -> AC	Substitution	76	97.4%	2,4E-215	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	N -> S	cfrA CDS
A	1042793	1042793	1	G -> A	SNP (transition)	80	98.8%	8E-235	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042796	1042796	1	A -> G	SNP (transition)	79	100.0%	1E-236	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1042805	1042805	1	C -> T	SNP (transition)	86	100.0%	4E-292	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	M -> I	cfrA CDS
A	1042829	1042829	1	G -> A	SNP (transition)	90	100.0%	1E-296	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042832	1042832	1	A -> G	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042835	1042835	1	G -> A	SNP (transition)	93	100.0%	1E-278	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042841	1042841	1	T -> G	SNP (transversion)	91	98.9%	9,1E-304	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
AG	1042850	1042851	2	GC -> AG	Substitution	104 -> 106	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	S -> T	cfrA CDS
GT	1042854	1042855	2	CC -> GT	Substitution	103 -> 107	96.1% -> 96.3%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	G -> T	cfrA CDS

CGCT	1042858	1042861	3	TCCC -> CGCT	Substitution	97	95.9% -> 97.9%	4,6E-281	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	GS -> SG	cfrA CDS
T	1042863	1042863	1	C -> T	SNP (transition)	101	97.0%	6,6E-269	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	S -> N	cfrA CDS
TG	1042866	1042867	2	GC -> TG	Substitution	101	97.0%	4E-283	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	A -> Q	cfrA CDS
A	1042880	1042880	1	G -> A	SNP (transition)	122	98.4%	7,3E-296	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042885	1042885	1	T -> C	SNP (transition)	119	99.2%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	N -> D	cfrA CDS
A	1042892	1042892	1	G -> A	SNP (transition)	120	96.7%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1042900	1042900	1	C -> T	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	D -> N	cfrA CDS
G	1042922	1042922	1	A -> G	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042937	1042937	1	T -> C	SNP (transition)	119	97.5%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042940	1042940	1	G -> A	SNP (transition)	114	98.2%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042964	1042964	1	G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042985	1042985	1	G -> A	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042994	1042994	1	T -> C	SNP (transition)	100	99.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043000	1043000	1	G -> T	SNP (transversion)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043087	1043087	1	T -> C	SNP (transition)	93	98.9%	2,3E-301	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043093	1043093	1	G -> A	SNP (transition)	98	99.0%	9,8E-289	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043099	1043099	1	G -> A	SNP (transition)	95	98.9%	3,8E-289	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043258	1043258	1	G -> A	SNP (transition)	89	100.0%	2E-293	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
TC	1043267	1043268	2	CT -> TC	Substitution	94	100.0%	1,6E-300	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	K -> R	cfrA CDS
G	1043271	1043271	1	A -> G	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	F -> S	cfrA CDS
C	1043584	1043584	1	G -> C	SNP (transversion)	89	100.0%	1,3E-275	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	L -> V	cfrA CDS
CAA	1043648	1043650	2	AAG -> CAA	Substitution	88 -> 89	97.7% -> 97.8%	4,4E-250	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GTT	1043657	1043659	2	ATC -> GTT	Substitution	86 -> 88	100.0%	2,5E-266	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	D -> N	cfrA CDS
G	1043669	1043669	1	A -> G	SNP (transition)	93	98.9%	3,7E-292	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043672	1043672	1	A -> G	SNP (transition)	92	100.0%	4E-294	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043690	1043690	1	A -> T	SNP (transversion)	86	98.8%	2,7E-278	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043717	1043717	1	A -> G	SNP (transition)	78	97.4%	7,5E-232	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043720	1043720	1	A -> C	SNP (transversion)	78	100.0%	4E-257	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043724	1043724	1	C -> T	SNP (transition)	80	100.0%	1E-215	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	S -> N	cfrA CDS
A	1043765	1043765	1	G -> A	SNP (transition)	77	94.8%	1,1E-190	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043769	1043769	1	A -> G	SNP (transition)	76	98.7%	7,6E-238	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	V -> A	cfrA CDS
C	1043774	1043774	1	T -> C	SNP (transition)	74	98.6%	1,9E-231	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
CAA	1043792	1043794	2	TAG -> CAA	Substitution	72	97.2%	7,1E-194	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043801	1043801	1	A -> G	SNP (transition)	70	100.0%	1E-223	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043861	1043861	1	C -> T	SNP (transition)	66	98.5%	2,1E-212	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043867	1043867	1	T -> C	SNP (transition)	63	98.4%	1,6E-202	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
TGC	1043870	1043872	2	AGA -> TGC	Substitution	63 -> 66	100.0%	2,5E-171	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	S -> A	cfrA CDS
T	1043876	1043876	1	C -> T	SNP (transition)	72	100.0%	1E-215	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043882	1043882	1	G -> A	SNP (transition)	81	97.5%	1,3E-201	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043891	1043891	1	G -> A	SNP (transition)	79	97.5%	3,9E-204	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043896	1043896	1	C -> T	SNP (transition)	87	98.9%	1,4E-238	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	D -> N	cfrA CDS
T	1043903	1043903	1	C -> T	SNP (transition)	85	98.8%	2,1E-241	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043912	1043912	1	A -> G	SNP (transition)	97	99.0%	6,1E-305	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GTC	1043922	1043924	3	CCA -> GTC	Substitution	93 -> 94	97.8% -> 97.9%	9,3E-274	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	SG -> ST	cfrA CDS
G	1043927	1043927	1	A -> G	SNP (transition)	96	100.0%	4E-278	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043930	1043930	1	G -> A	SNP (transition)	95	98.9%	2,4E-270	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043966	1043966	1	A -> G	SNP (transition)	104	99.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043999	1043999	1	T -> C	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044005	1044005	1	A -> G	SNP (transition)	106	99.1%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044024	1044024	1	G -> T	SNP (transversion)	112	97.3%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	P -> Q	cfrA CDS
A	1044029	1044029	1	T -> A	SNP (transversion)	111	97.3%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	R -> S	cfrA CDS
G	1044044	1044044	1	A -> G	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044047	1044047	1	A -> G	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044074	1044074	1	G -> A	SNP (transition)	89	100.0%	1,3E-275	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044110	1044110	1	A -> G	SNP (transition)	94	97.9%	6,9E-263	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1044128	1044128	1	T -> C	SNP (transition)	91	100.0%	1,3E-263	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044155	1044155	1	G -> A	SNP (transition)	91	95.6%	3,3E-228	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044191	1044191	1	C -> T	SNP (transition)	81	98.8%	8,1E-262	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044314	1044314	1	C -> T	SNP (transition)	101	97.0%	1E-278	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044662	1044662	1	A -> G	SNP (transition)	86	98.8%	2,7E-244	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044720	1044720	1	C -> G	SNP (transversion)	89	100.0%	2E-293	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	S -> T	cfrA CDS
G	1044722	1044722	1	A -> G	SNP (transition)	89	100.0%	1,6E-284	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GGT	1044761	1044763	2	AGC -> GGT	Substitution	82	97.6%	3,3E-236	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	A -> T	cfrA CDS
G	1044767	1044767	1	T -> G	SNP (transversion)	83	100.0%	6,3E-282	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1044781	1044781	1	T -> C	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	I -> V	cfrA CDS
T	1044785	1044785	1	C -> T	SNP (transition)	90	98.9%	9E-265	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044788	1044788	1	A -> G	SNP (transition)	94	98.9%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044791	1044791	1	G -> A	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044797	1044797	1	C -> T	SNP (transition)	99	100.0%	7,9E-287	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044815	1044815	1	A -> G	SNP (transition)	88	100.0%	1,6E-272	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044821	1044821	1	A -> G	SNP (transition)	95	96.8%	5,5E-289	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GCTT	1044824	1044827	4	AGCC -> GCTT	Substitution	95 -> 99	89.5% -> 90.8%	6,4E-240	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	LA -> LS	cfrA CDS
G	1044830	1044830	1	A -> G	SNP (transition)	97	92.8%	1,3E-286	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044833	1044833	1	G -> A	SNP (transition)	93	93.5%	9,5E-226	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044842	1044842	1	A -> G	SNP (transition)	87	100.0%	7,9E-287	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044848	1044848	1	C -> T	SNP (transition)	90	97.8%	2,5E-295	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044859	1044859	1	A -> T	SNP (transversion)	88	100.0%	1,6E-272	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	L -> I	cfrA CDS
T	1044863	1044863	1	C -> T	SNP (transition)	87	100.0%	2E-269	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044903	1044903	1	G -> A	SNP (transition)	84	100.0%	1E-251	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
	1048144	1048149	6	(TAAACA)3 -> (TAAACA	Deletion (tandem repeat)	241	100.0%	7,9E-24	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
CT	1048758	1048759	2	TC -> CT	Substitution	220 -> 222	98.2%	2,4E-61	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1048762	1048762	1	C -> A	SNP (transversion)	224	99.6%	1,4E-64	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1049147	1049147	1	A -> C	SNP (transversion)	206	99.0%	3,3E-57	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
	1052542	1052542	1	(A)3 -> (A)2	Deletion (tandem repeat)	217	100.0%	2E-21	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1052849	1052849	1	T -> C	SNP (transition)	219	99.5%	4,4E-63	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1060048	1060048	1	T -> C	SNP (transition)	80	98.8%	1,3E-250	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	N -> S	Phytase-like domain-containing protein CDS
C	1289372	1289372	1	T -> C	SNP (transition)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		ctb CDS
C	1290299	1290299	1	T -> C	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		ATP-dependent DNA helicase RecG CDS
T	1290463	1290463	1	C -> T	SNP (transition)	91	100.0%	3,2E-227	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	E -> K	ATP-dependent DNA helicase RecG CDS
G	1292034	1292034	1	A -> G	SNP (transition)	72	100.0%	4E-230	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		Insulinase family protein CDS
G	1292286	1292286	1	A -> G	SNP (transition)	88	100.0%	1E-263	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		Insulinase family protein CDS
C	1293565	1293565	1	T -> C	SNP (transition)	87	98.9%	2,2E-264	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	T -> A	cofH,mqnC CDS
C	1294638	1294638	1	T -> C	SNP (transition)	71	100.0%	6,3E-227	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
T	1294793	1294793	1	C -> T	SNP (transition)	91	98.9%	9,1E-286	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	T -> I	MFS transporter CDS
A	1295652	1295652	1	G -> A	SNP (transition)	77	98.7%	1,9E-233	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nusA CDS
T	1295733	1295733	1	C -> T	SNP (transition)	94	98.9%	1,9E-267	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		nusA CDS
C	1296710	1296710	1	T -> C	SNP (transition)	99	99.0%	1,6E-301	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		miaB CDS
A	1300322	1300322	1	G -> A	SNP (transition)	74	98.6%	3,7E-224	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	T -> I	thiC CDS
A	1303903	1303902	0	(A)7 -> (A)8	Insertion (tandem repeat)	87	87.4%	1,1E-206	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1304441	1304441	1	G -> A	SNP (transition)	71	97.2%	7,8E-169	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	E -> K	Chemotaxis protein CDS
G	1306198	1306198	1	A -> G	SNP (transition)	101	98.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		Ferric enterobactin receptor CDS
T	1307149	1307149	1	C -> T	SNP (transition)	77	97.4%	2,9E-236	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		Ferric enterobactin receptor CDS
G	1308269	1308269	1	A -> G	SNP (transition)	74	98.6%	1,5E-209	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	S -> P	CoA ester lyase CDS
T	1308298	1308298	1	C -> T	SNP (transition)	80	97.5%	3,2E-230	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	S -> N	CoA ester lyase CDS
C	1308320	1308320	1	T -> C	SNP (transition)	80	98.8%	1E-242	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	I -> V	CoA ester lyase CDS
G	1308428	1308428	1	A -> G	SNP (transition)	95	100.0%	3,2E-294	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	S -> P	CoA ester lyase CDS
A	1308485	1308485	1	T -> A	SNP (transversion)	91	100.0%	6,3E-291	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	I -> L	CoA ester lyase CDS
G	1308525	1308525	1	A -> G	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		CoA ester lyase CDS
A	1310083	1310083	1	G -> A	SNP (transition)	92	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	A -> V	hypothetical protein CDS
G	1311022	1311022	1	T -> G	SNP (transversion)	79	100.0%	1,3E-244	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
C	1311340	1311340	1	T -> C	SNP (transition)	87	97.7%	1,2E-242	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
T	1312069	1312069	1	C -> T	SNP (transition)	86	98.8%	8,6E-236	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
A	1312081	1312081	1	G -> A	SNP (transition)	87	100.0%	2,5E-243	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
C	1312087	1312087	1	T -> C	SNP (transition)	84	100.0%	1,6E-268	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
A	1312095	1312095	1	G -> A	SNP (transition)	87	100.0%	2E-269	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss	L -> F	MatC-N domain-containing protein CDS
A	1312289	1312289	1	T -> A	SNP (transversion)	106	98.1%	1,4E-297	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1312291	1312291	1	T -> C	SNP (transition)	99	98.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
AA	1312296	1312298	3	TTT -> AA	Deletion	98 -> 100	93.9% -> 94.0%	1,5E-165	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
TTT	1312313	1312315	3	AAG -> TTT	Substitution	100 -> 101	99.0%	1E-297	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
GT	1312330	1312331	2	TC -> GT	Substitution	95	100.0%	3,2E-294	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
AG	1312333	1312334	2	TA -> AG	Substitution	94 -> 95	97.9%	4,4E-272	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1312340	1312340	1	A -> C	SNP (transversion)	100	99.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1312342	1312342	1	T -> C	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1312352	1312352	1	T -> C	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1312383	1312383	1	A -> G	SNP (transition)	101	98.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1312394	1312394	1	A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1312407	1312407	1	C -> T	SNP (transition)	82	98.8%	5,2E-257	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1312413	1312413	1	G -> A	SNP (transition)	73	98.6%	2,9E-228	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1312415	1312415	1	C -> T	SNP (transition)	73	97.3%	2,6E-209	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
	1312427	1312427	1	(T)6 -> (T)5	Deletion (tandem repeat)	62	96.8%	1,8E-104	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1312433	1312433	1	T -> C	SNP (transition)	61	98.4%	6,1E-202	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
AG	1312440	1312441	2	GT -> AG	Substitution	59	100.0%	2E-194	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1312448	1312448	1	G -> A	SNP (transition)	57	100.0%	3,2E-199	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
TGTG	1312456	1312459	4	GCAT -> TGTG	Substitution	51 -> 52	94.1% -> 94.2%	5,1E-103	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
GC	1312461	1312460	0	+GC	Insertion	55	83.6%	1E-141	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1312465	1312465	1	A -> G	SNP (transition)	57	96.5%	5E-178	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1312470	1312470	1	G -> A	SNP (transition)	53	100.0%	5E-164	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1312481	1312481	1	G -> A	SNP (transition)	56	98.2%	1,8E-157	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1312485	1312485	1	T -> C	SNP (transition)	57	98.2%	3,6E-177	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1312487	1312487	1	A -> C	SNP (transversion)	57	91.2%	1E-164	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1312489	1312489	1	G -> A	SNP (transition)	52	90.4%	2,6E-134	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1312505	1312505	1	T -> C	SNP (transition)	45	97.8%	2,8E-143	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1312507	1312507	1	A -> C	SNP (transversion)	48	95.8%	1,8E-148	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
	1312512	1312512	1	-T	Deletion	46	93.5%	1,9E-94	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
GG	1312516	1312517	2	TT -> GG	Substitution	45 -> 47	91.1% -> 91.5%	2,6E-136	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
AT	1312519	1312520	2	TA -> AT	Substitution	47	95.7%	1,1E-131	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
TA	1312529	1312530	2	AC -> TA	Substitution	51	98.0%	5,1E-148	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1312538	1312538	1	T -> C	SNP (transition)	56	91.1%	1,5E-166	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
ATG	1312540	1312542	3	TGT -> ATG	Substitution	56 -> 57	89.5% -> 91.1%	2,9E-150	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1312544	1312545	2	GG -> A	Deletion	59 -> 60	85.0% -> 86.4%	7,1E-92	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
	1312551	1312551	1	-C	Deletion	62	98.4%	9,7E-108	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1312558	1312558	1	G -> A	SNP (transition)	63	98.4%	1,6E-171	Variants: BfR-CA-11057-TF15687-13_R	Concatemer BfR-CA-11057 - UniAss		

9 Appendix

T	1312560	1312560	1 C -> T	SNP (transition)	63	98.4%	4E-190	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1312565	1312565	1 T -> A	SNP (transversion)	65	96.9%	4,1E-179	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1312568	1312568	1 T -> G	SNP (transversion)	69	97.1%	9,3E-211	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1312570	1312570	1 A -> G	SNP (transition)	68	98.6%	2,7E-222	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1312577	1312577	1 A -> G	SNP (transition)	60	98.6%	4,3E-195	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1312580	1312580	1 A -> T	SNP (transversion)	70	98.6%	5,8E-198	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1312591	1312590	0 (A)3 -> (A)4	Insertion (tandem repeat)	78	85.9%	3,8E-181	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
GGG	1312610	1312612	3 TAA -> GGG	Substitution	86	95.3%	2E-235	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1312664	1312664	1 G -> A	SNP (transition)	92	98.9%	9,2E-271	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
A	1312674	1312674	1 G -> A	SNP (transition)	93	95.7%	1,5E-233	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss	A -> V	accA CDS
C	1312676	1312676	1 A -> C	SNP (transversion)	90	100.0%	1E-269	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
T	1312685	1312685	1 C -> T	SNP (transition)	90	96.7%	2,9E-238	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
T	1313231	1313231	1 C -> T	SNP (transition)	103	97.1%	1,8E-284	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
G	1314216	1314216	1 A -> G	SNP (transition)	86	98.8%	8,6E-270	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		fabF CDS
A	1314306	1314306	1 G -> A	SNP (transition)	82	98.8%	6,5E-249	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		fabF CDS
C	1314653	1314653	1 T -> C	SNP (transition)	97	99.0%	6,1E-305	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss	T -> A	fabF CDS
A	1316808	1316808	1 G -> A	SNP (transition)	93	98.9%	2,3E-301	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
G	1316877	1316877	1 A -> G	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
C	1316976	1316976	1 T -> C	SNP (transition)	79	98.7%	3,1E-255	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
A	1317402	1317402	1 G -> A	SNP (transition)	85	100.0%	3,2E-263	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss	L -> F	gpmI CDS
A	1317449	1317449	1 G -> A	SNP (transition)	82	98.8%	8,2E-241	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss	A -> V	gpmI CDS
A	1317469	1317469	1 G -> A	SNP (transition)	88	100.0%	6,3E-255	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317562	1317562	1 G -> A	SNP (transition)	72	98.6%	7,2E-211	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317946	1317946	1 G -> A	SNP (transition)	96	97.9%	1,8E-287	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317949	1317949	1 T -> C	SNP (transition)	99	100.0%	1E-296	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317958	1317958	1 A -> C	SNP (transversion)	101	100.0%	0	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss	D -> E	gpmI CDS
T	1317970	1317970	1 C -> T	SNP (transition)	103	99.0%	1,6E-293	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317973	1317973	1 A -> C	SNP (transversion)	105	99.0%	0	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317976	1317976	1 T -> C	SNP (transition)	108	99.1%	0	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317979	1317979	1 T -> A	SNP (transversion)	106	98.1%	1,4E-297	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss	E -> D	gpmI CDS
G	1318006	1318006	1 A -> G	SNP (transition)	85	100.0%	3,2E-263	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1318015	1318015	1 G -> C	SNP (transversion)	82	98.8%	8,2E-241	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318018	1318018	1 A -> G	SNP (transition)	83	100.0%	5E-257	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318207	1318207	1 A -> G	SNP (transition)	95	98.9%	6E-308	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318468	1318468	1 A -> G	SNP (transition)	94	97.9%	6,9E-261	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
T	1319026	1319026	1 C -> T	SNP (transition)	81	98.8%	8,1E-254	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		mraY CDS
C	1319170	1319170	1 T -> C	SNP (transition)	70	100.0%	1E-230	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		mraY CDS
T	1320129	1320129	1 C -> T	SNP (transition)	99	99.0%	9,9E-292	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		murD CDS
G	1320495	1320495	1 A -> G	SNP (transition)	87	97.7%	3,7E-251	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		murD CDS
A	1321063	1321002	0 (A)5 -> (A)6	Insertion (tandem repeat)	50	92.0%	3,6E-123	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
	1321702	1321707	6 (TAAACA)3 -> (TAAACA)2	Deletion (tandem repeat)	242	100.0%	6,3E-24	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
CT	1322316	1322317	2 TC -> CT	Substitution	220 -> 222	98.2%	2,4E-61	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
A	1322320	1322320	1 C -> A	SNP (transversion)	224	99.6%	1,4E-64	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1322705	1322705	1 A -> C	SNP (transversion)	206	99.0%	3,3E-57	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
	1326100	1326100	1 (A)3 -> (A)2	Deletion (tandem repeat)	217	100.0%	2E-21	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
C	1326407	1326407	1 T -> C	SNP (transition)	219	99.5%	4,4E-63	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1327851	1327851	1 A -> G	SNP (transition)	85	98.8%	5,8E-40	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
TT	1327864	1327863	0 +TT	Insertion	80	96.3%	2,9E-26	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1327866	1327866	1 A -> T	SNP (transversion)	80	96.3%	2,9E-26	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
	1327871	1327871	1 (T)3 -> (T)2	Deletion (tandem repeat)	79	97.5%	1,7E-12	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
G	1327896	1327896	1 A -> G	SNP (transition)	60	96.7%	8,4E-26	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1327911	1327911	1 C -> T	SNP (transition)	43	95.3%	1,3E-21	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1327914	1327913	0 (T)2 -> (T)3	Insertion (tandem repeat)	43	90.7%	1,6E-19	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		
T	1329416	1329416	1 G -> T	SNP (transversion)	87	100.0%	5E-252	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss	A -> D	Methyl-accepting chemotaxis protein CDS
A	1329562	1329562	1 G -> A	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		Methyl-accepting chemotaxis protein CDS
T	1329774	1329774	1 C -> T	SNP (transition)	111	99.1%	0	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss	E -> K	Methyl-accepting chemotaxis protein CDS
A	1330823	1330823	1 G -> A	SNP (transition)	89	98.9%	3,5E-244	Variants: BfR-CA-11057-TF156B7-13_R	Concatemer BfR-CA-11057 - UniAss		PMT-2 domain-containing protein CDS
G	24160	24160	1 T -> G	SNP (transversion)	113	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	K -> Q	yrgM CDS
T	24166	24166	1 G -> T	SNP (transversion)	93	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	H -> N	yrgM CDS
C	24170	24170	1 T -> C	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		yrgM CDS
G	24173	24173	1 A -> G	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		yrgM CDS
T	24185	24185	1 A -> T	SNP (transversion)	102	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		yrgM CDS
T	24212	24212	1 C -> T	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		yrgM CDS
T	24218	24218	1 G -> T	SNP (transversion)	119	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		yrgM CDS
G	24224	24224	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		yrgM CDS
A	24600	24600	1 G -> A	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		yrgM CDS
GC	24673	24674	2 AT -> GC	Substitution	82 -> 83	98.8%	3,3E-301	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		yrgM CDS
C	24710	24710	1 T -> C	SNP (transition)	70	98.6%	2,8E-246	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		yrgM CDS
G	25001	25001	1 A -> G	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	25286	25286	1 T -> C	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
T	25408	25408	1 C -> T	SNP (transition)	135	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	E -> K	RNA pseudouridylate synthase CDS
C	25489	25489	1 A -> C	SNP (transversion)	102	99.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
T	25474	25474	1 C -> T	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	E -> K	RNA pseudouridylate synthase CDS
A	25478	25478	1 T -> A	SNP (transversion)	105	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
A	25489	25489	1 G -> A	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	H -> Y	RNA pseudouridylate synthase CDS
A	25526	25526	1 G -> A	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
G	25538	25538	1 A -> G	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
G	25610	25610	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	25691	25691	1 T -> C	SNP (transition)	84	100.0%	1E-293	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	26306	26306	1 T -> C	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
A	26321	26321	1 G -> A	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
ACTT	26342	26345	3 GTA -> ACTT	Substitution	75 -> 81	98.7% -> 98.8%	3E-264	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
G	26348	26348	1 T -> G	SNP (transversion)	77	100.0%	1,3E-284	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
A	26369	26369	1 G -> A	SNP (transition)	85	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
T	27838	27838	1 C -> T	SNP (transition)	134	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	27892	27892	1 C -> T	SNP (transition)	122	99.2%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
C	27949	27949	1 T -> C	SNP (transition)	123	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
C	28003	28003	1 T -> C	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28015	28015	1 C -> T	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
C	28018	28018	1 T -> C	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
A	28024	28024	1 G -> A	SNP (transition)	102	98.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
GG	28135	28136	2 AA -> GG	Substitution	100 -> 101	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	VS -> VG	mrdA CDS
C	28213	28213	1 T -> C	SNP (transition)	110	98.2%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28216	28216	1 C -> T	SNP (transition)	114	99.1%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28237	28237	1 G -> T	SNP (transversion)	123	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
G	28780	28780	1 T -> G	SNP (transversion)	111	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28816	28816	1 C -> T	SNP (transition)	115	99.1%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28822	28822	1 C -> T	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	32037	32037	1 C -> T	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		pyrG CDS
A	33736	33736	1 G -> A	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33748	33748	1 T -> C	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33751	33751	1 T -> C	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
T	33757	33757	1 C -> T	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33769	33769	1 T -> C	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
A	36609	36609	1 G -> A	SNP (transition)	176	88.6%	5,7E-208	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	36674	36674	1 T -> C	SNP (transition)	193	85.9%	8,2E-181	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
G	38113	38113	1 A -> G	SNP (transition)	286	99.3%	6,4E-81	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
	38420	38420	1 (T)3 -> (T)2	Deletion (tandem repeat)	259	96.9%	1,3E-15	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
G	41815	41815	1 T -> G	SNP (transversion)	272	82.4%	1,8E-27	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
TTTGC	461516	461520	4 AGTTT -> TTTGC	Substitution	82 -> 83	80.5% -> 80.7%	6,1E-158	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	LNS -> LQT	DUF115 domain-containing protein CDS
TTT	461526	461528	2 ATC -> TTT	Substitution	81 -> 82	80.2% -> 81.7%	6,4E-153	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	D -> K	DUF115 domain-containing protein CDS
C	461537	461537	1 T -> C	SNP (transition)	83	100.0%	1,3E-190	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	N -> D	DUF115 domain-containing protein CDS
T	461547	461547	1 A -> T	SNP (transversion)	81	84.0%	2,3E-148	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	F -> L	DUF115 domain-containing protein CDS
C	1049147	1049147	1 A -> C	SNP (transversion)	272	82.4%	1,8E-27	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
	1052544	1052544	1 (A)3 -> (A)2	Deletion (tandem repeat)	257	97.7%	2,5E-17	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1052849	1052849	1 T -> C	SNP (transition)	286	99.3%	6,4E-81	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1056828	1056828	1 T -> C	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	E -> G	ccmA CDS
C	1058557	1058557	1 T -> C	SNP (transition)	83	98.8%	5,2E-299	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	I -> V	Putative ABC transport system permease CDS
T	1058795	1058795	1 G -> T	SNP (transversion)	74	100.0%	1,8E-273	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Putative ABC transport system permease CDS
T	1058819	1058819	1 C -> T	SNP (transition)	70	97.1%	3,8E-241	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	R -> K	ataC CDS
T	1058880	1058880	1 C -> T	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	V -> I	ataC CDS
G	1058884	1058884	1 A -> G	SNP (transition)	75	98.7%	7,6E-268	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1058971	1058971	1 G -> A	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059022	1059022	1 A -> G	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059108	1059108	1 G -> A	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059154	1059154	1 G -> A	SNP (transition)	79	98.7%	1,3E-278	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059162	1059162	1 A -> G	SNP (transition)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	F -> L	ataC CDS
T	1059259	1059259	1 C -> T	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059283	1059283	1 A -> G	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059487	1059487	1 A -> G	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
C	1059541	1059541	1 T -> C	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
CA	1059570	1059571	2 TG -> CA	Substitution	109	99.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	ST -> SA	ataC CDS
G	1059624	1059624	1 A -> G	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1059660	1059660	1 C -> T	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1059675	1059675	1 C -> T	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1059897	1059897	1 A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1059915	1059915	1 A -> G	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1059961	1059961	1 G -> A	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	A -> V	Phytase-like domain-containing protein CDS
G	1059973	1059973	1 A -> G	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	I -> T	Phytase-like domain-containing protein CDS
C	1060048	1060048	1 T -> C	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	N -> S	Phytase-like domain-containing protein CDS
G	1060134	1060134	1 A -> G	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1060458	1060458	1 G -> A	SNP (transition)	93	98.9%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1060491	1060491	1 G -> T	SNP (transversion)	90	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1060503	1060503	1 A -> G	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1060557	1060557	1 G -> A	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1060596	1060596	1 A -> G	SNP (transition)	87	98.9%	2,2E-307	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1060641	1060641	1 C -> T	SNP (transition)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
C	1061191	1061191	1 T -> C	SNP (transition)	83	100.0%	5,2E-290	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		aflA CDS
A	1061194	1061194	1 G -> A	SNP (transition)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		aflA CDS
A	1061399	1061399	1 G -> A	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	A -> V	aflA CDS
A	1061809	1061809	1 G -> A	SNP (transition)	98	99.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		aflA CDS
A	1061821	1061821	1 G -> A	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		aflA CDS

C	1062232	1062232	1	T -> C	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	V -> A	corA CDS
G	1062305	1062305	1	A -> G	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		corA CDS
G	1063367	1063367	1	A -> G	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	I -> V	moaB CDS
AGC	1065015	1065017	3	GCT -> AGC	Substitution	84 -> 86	98.8%	1,3E-296	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	A -> S	Peptidase, M48 family protein CDS
C	1065021	1065021	1	G -> C	SNP (transversion)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	V -> L	Peptidase, M48 family protein CDS
G	1065032	1065032	1	A -> G	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		Peptidase, M48 family protein CDS
G	1066684	1066684	1	A -> G	SNP (transition)	76	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	I -> V	flaC CDS
T	1066860	1066860	1	C -> T	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		flaC CDS
A	1067425	1067425	1	G -> A	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	A -> T	Pyridoxal phosphate homeostasis protein CDS
T	1068252	1068252	1	C -> T	SNP (transition)	87	98.9%	2,2E-307	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	G -> E	dnaE CDS
A	1068284	1068284	1	G -> A	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1068497	1068497	1	G -> A	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1069352	1069352	1	G -> A	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1070006	1070006	1	G -> A	SNP (transition)	114	99.1%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
G	1070291	1070291	1	A -> G	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1072148	1072148	1	G -> A	SNP (transition)	70	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
G	1072658	1072658	1	A -> G	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
T	1072835	1072835	1	C -> T	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
G	1072943	1072943	1	A -> G	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
G	1073012	1073012	1	A -> G	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		Phospho-2-dehydro-3-deoxyheptonate aldolase CDS
A	1073559	1073559	1	G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	H -> Y	uraH CDS
A	1073632	1073632	1	G -> A	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		uraH CDS
A	1073645	1073645	1	G -> A	SNP (transition)	75	98.7%	1,2E-271	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	A -> V	uraH CDS
C	1073813	1073813	1	T -> C	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	N -> S	uraH CDS
C	1074956	1074956	1	T -> C	SNP (transition)	70	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	N -> D	trmD CDS
G	1075095	1075095	1	A -> G	SNP (transition)	65	100.0%	3,2E-240	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	V -> A	rimM CDS
G	1075504	1075504	1	T -> G	SNP (transversion)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	K -> Q	rimM CDS
G	1075743	1075743	1	A -> G	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		RNA-binding protein CDS
C	1076616	1076616	1	T -> C	SNP (transition)	82	100.0%	1E-286	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	I -> M	ffh CDS
T	1078818	1078818	1	C -> T	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	R -> Q	3-deoxy-D-manno-octulosonic acid transferase CDS
T	1080585	1080585	1	G -> T	SNP (transversion)	70	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	L -> I	Nif3-like dinuclear metal center hexameric protein CDS
T	1081250	1081250	1	C -> T	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
T	1081253	1081253	1	C -> T	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
C	1081259	1081259	1	T -> C	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
C	1081469	1081469	1	T -> C	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
A	1081520	1081520	1	G -> A	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
C	1081523	1081523	1	T -> C	SNP (transition)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
A	1081526	1081526	1	T -> A	SNP (transversion)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
A	1081571	1081571	1	C -> A	SNP (transversion)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
C	1081580	1081580	1	T -> C	SNP (transition)	97	99.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
T	1081589	1081589	1	A -> T	SNP (transversion)	94	98.9%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		glyQ CDS
T	1081971	1081971	1	C -> T	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		DUF3972 domain-containing protein CDS
C	1083619	1083619	1	T -> C	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	S -> G	putative protease from collagenase family CDS
C	1084688	1084688	1	T -> C	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	N -> S	Chemotaxis protein CDS
C	1084756	1084756	1	T -> C	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1085392	1085392	1	G -> A	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	V -> I	glnA CDS
G	1087996	1087996	1	A -> G	SNP (transition)	73	98.6%	4,6E-257	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		flgG2 CDS
A	1088029	1088029	1	G -> A	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		flgG2 CDS
T	1088125	1088125	1	C -> T	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		flgG2 CDS
A	1088420	1088419	0	(A)6 -> (A)7	Insertion (tandem repeat)	80	91.3%	2,5E-260	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		
G	1088948	1088948	1	A -> G	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		ftsZ CDS
A	1089176	1089176	1	G -> A	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		ftsZ CDS
G	1089353	1089353	1	A -> G	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		ftsZ CDS
T	1090158	1090158	1	C -> T	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		ftsA CDS
G	1091208	1091208	1	A -> G	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	I -> T	Peptidylprolyl isomerase CDS
T	1091270	1091270	1	C -> T	SNP (transition)	112	99.1%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	M -> I	Peptidylprolyl isomerase CDS
C	1091511	1091511	1	T -> C	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	K -> R	Peptidylprolyl isomerase CDS
T	1091521	1091521	1	C -> T	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	D -> N	Peptidylprolyl isomerase CDS
G	1091616	1091616	1	A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	V -> A	Peptidylprolyl isomerase CDS
A	1093146	1093146	1	G -> A	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		mraW,rsmH CDS
A	1093703	1093703	1	G -> A	SNP (transition)	68	98.5%	8,6E-246	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		Membrane protein CDS
T	1093849	1093849	1	C -> T	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	T -> I	Membrane protein CDS
G	1093863	1093863	1	A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	K -> E	Membrane protein CDS
C	1093992	1093992	1	T -> C	SNP (transition)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	S -> P	Membrane protein CDS
T	1094028	1094028	1	C -> T	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		Membrane protein CDS
T	1096444	1096444	1	C -> T	SNP (transition)	87	98.9%	2,2E-307	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		pta CDS
T	1096752	1096752	1	C -> T	SNP (transition)	106	99.1%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	A -> T	pta CDS
A	1098210	1098210	1	G -> A	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	D -> N	flgH CDS
A	1099469	1099469	1	T -> A	SNP (transversion)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		ispG CDS
A	1099993	1099993	1	G -> A	SNP (transition)	97	99.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
A	1100197	1100197	1	G -> A	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
C	1100203	1100203	1	T -> C	SNP (transition)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
C	1100209	1100209	1	T -> C	SNP (transition)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
C	1100212	1100212	1	T -> C	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
C	1100218	1100218	1	T -> C	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
A	1100221	1100221	1	G -> A	SNP (transition)	88	100.0%	1E-307	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
T	1100230	1100230	1	C -> T	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
C	1100245	1100245	1	T -> C	SNP (transition)	82	100.0%	1E-286	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
C	1100263	1100263	1	T -> C	SNP (transition)	78	98.7%	4,9E-275	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
G	1100275	1100275	1	A -> G	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
C	1100281	1100281	1	T -> C	SNP (transition)	79	100.0%	4E-284	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
G	1100290	1100290	1	A -> G	SNP (transition)	80	100.0%	1E-279	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
C	1100487	1100487	1	T -> C	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	T -> A	priA CDS
C	1100504	1100504	1	T -> C	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	Q -> R	priA CDS
A	1100551	1100551	1	G -> A	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
T	1100934	1100934	1	C -> T	SNP (transition)	77	100.0%	1,3E-284	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	A -> T	priA CDS
A	1100947	1100947	1	G -> A	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
C	1100998	1100998	1	T -> C	SNP (transition)	79	100.0%	3,2E-276	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
AAC	1101004	1101006	2	GAT -> AAC	Substitution	82	100.0%	6,3E-295	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	I -> V	priA CDS
C	1101010	1101010	1	T -> C	SNP (transition)	77	100.0%	3,2E-269	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
T	1101220	1101220	1	G -> T	SNP (transversion)	63	100.0%	7,9E-233	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		priA CDS
A	1101396	1101396	1	G -> A	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	H -> Y	priA CDS
T	1103468	1103468	1	C -> T	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		uvrB CDS
A	1103471	1103471	1	G -> A	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		uvrB CDS
A	1104573	1104573	1	T -> A	SNP (transversion)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	F -> I	uvrB CDS
A	1104599	1104599	1	G -> A	SNP (transition)	76	100.0%	2,5E-273	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		uvrB CDS
T	1104865	1104865	1	C -> T	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		Anaerobic C4-dicarboxylate transporter CDS
G	1106155	1106155	1	C -> G	SNP (transversion)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		Anaerobic C4-dicarboxylate transporter CDS
G	1107577	1107577	1	A -> G	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		rpoN CDS
C	1107840	1107840	1	T -> C	SNP (transition)	79	98.7%	7,9E-271	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		lptB CDS
A	1107921	1107921	1	G -> A	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		lptB CDS
A	1109102	1109102	1	G -> A	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		
G	1109455	1109455	1	A -> G	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	R -> G	argG CDS
C	1109600	1109600	1	T -> C	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	V -> A	argG CDS
T	1110117	1110117	1	C -> T	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		argG CDS
C	1110276	1110276	1	T -> C	SNP (transition)	94	98.9%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		argG CDS
T	1110282	1110282	1	C -> T	SNP (transition)	98	99.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		argG CDS
C	1110321	1110321	1	T -> C	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		argG CDS
	1110352	1110352	1	(A)7 -> (A)6	Deletion (tandem repeat)	89	94.4%	1,6E-252	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	M ->	rplI CDS
C	1110399	1110399	1	T -> C	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		rplI CDS
T	1110423	1110423	1	C -> T	SNP (transition)	87	98.9%	2,2E-307	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		rplI CDS
T	1110474	1110474	1	C -> T	SNP (transition)	86	97.7%	1,5E-298	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		rplI CDS
C	1110492	1110492	1	T -> C	SNP (transition)	89	98.9%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		rplI CDS
T	1110501	1110501	1	C -> T	SNP (transition)	84	98.8%	6,7E-305	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		rplI CDS
G	1110516	1110516	1	A -> G	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		rplI CDS
T	1110531	1110531	1	C -> T	SNP (transition)	82	98.8%	2,6E-281	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		rplI CDS
C	1110615	1110615	1	T -> C	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		rplI CDS
G	1110618	1110618	1	A -> G	SNP (transition)	77	100.0%	1,3E-284	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		rplI CDS
C	1110633	1110633	1	T -> C	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		rplI CDS
T	1110762	1110762	1	C -> T	SNP (transition)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		rplI CDS
G	1111025	1111025	1	A -> G	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
A	1111058	1111058	1	G -> A	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
T	1111079	1111079	1	C -> T	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
G	1111082	1111082	1	A -> G	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
G	1111097	1111097	1	A -> G	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
T	1111130	1111130	1	C -> T	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
T	1111145	1111145	1	C -> T	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
A	1111148	1111148	1	G -> A	SNP (transition)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
C	1111166	1111166	1	T -> C	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
A	1111169	1111169	1	T -> A	SNP (transversion)	63	100.0%	7,9E-233	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
T	1111172	1111172	1	C -> T	SNP (transition)	70	98.6%	2,8E-246	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
T	1111181	1111181	1	C -> T	SNP (transition)	67	100.0%	6,3E-241	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
C	1111190	1111190	1	T -> C	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
T	1111193	1111193	1	C -> T	SNP (transition)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
A	1111196	1111196	1	G -> A	SNP (transition)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
T	1111205	1111205	1	A -> T	SNP (transversion)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
C	1111208	1111208	1	T -> C	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
T	1111277	1111277	1	C -> T	SNP (transition)	83	98.8%	5,2E-293	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslV CDS
A	1111387	1111387	1	G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslU CDS
T	1111516	1111516	1	C -> T	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hslU CDS
A	1112237	1112237	1	G -> A	SNP (transition)	71	98.6%	7,1E-257	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	A -> T	hslU CDS
C	1113039	1113039	1	T -> C	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		era CDS
G	1113381	1113381	1	A -> G	SNP (transition)	80	100.0%	1E-279	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		era CDS
T	1113874	1113874	1	C -> T	SNP (transition)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1114424	1114424	1	C -> G	SNP (transversion)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	H -> D	hypothetical protein CDS
T	1115463	1115463	1	A -> T	SNP (transversion)	89	98.9%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	E -> D	Xaa-Pro aminopeptidase CDS
T	1115790	1115790	1	C -> T	SNP (transition)	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		Xaa-Pro aminopeptidase CDS
A	1116040	1116040	1	G -> A	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	A -> T	Xaa-Pro aminopeptidase CDS
A	1116383	1116382	0	(A)6 -> (A)7	Insertion (tandem repeat)	93	89.2%	6,4E-294	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		Xaa-Pro aminopeptidase CDS
A	1116469	1116469	1	G -> A	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	G -> E	Xaa-Pro aminopeptidase CDS
T	1116748	1116748	1	C -> T	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss	T -> I	Xaa-Pro aminopeptidase CDS
C	1116929	1116929	1	T -> C	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-1_R	Concatemer BfR-CA-11057 - UniAss		Xaa-Pro aminopeptidase CDS

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G	1117008	1117008	1 A -> G	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	T -> A	Xaa-Pro aminopeptidase CDS
G	1117070	1117070	1 A -> G	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
A	1117259	1117259	1 G -> A	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
C	1117658	1117658	1 T -> C	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
C	1121111	1121111	1 T -> C	SNP (transition)	66	100.0%	1E-230	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		3-deoxy-D-manno-octulosonate 8-phosphate phosphatase K
G	1121401	1121402	0 +G	Insertion	102	91.2%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
G	1122140	1122140	1 A -> G	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Endolytic peptidoglycan transglycosylase RlpA CDS
T	1122572	1122572	1 C -> T	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	E -> K	Lytic transglycosylase CDS
C	1122840	1122840	1 T -> C	SNP (transition)	61	100.0%	2,5E-219	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Lytic transglycosylase CDS
G	1124431	1124431	1 A -> G	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Diguanylate cyclase response regulator CDS
C	1124825	1124825	1 T -> C	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	N -> S	Diguanylate cyclase response regulator CDS
A	1124951	1124951	1 T -> A	SNP (transversion)	87	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	N -> I	Diguanylate cyclase response regulator CDS
T	1125466	1125466	1 C -> T	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	A -> T	DNA repair protein RecN CDS
C	1126257	1126257	1 T -> C	SNP (transition)	70	100.0%	1E-251	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	N -> S	DNA repair protein RecN CDS
C	1126919	1126919	1 T -> C	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		DNA repair protein RecN CDS
C	1289372	1289372	1 T -> C	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		ctb CDS
C	1290299	1290299	1 T -> C	SNP (transition)	92	98.9%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		ATP-dependent DNA helicase RecG CDS
T	1290463	1290463	1 C -> T	SNP (transition)	110	98.2%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	E -> K	ATP-dependent DNA helicase RecG CDS
G	1292034	1292034	1 A -> G	SNP (transition)	55	100.0%	3,2E-203	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Insulinase family protein CDS
G	1292286	1292286	1 A -> G	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Insulinase family protein CDS
C	1293565	1293565	1 T -> C	SNP (transition)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	T -> A	coPrI_rnpnC CDS
C	1294638	1294638	1 T -> C	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
T	1294793	1294793	1 C -> T	SNP (transition)	88	98.9%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	T -> I	MFS transporter CDS
A	1295652	1295652	1 G -> A	SNP (transition)	70	100.0%	1E-251	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		nusA CDS
T	1295733	1295733	1 C -> T	SNP (transition)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		nusA CDS
C	1296710	1296710	1 T -> C	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		miaB CDS
A	1300322	1300322	1 G -> A	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	T -> I	tmC CDS
A	1303903	1303902	0 (A)7 -> (A)8	Insertion (tandem repeat)	101	87.1%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1304441	1304441	1 G -> A	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	E -> K	Chemotaxis protein CDS
G	1306198	1306198	1 A -> G	SNP (transition)	79	100.0%	4E-284	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Ferric enterobactin receptor CDS
T	1307149	1307149	1 C -> T	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Ferric enterobactin receptor CDS
G	1308269	1308269	1 A -> G	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	S -> P	CoA ester lyase CDS
T	1308298	1308298	1 C -> T	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	S -> N	CoA ester lyase CDS
C	1308320	1308320	1 T -> C	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	I -> V	CoA ester lyase CDS
G	1308478	1308428	1 A -> G	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	S -> P	CoA ester lyase CDS
A	1308485	1308485	1 T -> A	SNP (transversion)	75	100.0%	3,2E-262	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	I -> L	CoA ester lyase CDS
G	1308525	1308525	1 A -> G	SNP (transition)	83	98.8%	3,3E-301	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		CoA ester lyase CDS
A	1310083	1310083	1 G -> A	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	A -> V	hypothetical protein CDS
G	1311022	1311022	1 T -> G	SNP (transversion)	79	100.0%	4E-284	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
C	1311340	1311340	1 T -> C	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
T	1312069	1312069	1 C -> T	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
A	1312081	1312081	1 G -> A	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
C	1312087	1312087	1 T -> C	SNP (transition)	87	98.9%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
A	1312095	1312095	1 G -> A	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	L -> F	MatC-N domain-containing protein CDS
A	1312289	1312289	1 T -> A	SNP (transversion)	120	99.2%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1312291	1312291	1 T -> C	SNP (transition)	119	99.2%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
AA	1312296	1312298	3 TTT -> AA	Deletion	113 -> 114	95.6% -> 96.5%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
TTT	1312313	1312315	3 AAG -> TTT	Substitution	107 -> 108	99.1%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
GT	1312330	1312331	2 TC -> GT	Substitution	120 -> 121	99.2%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
AG	1312333	1312334	2 TA -> AG	Substitution	121 -> 123	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1312340	1312340	1 A -> C	SNP (transversion)	122	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1312342	1312342	1 T -> C	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1312352	1312352	1 T -> C	SNP (transition)	140	99.3%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
G	1312383	1312383	1 A -> G	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
G	1312394	1312394	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
T	1312407	1312407	1 C -> T	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1312413	1312413	1 G -> A	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
T	1312415	1312415	1 C -> T	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
	1312427	1312427	1 (T)6 -> (T)5	Deletion (tandem repeat)	74	98.6%	1,9E-231	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1312433	1312433	1 T -> C	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
AG	1312440	1312441	2 GT -> AG	Substitution	71	100.0%	2,5E-255	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1312448	1312448	1 G -> A	SNP (transition)	71	98.6%	7,1E-257	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
TGTG	1312456	1312459	4 GCAT -> TGTG	Substitution	66 -> 68	98.5%	6,6E-232	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
GC	1312461	1312460	0 +GC	Insertion	68	85.5%	1,7E-208	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
G	1312465	1312465	1 A -> G	SNP (transition)	74	97.3%	1,7E-255	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1312470	1312470	1 G -> A	SNP (transition)	64	100.0%	4E-230	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1312481	1312481	1 G -> A	SNP (transition)	60	98.3%	2,4E-210	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1312485	1312485	1 T -> C	SNP (transition)	60	96.7%	4,4E-211	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1312487	1312487	1 A -> C	SNP (transversion)	60	81.7%	1,7E-168	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1312489	1312489	1 G -> A	SNP (transition)	58	84.5%	4,2E-166	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1312505	1312505	1 T -> C	SNP (transition)	52	100.0%	6,3E-187	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1312507	1312507	1 A -> C	SNP (transversion)	50	98.0%	3,1E-174	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
	1312512	1312512	1 -T	Deletion	50	100.0%	1E-159	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
GG	1312516	1312517	2 TT -> GG	Substitution	48 -> 56	100.0%	2,5E-177	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
AT	1312519	1312520	2 TA -> AT	Substitution	56	100.0%	2,5E-201	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
TA	1312579	1312580	2 AC -> TA	Substitution	59 -> 62	100.0%	5E-218	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1312538	1312538	1 T -> C	SNP (transition)	65	96.9%	1,7E-229	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
ATG	1312540	1312542	3 TGT -> ATG	Substitution	66	95.5%	3,6E-228	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1312540	1312545	2 GG -> A	Deletion	66	95.5%	2,3E-190	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
	1312551	1312551	1 -C	Deletion	66	100.0%	6,3E-211	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1312558	1312558	1 G -> A	SNP (transition)	67	100.0%	1,3E-247	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
T	1312560	1312560	1 C -> T	SNP (transition)	68	100.0%	2,5E-251	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1312565	1312565	1 T -> A	SNP (transversion)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
G	1312568	1312568	1 T -> G	SNP (transversion)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
G	1312570	1312570	1 A -> G	SNP (transition)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
G	1312577	1312577	1 A -> G	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
T	1312580	1312580	1 A -> T	SNP (transversion)	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1312591	1312590	0 (A)3 -> (A)4	Insertion (tandem repeat)	81	86.4%	1,2E-238	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
GGG	1312610	1312612	3 TAA -> GGG	Substitution	84 -> 93	94.8% -> 98.9%	1,3E-296	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1312664	1312664	1 G -> A	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
A	1312674	1312674	1 G -> A	SNP (transition)	88	98.9%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	A -> V	accA CDS
C	1312676	1312676	1 A -> C	SNP (transversion)	87	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
T	1312685	1312685	1 C -> T	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
T	1313231	1313231	1 C -> T	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
G	1314216	1314216	1 A -> G	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		fabF CDS
A	1314306	1314306	1 G -> A	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		fabF CDS
C	1314653	1314653	1 T -> C	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	T -> A	fabF CDS
A	1316808	1316808	1 G -> A	SNP (transition)	111	99.1%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
G	1316877	1316877	1 A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
C	1316976	1316976	1 T -> C	SNP (transition)	77	97.4%	2,9E-266	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
A	1317402	1317402	1 G -> A	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	L -> F	gpmI CDS
A	1317449	1317449	1 G -> A	SNP (transition)	100	99.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	A -> V	gpmI CDS
A	1317469	1317469	1 G -> A	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317562	1317562	1 G -> A	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317946	1317946	1 G -> A	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317949	1317949	1 T -> C	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317958	1317958	1 A -> C	SNP (transversion)	109	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	D -> E	gpmI CDS
T	1317970	1317970	1 C -> T	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317973	1317973	1 A -> C	SNP (transversion)	115	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317976	1317976	1 T -> C	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317979	1317979	1 T -> A	SNP (transversion)	117	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	E -> D	gpmI CDS
G	1318006	1318006	1 A -> G	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1318015	1318015	1 G -> C	SNP (transversion)	102	99.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318018	1318018	1 A -> G	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318207	1318207	1 A -> G	SNP (transition)	137	99.3%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318468	1318468	1 A -> G	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
T	1319026	1319026	1 C -> T	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mraY CDS
C	1319170	1319170	1 T -> C	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		mraY CDS
T	1320129	1320129	1 C -> T	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		murD CDS
G	1320495	1320495	1 A -> G	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		murD CDS
C	1320908	1320907	0 (C)9 -> (C)10	Insertion (tandem repeat)	87	95.4%	5,6E-259	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1321003	1321002	0 (A)5 -> (A)6	Insertion (tandem repeat)	95	95.8%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1322705	1322705	1 A -> C	SNP (transversion)	272	82.4%	1,8E-27	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
	1326102	1326102	1 (A)3 -> (A)2	Deletion (tandem repeat)	257	97.7%	2,5E-17	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1326407	1326407	1 T -> C	SNP (transition)	286	99.3%	6,4E-81	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
G	1455441	1455441	1 A -> G	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
G	1455480	1455480	1 A -> G	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
G	1455569	1455569	1 A -> G	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
G	1455573	1455573	1 A -> G	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
T	1455720	1455720	1 C -> T	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	T -> I	MFS transporter CDS
A	1455914	1455914	1 G -> A	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	A -> T	MFS transporter CDS
T	1455919	1455919	1 A -> T	SNP (transversion)	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
C	1455925	1455925	1 A -> C	SNP (transversion)	103	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
C	1455931	1455931	1 T -> C	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
T	1455934	1455934	1 A -> T	SNP (transversion)	105	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
T	1455937	1455937	1 C -> T	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
	1455940	1455948	9 -TTGTATACT	Deletion	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	ACIL -> A	MFS transporter CDS
	1456055	1456055	1 (T)7 -> (T)6	Deletion (tandem repeat)	107	98.1%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
C	1457019	1457018	0 +C	Insertion	110	89.1%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1457198	1457197	0 (C)4 -> (C)5	Insertion (tandem repeat)	106	90.6%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1457765	1457765	1 A -> G	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	1457335	1457335	1 C -> A	SNP (transversion)	113	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	P -> H	hypothetical protein CDS
A	1457484	1457484	1 G -> A	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	A -> T	hypothetical protein CDS
C	1457688	1457688	1 T -> C	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	V -> A	cdtC CDS
C	1458468	1458468	1 T -> C	SNP (transition)	110	99.1%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss	I -> V	Zinc transporter ZupT CDS
T	1458529	1458529	1 C -> T	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Zinc transporter ZupT CDS
G	1458763	1458761	1 A -> G	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Zinc transporter ZupT CDS
T	1458820	1458820	1 G -> T	SNP (transversion)	95	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		Zinc transporter ZupT CDS
C	36624	36624	1 T -> C	SNP (transition)	242	100.0%	0	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
	36651	36651	1 (A)3 -> (A)2	Deletion (tandem repeat)	219	91.3%	8,5E-154	Variants: BfR-CA-11057-TF156B7-1_R	Concatemer BfR-CA-11057 - UniAss		
A	36654	36654	1 T -> A	SNP (transversion)	207	96.6%	0	Variants: BfR-CA-11057-TF156B7-2_R	Concatemer BfR-CA-11057 - UniAss		
AA	36660	36659	0 +AA	Insertion	203	87.2%	7,6E-285	Variants: BfR-CA-11057-TF156B7-2_R	Concatemer BfR-CA-11057 - UniAss		

9 Appendix

C	36669	36669	1 T -> C	SNP (transition)	204	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
G	38113	38113	1 A -> G	SNP (transition)	64	100.0%	6,3E-19	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	60299	60299	1 C -> T	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		Flagellar hook-length control protein CDS
T	60314	60314	1 C -> T	SNP (transition)	88	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		Flagellar hook-length control protein CDS
G	60855	60855	1 A -> G	SNP (transition)	85	97.6%	5,7E-295	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	I -> V	Flagellar hook-length control protein CDS
GCACGAGATAAACGCATTAACTCAAGAAAAGATA	61341	61340	0 +GCACGAGATAAAGCA	Insertion	66 -> 77	97.0% -> 100.0%	2,5E-237	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	-> ARDKALTQIH	Flagellar hook-length control protein CDS
	61435	61512	78 -AAAATATAAAAGATTTA	Deletion	95	100.0%	3,2E-294	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	KNIKDLINQALDK	Flagellar hook-length control protein CDS
T	69981	69981	1 C -> T	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	70027	70027	1 C -> T	SNP (transition)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> N	hypothetical protein CDS
AA	70079	70080	2 GT -> AA	Substitution	70	100.0%	1E-251	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> I	hypothetical protein CDS
A	70392	70392	1 G -> A	SNP (transition)	70	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	70058	70058	1 C -> T	SNP (transition)	70	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	V -> I	hypothetical protein CDS
T	70621	70621	1 C -> T	SNP (transition)	83	94.0%	2,9E-265	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		Iron-binding protein CDS
T	70875	70875	1 C -> T	SNP (transition)	79	100.0%	4E-284	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	G -> R	Iron-binding protein CDS
C	71259	71259	1 T -> C	SNP (transition)	81	100.0%	2E-299	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	T -> A	Iron-binding protein CDS
G	71595	71595	1 T -> G	SNP (transversion)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	72007	72007	1 T -> C	SNP (transition)	92	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	I -> T	2-oxoglutarate translocator CDS
G	72074	72074	1 A -> G	SNP (transition)	77	100.0%	1,3E-284	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		2-oxoglutarate translocator CDS
G	72143	72143	1 A -> G	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		2-oxoglutarate translocator CDS
C	72536	72536	1 T -> C	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		2-oxoglutarate translocator CDS
T	72968	72968	1 C -> T	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		2-oxoglutarate translocator CDS
GC	132831	132832	2 CT -> GC	Substitution	67 -> 72	100.0%	6,8E-241	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	LE -> LQ	dnaG CDS
TT	132837	132838	2 GG -> TT	Substitution	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	AL -> AI	dnaG CDS
C	132841	132841	1 T -> C	SNP (transition)	76	100.0%	2,5E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
G	132850	132850	1 A -> G	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
GTTT	132859	132862	3 ATGA -> GTTT	Substitution	79 -> 82	100.0%	4E-284	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	TH -> TN	dnaG CDS
G	132865	132865	1 A -> G	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
TAA	132868	132870	2 AAG -> TAA	Substitution	87	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
T	132877	132877	1 G -> T	SNP (transversion)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
A	132880	132880	1 T -> A	SNP (transversion)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
T	132883	132883	1 A -> T	SNP (transversion)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
T	132886	132886	1 A -> T	SNP (transversion)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
C	132889	132889	1 G -> C	SNP (transversion)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
A	132892	132892	1 C -> A	SNP (transversion)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
T	132895	132895	1 A -> T	SNP (transversion)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> K	dnaG CDS
T	132904	132904	1 C -> T	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
G	132916	132916	1 A -> G	SNP (transition)	84	98.8%	1,3E-296	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
T	132937	132937	1 A -> T	SNP (transversion)	79	98.7%	7,9E-271	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
A	132940	132940	1 T -> A	SNP (transversion)	76	100.0%	2,5E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	E -> D	dnaG CDS
G	132958	132958	1 A -> G	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
TAA	132961	132961	2 CAG -> TAA	Substitution	76 -> 77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
G	132969	132969	1 T -> G	SNP (transversion)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> H	dnaG CDS
G	132973	132973	1 A -> G	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
A	132991	132991	1 C -> A	SNP (transversion)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
C	133012	133012	1 A -> C	SNP (transversion)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
C	133272	133272	1 T -> C	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	K -> E	dnaG CDS
A	133403	133403	1 G -> A	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	T -> M	dnaG CDS
G	133462	133462	1 A -> G	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
A	133618	133618	1 G -> A	SNP (transition)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
A	133621	133621	1 T -> A	SNP (transversion)	64	98.4%	1E-224	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
G	133627	133627	1 A -> G	SNP (transition)	64	100.0%	4E-230	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
A	133630	133630	1 C -> A	SNP (transversion)	60	100.0%	1E-215	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
A	133648	133648	1 T -> A	SNP (transversion)	61	100.0%	3,2E-213	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
G	133654	133654	1 T -> G	SNP (transversion)	60	100.0%	1E-209	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
A	133657	133657	1 G -> A	SNP (transition)	60	98.3%	2,4E-210	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
G	133663	133663	1 T -> G	SNP (transversion)	64	100.0%	4E-230	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
C	133675	133675	1 A -> C	SNP (transversion)	56	100.0%	2,5E-201	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
G	133678	133678	1 A -> G	SNP (transition)	61	100.0%	2,5E-219	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
T	133687	133687	1 C -> T	SNP (transition)	63	100.0%	1,8E-226	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
A	133690	133690	1 G -> A	SNP (transition)	63	100.0%	1,8E-226	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
G	133693	133693	1 A -> G	SNP (transition)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
GATA	133702	133705	3 CACG -> GATA	Substitution	78	100.0%	1E-272	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	CV -> CI	dnaG CDS
C	133708	133708	1 A -> C	SNP (transversion)	75	100.0%	6,8E-281	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
A	133714	133714	1 G -> A	SNP (transition)	76	100.0%	2,5E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
A	133717	133717	1 T -> A	SNP (transversion)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
G	133720	133720	1 A -> G	SNP (transition)	70	100.0%	1E-251	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaG CDS
ATT	134278	134280	2 CTG -> ATT	Substitution	60	98.3%	2,4E-210	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	L -> I	hypothetical protein CDS
A	134283	134283	1 T -> A	SNP (transversion)	60	100.0%	1E-215	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	134286	134286	1 A -> C	SNP (transversion)	60	100.0%	1E-209	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	134299	134299	1 G -> A	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	A -> T	hypothetical protein CDS
C	134302	134302	1 T -> C	SNP (transition)	77	98.7%	7,7E-264	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	134307	134307	1 A -> G	SNP (transition)	78	98.7%	4,9E-275	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	134367	134367	1 T -> C	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GC	134394	134395	2 AA -> GC	Substitution	84	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	VK -> VQ	hypothetical protein CDS
G	134400	134400	1 A -> G	SNP (transition)	84	98.8%	1,3E-296	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	134486	134486	1 C -> T	SNP (transition)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	T -> I	hypothetical protein CDS
G	134514	134514	1 T -> G	SNP (transversion)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	F -> L	hypothetical protein CDS
G	134709	134709	1 A -> G	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	134956	134956	1 A -> G	SNP (transition)	77	100.0%	3,2E-269	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		mhA CDS
GC	134959	134960	2 AG -> GC	Substitution	76	98.7%	7,6E-268	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	AE -> AQ	mhA CDS
T	135115	135115	1 C -> T	SNP (transition)	69	100.0%	3,2E-241	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		mhA CDS
A	135118	135118	1 G -> A	SNP (transition)	68	100.0%	1E-237	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		mhA CDS
C	135425	135425	1 T -> C	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
C	135431	135431	1 T -> C	SNP (transition)	67	100.0%	6,3E-241	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
G	135623	135623	1 A -> G	SNP (transition)	55	100.0%	3,2E-192	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
T	135785	135785	1 C -> T	SNP (transition)	53	100.0%	3,2E-185	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
G	135788	135788	1 A -> G	SNP (transition)	52	100.0%	4E-192	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
G	135791	135791	1 A -> G	SNP (transition)	66	100.0%	7,5E-232	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
T	135794	135794	1 C -> T	SNP (transition)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
A	135800	135800	1 C -> A	SNP (transversion)	56	100.0%	6,3E-207	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
C	135815	135815	1 A -> C	SNP (transversion)	61	100.0%	3,2E-213	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
G	135830	135830	1 A -> G	SNP (transition)	58	100.0%	2,5E-214	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
T	135842	135842	1 C -> T	SNP (transition)	63	100.0%	7,9E-233	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
ATG	135849	135851	2 TTC -> ATG	Substitution	66 -> 67	98.5%	3,2E-240	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	F -> M	rnc CDS
G	135855	135855	1 A -> G	SNP (transition)	72	98.6%	1,4E-260	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> D	rnc CDS
TA	135860	135861	2 AC -> TA	Substitution	88	97.7%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	QQ -> GK	rnc CDS
A	135866	135866	1 G -> A	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
T	135878	135878	1 C -> T	SNP (transition)	98	99.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
A	135884	135884	1 G -> A	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		rnc CDS
GC	135889	135890	2 AT -> GC	Substitution	99 -> 100	99.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> S	rnc CDS
G	136066	136066	1 A -> G	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		aroC CDS
AA	136131	136132	2 GG -> AA	Substitution	91	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	R -> K	aroC CDS
T	136135	136135	1 G -> T	SNP (transversion)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		aroC CDS
T	136153	136153	1 A -> T	SNP (transversion)	89	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		aroC CDS
A	136162	136162	1 T -> A	SNP (transversion)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		aroC CDS
A	136168	136168	1 C -> A	SNP (transversion)	99	99.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		aroC CDS
C	136180	136180	1 T -> C	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		aroC CDS
A	136183	136183	1 T -> A	SNP (transversion)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		aroC CDS
A	136189	136189	1 G -> A	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	M -> I	aroC CDS
G	136192	136192	1 T -> G	SNP (transversion)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		aroC CDS
T	136195	136195	1 G -> T	SNP (transversion)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		aroC CDS
T	136201	136201	1 C -> T	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		aroC CDS
TGCC	136207	136210	3 CACA -> TGCC	Substitution	94 -> 95	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	NT -> NA	aroC CDS
C	136241	136241	1 T -> C	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		aroC CDS
T	136255	136255	1 C -> T	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		aroC CDS
T	413011	413011	1 C -> T	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		Vacuolating cytotoxin autotransporter CDS
A	413164	413164	1 G -> A	SNP (transition)	55	98.2%	8,7E-198	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	A -> T	Vacuolating cytotoxin autotransporter CDS
A	413181	413181	1 G -> A	SNP (transition)	57	100.0%	6,3E-205	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> N	Vacuolating cytotoxin autotransporter CDS
C	413317	413317	1 T -> C	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		Vacuolating cytotoxin autotransporter CDS
T	413319	413319	1 C -> T	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> L	Vacuolating cytotoxin autotransporter CDS
G	418431	418431	1 A -> G	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		ertA CDS
T	419001	419001	1 C -> T	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		ertA CDS
	419486	419487	2 -GT	Deletion	66	100.0%	2,5E-204	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
	419718	419718	1 (T)8 -> (T)7	Deletion (tandem repeat)	89	93.3%	1,5E-256	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	420119	420119	1 T -> C	SNP (transition)	87	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	I -> V	OrfA protein CDS
A	420216	420216	1 G -> A	SNP (transition)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		OrfA protein CDS
T	420249	420249	1 C -> T	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	M -> I	OrfA protein CDS
G	420462	420462	1 T -> G	SNP (transversion)	75	98.7%	1,2E-271	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	L -> F	OrfA protein CDS
T	421174	421174	1 C -> T	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		Enterochelin ABC transporter CeuBCDE, periplasmic substra
C	421887	421887	1 T -> C	SNP (transition)	56	100.0%	6,3E-207	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> S	ABC transporter ATP-binding protein CDS
C	422248	422248	1 T -> C	SNP (transition)	73	100.0%	1,8E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	T -> A	ABC transporter ATP-binding protein CDS
A	422285	422285	1 G -> A	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter ATP-binding protein CDS
T	423129	423129	1 C -> T	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	V -> I	Enterochelin ABC transporter CeuBCDE, permease protein C
C	423977	423977	1 T -> C	SNP (transition)	68	98.5%	1,1E-225	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter permease CDS
T	423983	423983	1 A -> T	SNP (transversion)	69	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter permease CDS
TAC	423989	423991	2 AAT -> TAC	Substitution	69 -> 73	98.6%	1,1E-242	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	I -> V	ABC transporter permease CDS
A	423995	423995	1 T -> A	SNP (transversion)	74	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter permease CDS
A	423998	423998	1 G -> A	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		ABC transporter permease CDS
T	424003	424003	1 G -> T	SNP (transversion)	79	100.0%	4E-284	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	L -> I	ABC transporter permease CDS
T	424006	424006	1 C -> T	SNP (transition)	76	100.0%	1E-265	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	A -> T	ABC transporter permease CDS
G	424541	424541	1 A -> G	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		Phospholipase A1 CDS
A	424553	424553	1 G -> A	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		Phospholipase A1 CDS
A	424580	424580	1 G -> A	SNP (transition)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		Phospholipase A1 CDS
G	424683	424683	1 T -> G	SNP (transversion)	75	98.7%	1,2E-271	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	Y -> S	Phospholipase A1 CDS
T	424688	424688	1 C -> T	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	M -> I	Phospholipase A1 CDS
C	424744	424744	1 T -> C	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	K -> E	Phospholipase A1 CDS
C	424780	424780	1 T -> C	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	I -> V	Phospholipase A1 CDS
T	424925	424925	1 C -> T	SNP (transition)	93	98.6%	1,7E-245	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		Phospholipase A1 CDS
C	461537	461537	1 T -> C	SNP (transition)	64	100.0%	2,5E-153	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> D	DUF115 domain-containing protein CDS
	566899	566899	1 (G)10 -> (G)9	Deletion (tandem repeat)	75	92.0%	2E-198	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	1009581	1009581	1 G -> A	SNP (transition)	57	98.2%	1,4E-199	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		LysE family translocator CDS
A	1009681	1009681	1 G -> A	SNP (transition)	56	100.0%	6,3E-207	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> F	LysE family translocator CDS

G	1010159	1010159	1	T -> G	SNP (transversion)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		Branched-chain amino acid ABC transporter CDS
C	1013811	1013811	1	T -> C	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hybA CDS
T	1013955	1013955	1	C -> T	SNP (transition)	82	100.0%	6,3E-295	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hybA CDS
A	1014180	1014180	1	G -> A	SNP (transition)	76	98.7%	2,4E-260	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hybA CDS
A	1014632	1014632	1	T -> A	SNP (transversion)	77	100.0%	1,3E-284	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		napA CDS
C	1014992	1014992	1	T -> C	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		napA CDS
C	1015338	1015338	1	T -> C	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> S	napA CDS
G	1017555	1017555	1	A -> G	SNP (transition)	67	100.0%	6,3E-241	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1019962	1019962	1	T -> C	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
C	1020030	1020030	1	T -> C	SNP (transition)	76	100.0%	2,5E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	K -> E	DNA helicase CDS
G	1020034	1020034	1	A -> G	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
G	1020043	1020043	1	A -> G	SNP (transition)	91	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
G	1020340	1020340	1	A -> G	SNP (transition)	78	98.7%	4,9E-275	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
T	1020478	1020478	1	C -> T	SNP (transition)	57	100.0%	1,3E-210	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
T	1020753	1020753	1	C -> T	SNP (transition)	69	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	G -> S	DNA helicase CDS
AA	1020795	1020796	2	GG -> AA	Substitution	61	100.0%	2,5E-219	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
A	1020811	1020811	1	G -> A	SNP (transition)	57	100.0%	1,3E-210	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
G	1020817	1020817	1	A -> G	SNP (transition)	58	100.0%	1,6E-208	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
C	1020952	1020952	1	T -> C	SNP (transition)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
A	1021000	1021000	1	G -> A	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
TAA	1021003	1021005	2	AAG -> TAA	Substitution	87	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
C	1021009	1021009	1	T -> C	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
C	1021012	1021012	1	T -> C	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
TTC	1021015	1021017	2	ATT -> TTC	Substitution	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> E	DNA helicase CDS
C	1021025	1021025	1	T -> C	SNP (transition)	71	100.0%	2,5E-255	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	K -> R	DNA helicase CDS
A	1021027	1021027	1	T -> A	SNP (transversion)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DNA helicase CDS
T	1021040	1021040	1	A -> T	SNP (transversion)	65	96.9%	3,3E-223	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
	1021050	1021050	1	-T	Deletion	64	98.4%	3,2E-193	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
CACG	1021056	1021059	4	TTAA -> CACG	Substitution	67 -> 68	100.0%	3,2E-234	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
G	1021067	1021067	1	A -> G	SNP (transition)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1021075	1021075	1	T -> A	SNP (transversion)	65	98.5%	2,6E-228	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
G	1021077	1021077	1	A -> G	SNP (transition)	64	98.4%	1E-224	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1021099	1021099	1	A -> C	SNP (transversion)	68	100.0%	2,5E-251	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
TA	1021103	1021104	2	AC -> TA	Substitution	69 -> 70	98.6%	1,1E-242	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
ATA	1021114	1021116	3	GAT -> ATA	Substitution	80 -> 85	100.0%	1E-295	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
	1021143	1021143	1	-C	Deletion	72	97.2%	2,6E-213	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1021159	1021159	1	G -> A	SNP (transition)	59	100.0%	4E-212	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
TAA	1021162	1021164	3	AGC -> TAA	Substitution	55 -> 57	82.5% -> 85.5%	2,2E-163	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
G	1021166	1021166	1	A -> G	SNP (transition)	55	89.1%	1,2E-168	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1021175	1021175	1	G -> T	SNP (transversion)	56	100.0%	6,3E-207	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	L -> F	hypothetical protein CDS
T	1021179	1021179	1	A -> T	SNP (transversion)	56	100.0%	6,3E-207	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	I -> F	hypothetical protein CDS
A	1021196	1021196	1	T -> A	SNP (transversion)	57	100.0%	6,3E-205	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1021199	1021199	1	C -> G	SNP (transversion)	57	100.0%	6,3E-205	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021202	1021202	1	A -> T	SNP (transversion)	54	100.0%	4E-194	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GTC	1021206	1021208	2	ATT -> GTC	Substitution	49 -> 54	100.0%	5E-181	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	I -> V	hypothetical protein CDS
T	1021210	1021210	1	C -> T	SNP (transition)	47	100.0%	1,3E-173	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	A -> V	hypothetical protein CDS
G	1021214	1021214	1	T -> G	SNP (transversion)	47	100.0%	1,3E-173	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021218	1021218	1	G -> T	SNP (transversion)	47	100.0%	1,3E-173	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	V -> L	hypothetical protein CDS
CTTAGC	1021224	1021229	4	TTAGGT -> CTTAGC	Substitution	46 -> 47	100.0%	2,5E-165	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	LG -> LS	hypothetical protein CDS
T	1021235	1021235	1	C -> T	SNP (transition)	44	100.0%	1,6E-162	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1021241	1021241	1	T -> C	SNP (transition)	44	100.0%	1,6E-162	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1021253	1021253	1	A -> G	SNP (transition)	42	100.0%	4E-155	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021259	1021259	1	A -> T	SNP (transversion)	40	100.0%	1E-147	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GTGCTT	1021782	1021787	4	ATTTTA -> GTGCTT	Substitution	42 -> 45	100.0%	6,3E-151	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	IL -> VL	hypothetical protein CDS
T	1021793	1021793	1	A -> T	SNP (transversion)	49	100.0%	5E-181	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1021799	1021799	1	T -> C	SNP (transition)	49	100.0%	5E-181	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GAT	1021806	1021808	2	CAA -> GAT	Substitution	49 -> 51	98.0%	2,5E-177	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	Q -> D	hypothetical protein CDS
T	1021811	1021811	1	C -> T	SNP (transition)	52	100.0%	6,3E-187	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	1021814	1021814	1	G -> A	SNP (transition)	51	100.0%	2,5E-183	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1021820	1021820	1	T -> G	SNP (transversion)	51	98.0%	5,1E-178	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> K	hypothetical protein CDS
T	1021823	1021823	1	G -> T	SNP (transversion)	51	100.0%	2,5E-183	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021836	1021836	1	C -> T	SNP (transition)	57	100.0%	6,3E-205	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GCGA	1021839	1021842	4	AGCG -> GCGA	Substitution	58 -> 59	93.1% -> 93.2%	1,7E-188	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	SV -> AI	hypothetical protein CDS
G	1021848	1021848	1	C -> G	SNP (transversion)	58	100.0%	2,5E-214	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	Q -> E	hypothetical protein CDS
TCT	1021857	1021859	2	GCA -> TCT	Substitution	60 -> 64	100.0%	1E-221	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	A -> S	hypothetical protein CDS
C	1021865	1021865	1	T -> C	SNP (transition)	67	100.0%	6,3E-241	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021868	1021868	1	C -> T	SNP (transition)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021870	1021870	1	A -> T	SNP (transversion)	69	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	Y -> F	hypothetical protein CDS
T	1021874	1021874	1	A -> T	SNP (transversion)	69	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1021895	1021895	1	A -> G	SNP (transition)	63	100.0%	1,6E-226	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021898	1021898	1	A -> T	SNP (transversion)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1021901	1021901	1	A -> G	SNP (transition)	62	98.4%	2E-211	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GT	1021912	1021913	2	AA -> GT	Substitution	59	100.0%	3,2E-206	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	K -> S	hypothetical protein CDS
T	1021922	1021922	1	C -> T	SNP (transition)	56	98.2%	1,8E-201	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1021925	1021925	1	T -> C	SNP (transition)	56	100.0%	2,5E-201	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021928	1021928	1	C -> T	SNP (transition)	57	100.0%	1,3E-210	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021934	1021934	1	A -> T	SNP (transversion)	51	100.0%	2E-188	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	E -> D	hypothetical protein CDS
T	1021940	1021940	1	C -> T	SNP (transition)	48	97.9%	3E-167	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1021943	1021943	1	T -> C	SNP (transition)	46	97.8%	1,5E-164	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021946	1021946	1	A -> T	SNP (transversion)	45	100.0%	1E-161	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1021959	1021959	1	G -> T	SNP (transversion)	41	100.0%	2,5E-147	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	A -> S	hypothetical protein CDS
A	1021998	1021998	1	T -> A	SNP (transversion)	40	82.5%	1,5E-114	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	L -> I	hypothetical protein CDS
G	1022060	1022060	1	A -> G	SNP (transition)	41	100.0%	2,5E-147	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1022068	1022068	1	T -> C	SNP (transition)	42	97.6%	8,4E-150	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	I -> T	hypothetical protein CDS
A	1022078	1022078	1	T -> A	SNP (transversion)	43	100.0%	1,6E-154	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	D -> E	hypothetical protein CDS
A	1022081	1022081	1	C -> A	SNP (transversion)	44	100.0%	4E-158	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	1022093	1022093	1	T -> A	SNP (transversion)	48	100.0%	1,6E-172	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	D -> E	hypothetical protein CDS
G	1022102	1022102	1	A -> G	SNP (transition)	49	98.0%	1,2E-175	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	1022108	1022108	1	C -> A	SNP (transversion)	58	100.0%	1,6E-208	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1022111	1022111	1	A -> T	SNP (transversion)	60	100.0%	1E-215	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	K -> N	hypothetical protein CDS
C	1022114	1022114	1	T -> C	SNP (transition)	62	100.0%	4E-229	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	1022117	1022117	1	G -> A	SNP (transition)	63	100.0%	7,9E-233	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1022132	1022132	1	T -> C	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
AG	1022134	1022135	2	CA -> AG	Substitution	69	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	T -> K	hypothetical protein CDS
T	1022138	1022138	1	A -> T	SNP (transversion)	67	100.0%	6,3E-241	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1022144	1022144	1	T -> C	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1022147	1022147	1	C -> T	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1022150	1022150	1	C -> T	SNP (transition)	70	100.0%	1E-251	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
A	1022153	1022153	1	G -> A	SNP (transition)	70	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1022165	1022165	1	T -> C	SNP (transition)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
CT	1022176	1022177	2	GC -> CT	Substitution	57	100.0%	3,2E-199	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> T	hypothetical protein CDS
CGTA	1022180	1022183	3	TATT -> CGTA	Substitution	54 -> 56	98.1% -> 98.2%	4,3E-194	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	SI -> SV	hypothetical protein CDS
CGCGTA	1022192	1022197	6	TAAAAC -> CGCGTA	Substitution	55 -> 62	88.7% -> 100.0%	4,9E-189	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
	1022200	1022200	1	-T	Deletion	63	85.7%	9,4E-157	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1022206	1022206	1	C -> T	SNP (transition)	60	98.3%	3E-216	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
AAA	1022210	1022209	0	+AAA	Insertion	61	88.5%	6,9E-191	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
GCA	1022225	1022227	3	ATT -> GCA	Substitution	63 -> 65	100.0%	1,6E-226	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	NL -> SI	valS CDS
ACA	1022236	1022238	3	GAG -> ACA	Substitution	67	95.5%	7,6E-232	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	E -> T	valS CDS
G	1022259	1022259	1	A -> G	SNP (transition)	61	100.0%	2E-225	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
T	1022262	1022262	1	C -> T	SNP (transition)	70	100.0%	1E-251	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
G	1022265	1022265	1	A -> G	SNP (transition)	70	100.0%	1E-244	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
A	1022283	1022283	1	C -> A	SNP (transversion)	65	100.0%	3,2E-240	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
G	1022290	1022290	1	A -> G	SNP (transition)	67	98.5%	1,7E-235	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	T -> A	valS CDS
C	1022451	1022451	1	T -> C	SNP (transition)	76	100.0%	2,5E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
T	1022454	1022454	1	C -> T	SNP (transition)	70	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
A	1022460	1022460	1	T -> A	SNP (transversion)	76	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
T	1022529	1022529	1	C -> T	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		valS CDS
A	1028995	1028995	1	G -> A	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> N	DL-methionine ABC transporter MetINQ, substrate-binding
G	1029015	1029015	1	A -> G	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> D	DL-methionine ABC transporter MetINQ, substrate-binding
T	1029122	1029122	1	C -> T	SNP (transition)	85	98.8%	3,4E-300	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		DL-methionine ABC transporter MetINQ, substrate-binding
A	1029394	1029394	1	G -> A	SNP (transition)	60	100.0%	1E-215	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1029442	1029442	1	C -> T	SNP (transition)	69	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1029517	1029517	1	T -> C	SNP (transition)	67	100.0%	3,2E-234	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
CC	1029544	1029545	2	TT -> CC	Substitution	60 -> 62	100.0%	1E-215	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1029550	1029550	1	T -> C	SNP (transition)	57	100.0%	3,2E-199	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1029556	1029556	1	T -> C	SNP (transition)	60	100.0%	1E-215	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029559	1029559	1	C -> T	SNP (transition)	56	100.0%	2,5E-201	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
A	1029622	1029622	1	G -> A	SNP (transition)	65	100.0%	3,2E-240	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029748	1029748	1	C -> T	SNP (transition)	70	100.0%	1E-244	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029757	1029757	1	C -> T	SNP (transition)	65	98.5%	2,6E-228	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
G	1029760	1029760	1	A -> G	SNP (transition)	69	98.6%	1,7E-249	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029769	1029769	1	C -> T	SNP (transition)	69	98.6%	1,1E-242	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
GG	1029777	1029778	2	AA -> GG	Substitution	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	K -> R	flgA CDS
T	1029790	1029790	1	C -> T	SNP (transition)	70	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029901	1029901	1	C -> T	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
ATC	1029914	1029916	2	GTT -> ATC	Substitution	86	97.7%	5,8E-307	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	V -> I	flgA CDS
C	1029922	1029922	1	T -> C	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
G	1029943	1029943	1	A -> G	SNP (transition)	81	100.0%	2E-299	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1030030	1030030	1	T -> C	SNP (transition)	79	100.0%	4E-284	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1030264	1030264	1	G -> T	SNP (transversion)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	A -> S	3-octaprenyl-4-hydroxybenzoate carboxy-lyase CDS
A	1030581	1030581	1	G -> A	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		3-octaprenyl-4-hydroxybenzoate carboxy-lyase CDS
G	1030821	1030821	1	A -> G	SNP (transition)	79	98.7%	2E-286	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		coaD CDS
G	1032161	1032161	1	A -> G	SNP (transition)	66	100.0%	1E-230	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> G	hisS CDS
T	1032172	1032172	1	C -> T	SNP (transition)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
AG	1032227	1032228	2	GA -> AG	Substitution	66	100.0%	1E-230	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	E -> R	hisS CDS
G	1032244	1032244	1	A -> G	SNP (transition)	56	98.2%	1,8E-190	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032250	1032250	1	T -> C	SNP (transition)	51	100.0%	3,2E-178	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032265	1032265	1	C -> T	SNP (transition)	59	100.0%	5E-218	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032304	1032304	1	C -> T	SNP (transition)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032307	1032307	1	T -> C	SNP (transition)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
A	1032310	1032310	1	G -> A	SNP (transition)	64	100.0%	1,6E-236	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
GC	1032325	1032326	2	AT -> GC	Substitution	68 -> 69	100.0%	2,5E-251	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	EY -> EH	hisS CDS

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G	1032355	1032355	1 A -> G	SNP (transition)	59	100.0%	4E-212	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1032361	1032361	1 A -> G	SNP (transition)	61	100.0%	2,5E-219	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032376	1032376	1 T -> C	SNP (transition)	59	100.0%	4E-212	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1032406	1032406	1 A -> G	SNP (transition)	52	98.1%	1E-186	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032466	1032466	1 C -> T	SNP (transition)	74	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1032523	1032523	1 A -> G	SNP (transition)	60	98.3%	1,9E-204	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032526	1032526	1 C -> T	SNP (transition)	62	100.0%	6,8E-223	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032529	1032529	1 C -> T	SNP (transition)	61	100.0%	2,5E-219	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032532	1032532	1 T -> C	SNP (transition)	61	98.4%	6,1E-208	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1038237	1038237	1 A -> G	SNP (transition)	71	98.6%	7,1E-243	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	I -> T	MBL fold metallo-hydrolase CDS
G	1038273	1038273	1 A -> G	SNP (transition)	59	100.0%	5E-218	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1040325	1040325	1 G -> A	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		dnaK CDS
T	1042179	1042179	1 C -> T	SNP (transition)	50	100.0%	1E-184	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042182	1042182	1 G -> A	SNP (transition)	56	100.0%	2,5E-201	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
AC	1042187	1042188	2 GT -> AC	Substitution	57 -> 58	98.2% -> 98.3%	1,4E-199	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
T	1042191	1042191	1 C -> T	SNP (transition)	57	100.0%	6,8E-205	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
C	1042194	1042194	1 T -> C	SNP (transition)	58	100.0%	1,6E-208	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042208	1042208	1 A -> G	SNP (transition)	57	100.0%	1,3E-210	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042218	1042218	1 A -> G	SNP (transition)	59	100.0%	5E-218	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042221	1042221	1 G -> A	SNP (transition)	59	100.0%	5E-218	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
T	1042233	1042233	1 C -> T	SNP (transition)	67	98.5%	1,7E-235	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
C	1042249	1042249	1 T -> C	SNP (transition)	60	100.0%	1E-221	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> S	hrcA CDS
A	1042293	1042293	1 G -> A	SNP (transition)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042371	1042371	1 G -> A	SNP (transition)	70	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042431	1042431	1 A -> G	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042479	1042479	1 A -> G	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1042488	1042488	1 C -> T	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1042490	1042490	1 T -> A	SNP (transversion)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
G	1042492	1042492	1 T -> G	SNP (transversion)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
AG	1042520	1042521	2 TA -> AG	Substitution	79 -> 89	100.0%	4E-284	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1042591	1042591	1 A -> T	SNP (transversion)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1042596	1042596	1 G -> A	SNP (transition)	81	100.0%	2E-299	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1042608	1042608	1 G -> A	SNP (transition)	81	98.8%	8,1E-294	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
G	1042632	1042632	1 A -> G	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1042634	1042634	1 C -> A	SNP (transversion)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1042638	1042638	1 C -> A	SNP (transversion)	60	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1042642	1042642	1 T -> C	SNP (transition)	58	100.0%	2,5E-214	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
GT	1042650	1042651	2 AA -> GT	Substitution	55	100.0%	3,2E-203	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
ACAG	1042654	1042657	4 TGCA -> ACAG	Substitution	53 -> 55	100.0%	7,9E-196	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
G	1042659	1042658	0 +G	Insertion	51	98.0%	5,1E-183	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1042687	1042687	1 T -> A	SNP (transversion)	52	96.2%	1,9E-181	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1042690	1042690	1 A -> T	SNP (transversion)	49	91.8%	2,1E-158	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1042692	1042692	1 T -> C	SNP (transition)	49	91.8%	6,7E-161	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
AA	1042696	1042697	2 TG -> AA	Substitution	53	84.9%	2,8E-157	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1042699	1042699	1 C -> T	SNP (transition)	54	83.3%	1,7E-156	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1042729	1042729	1 T -> C	SNP (transition)	58	98.3%	7,3E-209	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
AC	1042750	1042751	2 GA -> AC	Substitution	55	100.0%	1E-197	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1042763	1042763	1 T -> C	SNP (transition)	56	100.0%	6,3E-207	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1042765	1042765	1 C -> T	SNP (transition)	56	100.0%	6,3E-207	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
AC	1042784	1042785	2 GT -> AC	Substitution	62	98.4%	6,3E-223	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> S	cfrA CDS
A	1042793	1042793	1 G -> A	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042796	1042796	1 A -> G	SNP (transition)	70	100.0%	1E-251	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1042805	1042805	1 C -> T	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	M -> I	cfrA CDS
A	1042829	1042829	1 G -> A	SNP (transition)	74	100.0%	1,8E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042832	1042832	1 A -> G	SNP (transition)	76	100.0%	2,5E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042835	1042835	1 G -> A	SNP (transition)	75	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042841	1042841	1 T -> G	SNP (transversion)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
AG	1042850	1042851	2 GC -> AG	Substitution	86	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> T	cfrA CDS
GT	1042854	1042855	2 CC -> GT	Substitution	83 -> 83	100.0%	2E-299	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	G -> T	cfrA CDS
CGCT	1042858	1042861	3 TCCC -> CGCT	Substitution	78 -> 79	98.7%	4E-284	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	GS -> SG	cfrA CDS
T	1042863	1042863	1 C -> T	SNP (transition)	76	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> N	cfrA CDS
TG	1042866	1042867	2 GC -> TG	Substitution	76	98.7%	2,4E-275	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	A -> Q	cfrA CDS
A	1042880	1042880	1 G -> A	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042885	1042885	1 T -> C	SNP (transition)	85	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> D	cfrA CDS
A	1042892	1042892	1 G -> A	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1042900	1042900	1 C -> T	SNP (transition)	78	100.0%	1,8E-280	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	D -> N	cfrA CDS
G	1042922	1042922	1 A -> G	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042937	1042937	1 T -> C	SNP (transition)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042940	1042940	1 G -> A	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042964	1042964	1 G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042985	1042985	1 G -> A	SNP (transition)	85	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042994	1042994	1 T -> C	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043000	1043000	1 G -> T	SNP (transversion)	71	97.2%	9,9E-245	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043087	1043087	1 T -> C	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043093	1043093	1 G -> A	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043099	1043099	1 G -> A	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043258	1043258	1 G -> A	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
TC	1043267	1043268	2 CT -> TC	Substitution	84	98.8%	6,7E-305	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	K -> R	cfrA CDS
G	1043271	1043271	1 A -> G	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	F -> S	cfrA CDS
C	1043584	1043584	1 G -> C	SNP (transversion)	74	98.6%	5,9E-268	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	L -> V	cfrA CDS
CAA	1043648	1043650	2 AAG -> CAA	Substitution	61	100.0%	3,2E-213	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GTT	1043657	1043659	2 ATC -> GTT	Substitution	64	100.0%	4E-230	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	D -> N	cfrA CDS
G	1043669	1043669	1 A -> G	SNP (transition)	69	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043672	1043672	1 A -> G	SNP (transition)	73	100.0%	1,8E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043690	1043690	1 A -> T	SNP (transversion)	64	100.0%	1,6E-230	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043717	1043717	1 A -> G	SNP (transition)	61	100.0%	2,5E-219	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043720	1043720	1 A -> C	SNP (transversion)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043724	1043724	1 C -> T	SNP (transition)	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> N	cfrA CDS
A	1043765	1043765	1 G -> A	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043769	1043769	1 A -> G	SNP (transition)	92	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	V -> A	cfrA CDS
C	1043774	1043774	1 T -> C	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
CAA	1043792	1043794	2 TAG -> CAA	Substitution	94	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043801	1043801	1 A -> G	SNP (transition)	96	97.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043917	1043917	1 A -> G	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GTC	1043922	1043924	3 CCA -> GTC	Substitution	60 -> 61	98.3% -> 98.4%	6,1E-220	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	SG -> ST	cfrA CDS
G	1043927	1043927	1 A -> G	SNP (transition)	57	98.2%	3,8E-209	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043930	1043930	1 G -> A	SNP (transition)	57	100.0%	1,3E-210	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043966	1043966	1 A -> G	SNP (transition)	56	100.0%	6,8E-207	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043999	1043999	1 T -> C	SNP (transition)	63	100.0%	1,6E-226	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044005	1044005	1 A -> G	SNP (transition)	62	100.0%	4E-229	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044024	1044024	1 G -> T	SNP (transversion)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	P -> Q	cfrA CDS
A	1044029	1044029	1 T -> A	SNP (transversion)	60	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	R -> S	cfrA CDS
G	1044044	1044044	1 A -> G	SNP (transition)	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044047	1044047	1 A -> G	SNP (transition)	64	100.0%	4E-230	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044074	1044074	1 G -> A	SNP (transition)	62	100.0%	6,8E-223	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044110	1044110	1 A -> G	SNP (transition)	66	100.0%	2,5E-237	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1044128	1044128	1 T -> C	SNP (transition)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044155	1044155	1 G -> A	SNP (transition)	67	100.0%	6,3E-241	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044191	1044191	1 C -> T	SNP (transition)	66	100.0%	2,5E-237	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044314	1044314	1 C -> T	SNP (transition)	64	100.0%	4E-230	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044662	1044662	1 A -> G	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044720	1044720	1 C -> G	SNP (transversion)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> T	cfrA CDS
G	1044722	1044722	1 A -> G	SNP (transition)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GGT	1044761	1044763	2 AGC -> GGT	Substitution	64 -> 66	100.0%	1,6E-238	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	A -> T	cfrA CDS
G	1044767	1044767	1 T -> G	SNP (transversion)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1044781	1044781	1 T -> C	SNP (transition)	65	96.9%	1,7E-229	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	I -> V	cfrA CDS
T	1044785	1044785	1 C -> T	SNP (transition)	65	98.5%	2,6E-229	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044788	1044788	1 A -> G	SNP (transition)	69	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044791	1044791	1 G -> A	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044797	1044797	1 C -> T	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044815	1044815	1 A -> G	SNP (transition)	74	98.6%	1,2E-260	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044821	1044821	1 A -> G	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GCTT	1044824	1044827	4 AGCC -> GCTT	Substitution	78 -> 79	93.6% -> 93.7%	1,7E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	LA -> LS	cfrA CDS
G	1044830	1044830	1 A -> G	SNP (transition)	77	94.8%	1,1E-263	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044833	1044833	1 G -> A	SNP (transition)	74	100.0%	1,8E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044842	1044842	1 A -> G	SNP (transition)	66	100.0%	2,5E-237	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044848	1044848	1 C -> T	SNP (transition)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044859	1044859	1 A -> T	SNP (transversion)	71	100.0%	2,5E-255	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	L -> I	cfrA CDS
T	1044863	1044863	1 C -> T	SNP (transition)	70	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1052849	1052849	1 T -> C	SNP (transition)	83	100.0%	1,3E-24	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1056828	1056828	1 T -> C	SNP (transition)	79	97.5%	9,7E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	E -> G	ccmA CDS
G	1308269	1308269	1 A -> G	SNP (transition)	82	100.0%	6,8E-299	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> P	CoA ester lyase CDS
T	1308298	1308298	1 C -> T	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> N	CoA ester lyase CDS
C	1308320	1308320	1 T -> C	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	I -> V	CoA ester lyase CDS
G	1308428	1308428	1 A -> G	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	S -> P	CoA ester lyase CDS
A	1308485	1308485	1 T -> A	SNP (transversion)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	I -> L	CoA ester lyase CDS
G	1308525	1308525	1 A -> G	SNP (transition)	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		CoA ester lyase CDS
A	1310083	1310083	1 G -> A	SNP (transition)	76	100.0%	1E-265	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	A -> V	hypothetical protein CDS
G	1311022	1311022	1 T -> G	SNP (transversion)	87	100.0%	3,2E-304	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
C	1311340	1311340	1 T -> C	SNP (transition)	82	100.0%	6,3E-295	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
T	1312069	1312069	1 C -> T	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
A	1312081	1312081	1 G -> A	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
C	1312087	1312087	1 T -> C	SNP (transition)	70	100.0%	1E-251	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
A	1312095	1312095	1 G -> A	SNP (transition)	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	L -> F	MatC-N domain-containing protein CDS
A	1312289	1312289	1 T -> A	SNP (transversion)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1312291	1312291	1 T -> C	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
AA	1312296	1312298	3 TTT -> AA	Deletion	67 -> 70	95.7% -> 100.0%	5,5E-196	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
TTT	1312313	1312315	3 AAG -> TTT	Substitution	71	98.6%	7,1E-250	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
GT	1312330	1312331	2 TC -> GT	Substitution	70 -> 71	95.7% -> 95.8%	6,1E-248	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
AG	1312333	1312334	2 TA -> AG	Substitution	71 -> 74	97.2% -> 97.3%	1,2E-251	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1312340	1312340	1 A -> C	SNP (transversion)	74	98.6%	1,2E-260	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1312342	1312342	1 T -> C	SNP (transition)	78	98.7%	4,8E-275	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		

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C	1312352	1312352	1 T -> C	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
G	1312383	1312383	1 A -> G	SNP (transition)	70	98.6%	2,8E-246	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
G	1312394	1312394	1 A -> G	SNP (transition)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1312407	1312407	1 C -> T	SNP (transition)	61	98.4%	6,3E-214	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1312413	1312413	1 G -> A	SNP (transition)	55	100.0%	1E-197	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1312415	1312415	1 C -> T	SNP (transition)	55	100.0%	1E-197	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
	1312427	1312427	1 (T)6 -> (T)5	Deletion (tandem repeat)	47	97.9%	1,9E-131	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1312433	1312433	1 T -> C	SNP (transition)	44	97.7%	1,4E-148	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
AG	1312440	1312441	2 GT -> AG	Substitution	44	100.0%	4E-158	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1312448	1312448	1 G -> A	SNP (transition)	43	100.0%	1,6E-154	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
TG	1312456	1312457	2 GC -> TG	Substitution	41	97.6%	4,1E-134	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
GC	1312461	1312460	0 +GC	Insertion	42	81.0%	4,7E-114	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
G	1312465	1312465	1 A -> G	SNP (transition)	46	100.0%	1E-160	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1312470	1312470	1 G -> A	SNP (transition)	43	100.0%	7,9E-159	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1312481	1312481	1 G -> A	SNP (transition)	51	100.0%	2,5E-183	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1312485	1312485	1 T -> C	SNP (transition)	51	96.1%	4E-168	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1312487	1312487	1 A -> C	SNP (transversion)	51	82.4%	1,9E-147	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1312489	1312489	1 G -> A	SNP (transition)	50	84.0%	5,4E-138	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1312505	1312505	1 T -> C	SNP (transition)	52	100.0%	6,3E-187	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1312507	1312507	1 A -> C	SNP (transversion)	52	98.1%	1E-189	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
	1312512	1312512	1 -T	Deletion	50	100.0%	1E-159	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
GG	1312516	1312517	2 TT -> GG	Substitution	50 -> 54	100.0%	1E-179	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
AT	1312519	1312520	2 TA -> AT	Substitution	54	100.0%	4E-194	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
TA	1312529	1312530	2 AC -> TA	Substitution	57 -> 58	100.0%	1,3E-210	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1312538	1312538	1 T -> C	SNP (transition)	62	95.2%	1,3E-213	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
ATG	1312540	1312542	3 TGT -> ATG	Substitution	65	90.8%	4,1E-210	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1312544	1312544	1 G -> A	SNP (transition)	66	100.0%	2,5E-237	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
	1312545	1312545	1 -G	Deletion	67	86.6%	4,2E-163	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
	1312551	1312551	1 -C	Deletion	67	100.0%	4E-214	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1312558	1312558	1 G -> A	SNP (transition)	68	100.0%	2,5E-251	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1312560	1312560	1 C -> T	SNP (transition)	68	100.0%	2,5E-251	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1312565	1312565	1 T -> A	SNP (transversion)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
G	1312568	1312568	1 T -> G	SNP (transversion)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
G	1312570	1312570	1 A -> G	SNP (transition)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
G	1312577	1312577	1 A -> G	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1312580	1312580	1 A -> T	SNP (transversion)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1312591	1312590	0 (A)3 -> (A)4	Insertion (tandem repeat)	75	98.7%	1,2E-271	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
GGG	1312610	1312612	3 TAA -> GGG	Substitution	78 -> 88	98.7% -> 98.9%	2,5E-288	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1312664	1312664	1 G -> A	SNP (transition)	67	100.0%	1,3E-247	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
A	1312674	1312674	1 G -> A	SNP (transition)	64	100.0%	1E-223	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	A -> V	accA CDS
C	1312676	1312676	1 A -> C	SNP (transversion)	65	100.0%	1E-231	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
T	1312685	1312685	1 C -> T	SNP (transition)	63	100.0%	1,6E-228	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
T	1313231	1313231	1 C -> T	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
G	1314216	1314216	1 A -> G	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		fabF CDS
A	1314306	1314306	1 G -> A	SNP (transition)	81	100.0%	2E-299	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		fabF CDS
C	1314653	1314653	1 T -> C	SNP (transition)	67	100.0%	1,3E-247	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	T -> A	fabF CDS
A	1316808	1316808	1 G -> A	SNP (transition)	75	98.7%	1,7E-271	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
G	1316877	1316877	1 A -> G	SNP (transition)	78	98.7%	4,9E-275	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
C	1316976	1316976	1 T -> C	SNP (transition)	74	98.6%	1,2E-260	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
A	1317402	1317402	1 G -> A	SNP (transition)	86	98.8%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	L -> F	gpmI CDS
A	1317449	1317449	1 G -> A	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	A -> V	gpmI CDS
A	1317469	1317469	1 G -> A	SNP (transition)	86	98.8%	8,6E-304	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317562	1317562	1 G -> A	SNP (transition)	78	98.7%	2,5E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317946	1317946	1 G -> A	SNP (transition)	85	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317949	1317949	1 T -> C	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317958	1317958	1 A -> C	SNP (transversion)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	Q -> E	gpmI CDS
T	1317970	1317970	1 C -> T	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317973	1317973	1 A -> C	SNP (transversion)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
T	1317976	1317976	1 T -> C	SNP (transition)	90	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317979	1317979	1 T -> A	SNP (transversion)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	E -> D	gpmI CDS
G	1318006	1318006	1 A -> G	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1318015	1318015	1 G -> C	SNP (transversion)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318018	1318018	1 A -> G	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318207	1318207	1 A -> G	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318468	1318468	1 A -> G	SNP (transition)	94	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
T	1319028	1319026	1 C -> T	SNP (transition)	73	100.0%	1,8E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		mraY CDS
C	1319170	1319170	1 T -> C	SNP (transition)	70	98.6%	2,8E-246	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		mraY CDS
T	1320129	1320129	1 C -> T	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		murD CDS
G	1320495	1320495	1 A -> G	SNP (transition)	79	96.2%	2E-268	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		murD CDS
C	1320908	1320907	0 (C)9 -> (C)10	Insertion (tandem repeat)	69	97.1%	9,3E-231	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
A	1321002	1321002	0 (A)5 -> (A)6	Insertion (tandem repeat)	72	95.8%	2,4E-243	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
	1326102	1326102	1 (A)3 -> (A)2	Deletion (tandem repeat)	81	98.8%	0,0000017	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
C	1326407	1326407	1 T -> C	SNP (transition)	72	100.0%	2,5E-21	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1329416	1329416	1 G -> T	SNP (transversion)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	A -> D	Methyl-accepting chemotaxis protein CDS
A	1329562	1329562	1 G -> A	SNP (transition)	77	97.4%	2,8E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		Methyl-accepting chemotaxis protein CDS
T	1329774	1329774	1 C -> T	SNP (transition)	57	98.2%	5,7E-194	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	E -> K	Methyl-accepting chemotaxis protein CDS
A	1330823	1330823	1 G -> A	SNP (transition)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		PMT-2 domain-containing protein CDS
G	1330927	1330927	1 A -> G	SNP (transition)	75	100.0%	3,2E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	F -> L	PMT-2 domain-containing protein CDS
A	1543802	1543802	1 G -> A	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	V -> I	torA CDS
G	1544587	1544587	1 A -> G	SNP (transition)	79	100.0%	4E-284	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	I -> M	torA CDS
A	1544639	1544639	1 G -> A	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	G -> R	torA CDS
G	1561539	1561539	1 A -> G	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	Y -> H	sdaA CDS
T	1561669	1561669	1 C -> T	SNP (transition)	76	100.0%	2,5E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		sdaA CDS
CAA	1568800	1568802	2 TAG -> CAA	Substitution	88 -> 87	100.0%	1E-300	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		Ferric iron ABC transporter, permease protein CDS
T	1569715	1569715	1 C -> T	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
A	1569736	1569736	1 G -> A	SNP (transition)	81	100.0%	2E-299	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
G	1569781	1569781	1 A -> G	SNP (transition)	59	98.3%	9,3E-207	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
A	1569913	1569913	1 G -> A	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
T	1569961	1569961	1 C -> T	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
A	1570018	1570018	1 G -> A	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
A	1570090	1570090	1 G -> A	SNP (transition)	77	100.0%	1,3E-284	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
CCCCCT	1570749	1570748	0 +CCCCCT	Insertion	75 -> 76	98.7%	4E-258	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		
T	1571442	1571442	1 C -> T	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
A	1571499	1571499	1 G -> A	SNP (transition)	76	98.7%	7,6E-268	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
T	1571502	1571502	1 C -> T	SNP (transition)	83	97.6%	8,5E-288	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
T	1571553	1571553	1 C -> T	SNP (transition)	78	98.7%	4,9E-275	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
GC	1571565	1571566	2 AT -> GC	Substitution	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
T	1571634	1571634	1 A -> T	SNP (transversion)	93	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
GT	1571659	1571660	2 AC -> GT	Substitution	78 -> 79	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	T -> V	phuW CDS
T	1571664	1571664	1 C -> T	SNP (transition)	79	98.7%	2E-288	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
A	1571667	1571667	1 G -> A	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
C	1571677	1571677	1 T -> C	SNP (transition)	82	100.0%	6,3E-295	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
A	1571685	1571685	1 G -> A	SNP (transition)	87	100.0%	3,2E-304	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
T	1571700	1571700	1 C -> T	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
A	1571703	1571703	1 G -> A	SNP (transition)	86	98.8%	8,6E-304	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
CAG	1571742	1571744	3 TCA -> CAG	Substitution	85 -> 86	98.8%	8,6E-304	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	SD -> SS	phuW CDS
T	1571757	1571757	1 C -> T	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
A	1571760	1571760	1 G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		phuW CDS
G	1571771	1571771	1 A -> G	SNP (transition)	90	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> S	phuW CDS
T	1571783	1571783	1 G -> T	SNP (transversion)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	R -> I	phuW CDS
C	1571878	1571878	1 A -> C	SNP (transversion)	66	100.0%	2,5E-237	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	N -> H	TonB-dependent receptor CDS
T	1571892	1571892	1 C -> T	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
G	1571901	1571901	1 A -> G	SNP (transition)	71	100.0%	3,2E-248	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
T	1571967	1571967	1 C -> T	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
G	1571985	1571985	1 A -> G	SNP (transition)	71	100.0%	2,5E-255	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
G	1572081	1572081	1 A -> G	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
G	1572114	1572114	1 A -> G	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
C	1572173	1572173	1 A -> C	SNP (transversion)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
G	1572144	1572144	1 A -> G	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
C	1572156	1572156	1 T -> C	SNP (transition)	93	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
C	1572165	1572165	1 T -> C	SNP (transition)	94	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
C	1572177	1572177	1 T -> C	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
A	1572181	1572181	1 G -> A	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
T	1572210	1572210	1 C -> T	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
G	1572531	1572531	1 A -> G	SNP (transition)	70	100.0%	1E-251	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
ATC	1572538	1572540	2 TTT -> ATC	Substitution	67 -> 70	100.0%	6,3E-241	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	F -> I	TonB-dependent receptor CDS
T	1572543	1572543	1 C -> T	SNP (transition)	76	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
T	1573242	1573242	1 C -> T	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
C	1573263	1573263	1 T -> C	SNP (transition)	87	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
AT	1573333	1573334	2 GA -> AT	Substitution	87	98.9%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	E -> M	TonB-dependent receptor CDS
GC	1573403	1573404	2 CA -> GC	Substitution	91	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	T -> S	TonB-dependent receptor CDS
C	1573419	1573419	1 T -> C	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
G	1573444	1573444	1 A -> G	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	M -> V	TonB-dependent receptor CDS
T	1573509	1573509	1 C -> T	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
G	1573530	1573530	1 A -> G	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
G	1573575	1573575	1 A -> G	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
C	1573692	1573692	1 T -> C	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
G	1573761	1573761	1 A -> G	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
T	1573765	1573765	1 C -> T	SNP (transition)	79	98.7%	2E-286	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
T	1573770	1573770	1 A -> T	SNP (transversion)	77	100.0%	1,3E-284	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
A	1573800	1573800	1 G -> A	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
A	1574031	1574031	1 G -> A	SNP (transition)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
T	1574070	1574070	1 C -> T	SNP (transition)	83	100.0%	1,8E-298	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		TonB-dependent receptor CDS
G	1574154	1574154	1 A -> G	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		tolQ CDS
GCG	1574191	1574193	2 ACA -> GCG	Substitution	82 -> 83	100.0%	6,3E-295	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	T -> A	tolQ CDS
G	1574238	1574238	1 A -> G	SNP (transition)	75	98.7%	3E-264	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		tolQ CDS
T	1574271	1574271	1 C -> T	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		tolQ CDS
C	1574301	1574301	1 T -> C	SNP (transition)	74	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		tolQ CDS
CA	1574387	1574388	2 TC -> CA	Substitution	70	98.6%	2,8E-248	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	F -> S	tolQ CDS
C	1574391	1574391	1 T -> C	SNP (transition)	71	98.6%	7,1E-243	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss		tolQ CDS
A	1574397	1574397	1 C -> A	SNP (transversion)	64	98.4%	2E-218	Variants: BfR-CA-11057-TF15687-2_R	Concatemer BfR-CA-11057 - UniAss	H -> Q	tolQ CDS
AA		36609	G -> AA	Insertion	232	100.0%	0	Variants: BfR-CA-11057 - UniAss	Concatemer BfR-CA-11057 - UniAss		

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A	6399	6399	1 G -> A	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	G -> E	putative p-cresol methylhydroxylase subunit CDS
C	6704	6704	1 T -> C	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	F -> S	Chain B, Stru CDS
	6882	6882	1 (AT -> (AG	Deletion (tandem repeat)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		Cytochrome c CDS
	7425	7425	1 (T)8 -> (T)7	Deletion (tandem repeat)	107	97.2%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
T	8868	8868	1 C -> T	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		actP CDS
G	10257	10257	1 A -> G	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		Sodium:proton antiporter CDS
C	10326	10326	1 G -> C	SNP (transversion)	115	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	M -> I	Sodium:proton antiporter CDS
T	10353	10353	1 C -> T	SNP (transition)	121	98.3%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		Sodium:proton antiporter CDS
T	11197	11197	1 C -> T	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	11386	11386	1 T -> G	SNP (transversion)	124	99.2%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	11560	11560	1 A -> G	SNP (transition)	115	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	11572	11572	1 C -> T	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
AAATA	11574	11578	4 CGCTT -> AAATA	Substitution	118	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	TV -> KI	gltB3 CDS
G	11580	11580	1 A -> G	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	N -> S	gltB3 CDS
G	11593	11593	1 A -> G	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	11605	11605	1 A -> G	SNP (transition)	130	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
AG	11612	11613	2 GC -> AG	Substitution	132	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	A -> S	gltB3 CDS
ACG	11615	11617	3 TGT -> ACG	Substitution	111 -> 113	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	C -> T	gltB3 CDS
A	11623	11623	1 T -> A	SNP (transversion)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	11653	11653	1 T -> A	SNP (transversion)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	11671	11671	1 C -> T	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11686	11686	1 T -> C	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	11713	11713	1 T -> A	SNP (transversion)	127	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11725	11725	1 T -> C	SNP (transition)	128	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11770	11770	1 T -> C	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11788	11788	1 T -> C	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	11812	11812	1 C -> T	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11824	11824	1 T -> C	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	11836	11836	1 C -> T	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	11863	11863	1 C -> T	SNP (transition)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11866	11866	1 T -> C	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	11872	11872	1 A -> C	SNP (transversion)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	11881	11881	1 C -> T	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
CAA	11912	11914	2 GAG -> CAA	Substitution	128	98.4%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	E -> Q	gltB3 CDS
T	11917	11917	1 C -> T	SNP (transition)	125	99.2%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	11920	11920	1 A -> G	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	11980	11980	1 T -> A	SNP (transversion)	130	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	12011	12011	1 T -> C	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	12349	12349	1 T -> C	SNP (transition)	100	99.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12607	12607	1 T -> A	SNP (transversion)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12616	12616	1 G -> A	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	12751	12751	1 A -> T	SNP (transversion)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	12760	12760	1 T -> C	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12769	12769	1 G -> A	SNP (transition)	91	98.9%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	12772	12772	1 T -> C	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12775	12775	1 T -> A	SNP (transversion)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
AGCC	12781	12784	3 TTCT -> AGCC	Substitution	96 -> 97	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	IS -> IA	gltB3 CDS
GTG	12791	12793	2 ATT -> GTG	Substitution	101	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	I -> V	gltB3 CDS
A	12796	12796	1 T -> A	SNP (transversion)	100	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12808	12808	1 G -> A	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	12814	12814	1 C -> T	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12817	12817	1 G -> A	SNP (transition)	86	98.8%	8,6E-304	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	12823	12823	1 A -> G	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	12826	12826	1 C -> T	SNP (transition)	95	98.9%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	12832	12832	1 C -> T	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12835	12835	1 T -> A	SNP (transversion)	94	97.9%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	N -> K	gltB3 CDS
T	12838	12838	1 C -> T	SNP (transition)	94	96.8%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	12965	12965	1 C -> A	SNP (transversion)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	Q -> K	gltB3 CDS
C	13275	13275	1 T -> C	SNP (transition)	138	99.3%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	13231	13231	1 A -> G	SNP (transition)	137	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	13273	13273	1 A -> G	SNP (transition)	135	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	13282	13282	1 T -> C	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	13285	13285	1 A -> G	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	13303	13303	1 T -> C	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	13306	13306	1 T -> A	SNP (transversion)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	13315	13315	1 G -> A	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	13319	13319	1 T -> C	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	13354	13354	1 T -> C	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	13365	13365	1 T -> C	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	I -> T	gltB3 CDS
C	13411	13411	1 T -> C	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	13501	13501	1 C -> T	SNP (transition)	101	99.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	13819	13819	1 C -> T	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	14023	14023	1 T -> G	SNP (transversion)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	14029	14029	1 C -> T	SNP (transition)	110	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14032	14032	1 G -> A	SNP (transition)	109	98.2%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14035	14035	1 T -> A	SNP (transversion)	108	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14059	14059	1 T -> A	SNP (transversion)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14062	14062	1 G -> A	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	14170	14170	1 A -> T	SNP (transversion)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	14173	14173	1 A -> G	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	14179	14179	1 A -> C	SNP (transversion)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	14431	14431	1 T -> C	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14662	14662	1 T -> A	SNP (transversion)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
GCTA	14665	14668	3 AGTG -> GCTA	Substitution	105 -> 106	98.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	KV -> KL	gltB3 CDS
G	14674	14674	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	15274	15274	1 G -> A	SNP (transition)	92	97.8%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	15526	15526	1 A -> G	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	15538	15538	1 C -> T	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	17240	17240	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrhB CDS
C	17383	17383	1 T -> C	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	K -> E	nrhB CDS
G	17889	17889	1 A -> G	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		Desulfoferrodoxin Fe(4 iron-binding domain-containing pro
T	18297	18297	1 C -> T	SNP (transition)	85	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		Desulfoferrodoxin Fe(4 iron-binding domain-containing pro
T	18372	18372	1 C -> T	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
A	19670	19670	1 G -> A	SNP (transition)	178	99.2%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		ilvD CDS
G	20635	20635	1 T -> G	SNP (transversion)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20638	20638	1 G -> A	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20644	20644	1 G -> A	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	20656	20656	1 T -> C	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20659	20659	1 A -> T	SNP (transversion)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
CAA	20662	20664	2 TAC -> CAA	Substitution	95 -> 97	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	20674	20674	1 T -> C	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20680	20680	1 G -> A	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20692	20692	1 G -> A	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	20695	20695	1 T -> C	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	20709	20709	1 T -> C	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	N -> D	comGF CDS
C	20716	20716	1 T -> C	SNP (transition)	85	98.8%	3,4E-300	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20725	20725	1 A -> T	SNP (transversion)	82	100.0%	1E-286	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	20731	20731	1 A -> G	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	20755	20755	1 T -> C	SNP (transition)	87	98.9%	8,7E-299	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	20776	20776	1 A -> C	SNP (transversion)	79	98.7%	7,9E-271	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	20779	20779	1 A -> G	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20785	20785	1 A -> T	SNP (transversion)	76	100.0%	2,5E-273	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20797	20797	1 G -> A	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20812	20812	1 C -> T	SNP (transition)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	20821	20821	1 A -> G	SNP (transition)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20830	20830	1 C -> T	SNP (transition)	77	100.0%	3,2E-268	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
AAG	20836	20838	2 TAA -> AAG	Substitution	82 -> 83	95.1% -> 95.2%	2,8E-274	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20842	20842	1 G -> A	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20845	20845	1 G -> A	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	20851	20851	1 T -> G	SNP (transversion)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20854	20854	1 G -> T	SNP (transversion)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
TAA	20866	20868	2 AAG -> TAA	Substitution	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20872	20872	1 G -> A	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20890	20890	1 G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	20893	20893	1 T -> C	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	20899	20899	1 A -> G	SNP (transition)	85	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20908	20908	1 C -> T	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	20917	20917	1 A -> T	SNP (transversion)	84	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	D -> E	comGF CDS
A	20970	20970	1 G -> A	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	20976	20976	1 A -> G	SNP (transition)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20932	20932	1 G -> A	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	20941	20941	1 G -> A	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21001	21001	1 G -> A	SNP (transition)	90	98.9%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21004	21004	1 G -> T	SNP (transversion)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21007	21007	1 T -> A	SNP (transversion)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21010	21010	1 A -> T	SNP (transversion)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21034	21034	1 G -> A	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
AGC	21040	21042	2 GGT -> AGC	Substitution	117 -> 125	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	T -> A	comGF CDS
A	21046	21046	1 G -> A	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	21049	21049	1 A -> G	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21054	21054	1 G -> A	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21058	21058	1 T -> C	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	21075	21075	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21079	21079	1 C -> T	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21082	21082	1 T -> C	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21106	21106	1 G -> A	SNP (transition)	118	98.3%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	21118	21118	1 A -> G	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21136	21136	1 C -> A	SNP (transversion)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21139	21139	1 C -> T	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21142	21142	1 T -> A	SNP (transversion)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21154	21154	1 G -> A	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21157	21157	1 T -> C	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS

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C	21172	21172	1 T -> C	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21193	21193	1 A -> T	SNP (transversion)	70	98.6%	2,8E-246	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21196	21196	1 T -> C	SNP (transition)	78	98.7%	2,5E-267	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21202	21202	1 G -> A	SNP (transition)	78	98.7%	4,8E-275	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21205	21205	1 G -> A	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21214	21214	1 T -> C	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21226	21226	1 A -> C	SNP (transversion)	83	100.0%	1,8E-298	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
CA	21238	21239	2 AG -> CA	Substitution	85 -> 87	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	A -> V	comGF CDS
T	21244	21244	1 C -> T	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	M -> I	comGF CDS
A	21268	21268	1 T -> A	SNP (transversion)	94	98.9%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	21271	21271	1 A -> G	SNP (transition)	92	98.9%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21274	21274	1 G -> A	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21280	21280	1 A -> T	SNP (transversion)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
G	21283	21283	1 T -> G	SNP (transversion)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21298	21298	1 C -> A	SNP (transversion)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21313	21313	1 C -> T	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
A	21316	21316	1 G -> A	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
C	21319	21319	1 T -> C	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		comGF CDS
T	21418	21417	0 (T)6 -> (T)7	Insertion (tandem repeat)	111	94.6%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
T	21682	21682	1 C -> T	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		quaC CDS
A	22093	22093	1 G -> A	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		quaC CDS
C	22173	22173	1 T -> C	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
A	22276	22276	1 G -> A	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
T	22282	22282	1 G -> T	SNP (transversion)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
T	22291	22291	1 C -> T	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
C	22294	22294	1 T -> C	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
AG	22306	22307	2 GT -> AG	Substitution	107	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	D -> A	dsbI CDS
G	22315	22315	1 A -> G	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
TA	22370	22321	2 CG -> TA	Substitution	104 -> 106	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	AV -> AI	dsbI CDS
G	22324	22324	1 A -> G	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
CT	22604	22605	2 TC -> CT	Substitution	111	96.4%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	D -> S	dsbI CDS
CG	22608	22609	2 TT -> CG	Substitution	114 -> 115	96.5%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	GK -> GE	dsbI CDS
C	22834	22834	1 T -> C	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
ATC	22864	22866	2 GTT -> ATC	Substitution	101 -> 103	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	N -> D	dsbI CDS
A	22870	22870	1 G -> A	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
T	22891	22891	1 G -> T	SNP (transversion)	120	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
A	22897	22897	1 G -> A	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
GA	22921	22922	2 TG -> GA	Substitution	87 -> 90	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	T -> I	dsbI CDS
A	22924	22924	1 G -> A	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
GTCA	22939	22942	3 ATTG -> GTCA	Substitution	112 -> 114	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	IN -> ID	dsbI CDS
C	22947	22947	1 T -> C	SNP (transition)	117	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	K -> E	dsbI CDS
A	22959	22959	1 C -> A	SNP (transversion)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	A -> S	dsbI CDS
A	22963	22963	1 G -> A	SNP (transition)	118	99.2%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
TG	22966	22967	2 GA -> TG	Substitution	117 -> 118	99.1% -> 99.2%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	I -> T	dsbI CDS
T	22971	22971	1 C -> T	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	D -> N	dsbI CDS
A	22987	22987	1 G -> A	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
CAA	22990	22992	2 AAG -> CAA	Substitution	119 -> 123	97.5% -> 97.6%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
C	23002	23002	1 T -> C	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
A	23038	23038	1 G -> A	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
C	23041	23041	1 T -> C	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
G	24160	24160	1 T -> G	SNP (transversion)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	K -> Q	yceJ CDS
T	24166	24166	1 G -> T	SNP (transversion)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	H -> N	yceJ CDS
C	24170	24170	1 T -> C	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		yceJ CDS
G	24173	24173	1 A -> G	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		yceJ CDS
T	24185	24185	1 A -> T	SNP (transversion)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		yceJ CDS
G	24224	24224	1 A -> G	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		yceJ CDS
A	24500	24500	1 G -> A	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		yceJ CDS
GC	24673	24674	2 AT -> GC	Substitution	99 -> 101	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		yceJ CDS
T	24710	24710	1 T -> C	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		yceJ CDS
G	25001	25001	1 A -> G	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	25286	25286	1 T -> C	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
T	25408	25408	1 C -> T	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	E -> K	RNA pseudouridylate synthase CDS
C	25469	25469	1 A -> C	SNP (transversion)	105	99.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
T	25474	25474	1 C -> T	SNP (transition)	114	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	E -> K	RNA pseudouridylate synthase CDS
A	25478	25478	1 T -> A	SNP (transversion)	114	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
A	25485	25485	1 G -> A	SNP (transition)	114	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	H -> Y	RNA pseudouridylate synthase CDS
A	25526	25526	1 G -> A	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
G	25538	25538	1 A -> G	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
G	25610	25610	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	25691	25691	1 T -> C	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	26306	26306	1 T -> C	SNP (transition)	85	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
A	26321	26321	1 G -> A	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
ACTT	26342	26345	3 GTTA -> ACTT	Substitution	79 -> 82	100.0%	4E-284	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
G	26348	26348	1 T -> G	SNP (transversion)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
A	26369	26369	1 G -> A	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
T	27838	27836	1 C -> T	SNP (transition)	139	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	27892	27892	1 C -> T	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
C	27949	27949	1 T -> C	SNP (transition)	95	97.9%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
C	28003	28003	1 T -> C	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28015	28015	1 C -> T	SNP (transition)	67	100.0%	6,3E-241	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
C	28018	28018	1 T -> C	SNP (transition)	65	100.0%	3,2E-227	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
A	28024	28024	1 G -> A	SNP (transition)	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
GG	28135	28136	2 AA -> GG	Substitution	103	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	VS -> VG	nrdA CDS
C	28213	28213	1 T -> C	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28216	28216	1 C -> T	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28237	28237	1 G -> T	SNP (transversion)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
G	28780	28780	1 T -> G	SNP (transversion)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28816	28816	1 C -> T	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	28822	28822	1 C -> T	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		nrdA CDS
T	32037	32037	1 C -> T	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		pyrG CDS
A	33736	33736	1 G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33748	33748	1 T -> C	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33751	33751	1 T -> C	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
T	33757	33757	1 C -> T	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33769	33769	1 T -> C	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
A	36609	36609	1 G -> A	SNP (transition)	203	99.5%	3,1E-280	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
A	36610	36609	0 +A	Insertion	201	87.6%	7,5E-215	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
C	36624	36624	1 T -> C	SNP (transition)	219	99.5%	5,2E-259	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
T	36651	36651	1 (A)3 -> (A)2	Deletion (tandem repeat)	233	94.0%	2,3E-68	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
A	36654	36654	1 T -> A	SNP (transversion)	223	98.2%	4,7E-189	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
AA	36660	36659	0 +AA	Insertion	219	95.4%	4,8E-155	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
C	36669	36669	1 T -> C	SNP (transition)	227	99.6%	3E-178	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
G	38113	38113	1 A -> G	SNP (transition)	283	99.6%	3,6E-82	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
	38420	38420	1 (T)3 -> (T)2	Deletion (tandem repeat)	252	98.0%	6,5E-18	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
G	40889	40889	1 T -> G	SNP (transversion)	302	99.7%	7,6E-88	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
T	42300	42300	1 G -> T	SNP (transversion)	312	99.4%	1,7E-88	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
AG	42203	42204	2 GA -> AG	Substitution	318 -> 331	95.9% -> 96.1%	7,1E-74	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
	42429	42429	1 (A)7 -> (A)8	Deletion (tandem repeat)	317	92.4%	1,7E-09	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
C	42643	42643	1 T -> C	SNP (transition)	287	100.0%	7,9E-86	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
	42797	42802	6 (TTTATG)3 -> (TTTATG)2	Deletion (tandem repeat)	266	100.0%	2,5E-26	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
A	43128	43128	1 G -> A	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	T -> I	hypothetical protein CDS
C	4615137	4615137	1 T -> C	SNP (transition)	86	88.4%	3,4E-177	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	N -> D	DUF115 domain-containing protein CDS
A	1028995	1028995	1 G -> A	SNP (transition)	98	99.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	S -> N	DL-methionine ABC transporter: MetINQ, substrate-binding
G	1029015	1029015	1 A -> G	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	N -> D	DL-methionine ABC transporter: MetINQ, substrate-binding
T	1029122	1029122	1 C -> T	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		DL-methionine ABC transporter: MetINQ, substrate-binding
A	1029394	1029394	1 G -> A	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		
T	1029442	1029442	1 C -> T	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1029517	1029517	1 T -> C	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
CC	1029540	1029545	2 TT -> CC	Substitution	84 -> 90	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1029550	1029550	1 T -> C	SNP (transition)	82	100.0%	1E-286	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1029556	1029556	1 T -> C	SNP (transition)	76	98.7%	7,6E-268	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029559	1029559	1 C -> T	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
A	1029622	1029623	1 G -> A	SNP (transition)	78	100.0%	1E-272	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029748	1029748	1 C -> T	SNP (transition)	85	97.6%	2,8E-303	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029757	1029757	1 C -> T	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
G	1029760	1029760	1 A -> G	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029769	1029769	1 C -> T	SNP (transition)	92	98.9%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
GG	1029777	1029778	2 AA -> GG	Substitution	96 -> 97	99.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	K -> R	flgA CDS
T	1029790	1029790	1 C -> T	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029901	1029901	1 C -> T	SNP (transition)	108	97.2%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
ATC	1029914	1029916	2 GTT -> ATC	Substitution	94 -> 96	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	V -> I	flgA CDS
C	1029922	1029922	1 T -> C	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
G	1029943	1029943	1 A -> G	SNP (transition)	87	98.9%	2,2E-307	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1030030	1030030	1 T -> C	SNP (transition)	123	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1030264	1030264	1 G -> T	SNP (transversion)	109	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	A -> S	3-octaprenyl-4-hydroxybenzoate carboxy-lyase CDS
A	1030581	1030581	1 G -> A	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		3-octaprenyl-4-hydroxybenzoate carboxy-lyase CDS
G	1032161	1032161	1 A -> G	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	S -> G	hisS CDS
T	1032172	1032172	1 C -> T	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
AG	1032227	1032228	2 GA -> AG	Substitution	86	100.0%	1E-300	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	E -> R	hisS CDS
G	1032244	1032244	1 A -> G	SNP (transition)	82	100.0%	6,3E-295	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032750	1032750	1 T -> C	SNP (transition)	76	100.0%	7,5E-273	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032765	1032765	1 C -> T	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032304	1032304	1 C -> T	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032307	1032307	1 T -> C	SNP (transition)	98	99.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
A	1032310	1032310	1 G -> A	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
GC	1032325	1032326	2 AT -> GC	Substitution	96	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	EY -> EH	hisS CDS
G	1032355	1032355	1 A -> G	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1032361	1032361	1 A -> G	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032376	1032376	1 T -> C	SNP (transition)	76	98.7%	7,8E-268	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1032406	1032406	1 A -> G	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032466	1032466	1 C -> T	SNP (transition)	69	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1032523	1032523	1 A -> G	SNP (transition)	71	100.0%	2,5E-255	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS

9 Appendix

T	1032528	1032528	1 C -> T	SNP (transition)	69	100.0%	4E-248	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032529	1032529	1 C -> T	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032532	1032532	1 T -> C	SNP (transition)	70	100.0%	1E-244	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1038237	1038237	1 A -> G	SNP (transition)	87	98.9%	2,2E-307	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	I -> T	MBL fold metallo-hydrolase CDS
G	1038273	1038273	1 A -> G	SNP (transition)	78	100.0%	7,5E-288	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
A	1040325	1040325	1 G -> A	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		dnaK CDS
T	1042179	1042179	1 C -> T	SNP (transition)	90	98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042182	1042182	1 G -> A	SNP (transition)	95	98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
AC	1042187	1042188	2 GT -> AC	Substitution	96	96.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
T	1042191	1042191	1 C -> T	SNP (transition)	90	97.8%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
C	1042194	1042194	1 T -> C	SNP (transition)	93	97.8%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042206	1042206	1 A -> G	SNP (transition)	91	97.8%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042218	1042218	1 A -> G	SNP (transition)	95	97.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042221	1042221	1 G -> A	SNP (transition)	98	98.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
T	1042233	1042233	1 C -> T	SNP (transition)	106	98.1%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
C	1042249	1042249	1 T -> C	SNP (transition)	101	98.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	N -> S	hrcA CDS
A	1042793	1042793	1 G -> A	SNP (transition)	91	98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042371	1042371	1 G -> A	SNP (transition)	94	98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042431	1042431	1 A -> G	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042479	1042479	1 A -> G	SNP (transition)	101	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
T	1042488	1042488	1 C -> T	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
A	1042490	1042490	1 T -> A	SNP (transversion)	113	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
G	1042492	1042492	1 T -> G	SNP (transversion)	114	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
AG	1042520	1042521	2 TA -> AG	Substitution	111 -> 118	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
T	1042591	1042591	1 A -> T	SNP (transversion)	81	100.0%	2E-299	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
A	1042596	1042596	1 G -> A	SNP (transition)	77	100.0%	6,8E-277	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
A	1042608	1042608	1 G -> A	SNP (transition)	72	98.6%	1,4E-260	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
G	1042632	1042632	1 A -> G	SNP (transition)	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
A	1042634	1042634	1 C -> A	SNP (transversion)	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
A	1042638	1042638	1 C -> A	SNP (transversion)	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
C	1042642	1042642	1 T -> C	SNP (transition)	60	100.0%	1E-221	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
GT	1042650	1042651	2 AA -> GT	Substitution	55	100.0%	1E-197	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
ACAG	1042654	1042657	4 TGCA -> ACAG	Substitution	49 -> 55	95.9% -> 100.0%	1,5E-170	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
G	1042659	1042658	0 +G	Insertion	44	95.5%	3,8E-152	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
A	1042687	1042687	1 T -> A	SNP (transversion)	50	100.0%	1E-184	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
T	1042690	1042690	1 A -> T	SNP (transversion)	51	84.3%	5,1E-150	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
C	1042692	1042692	1 T -> C	SNP (transition)	52	84.6%	1,2E-153	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
C	1042729	1042729	1 T -> C	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
AC	1042750	1042751	2 GA -> AC	Substitution	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
C	1042763	1042763	1 T -> C	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
T	1042765	1042765	1 C -> T	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
AC	1042784	1042785	2 GT -> AC	Substitution	81 -> 83	100.0%	2E-299	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	N -> S	ctrA CDS
A	1042793	1042793	1 G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1042796	1042796	1 A -> G	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
T	1042805	1042805	1 C -> T	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	M -> I	ctrA CDS
A	1042829	1042829	1 G -> A	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1042832	1042832	1 A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1042835	1042835	1 G -> A	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1042841	1042841	1 T -> G	SNP (transversion)	93	98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
AG	1042850	1042851	2 GC -> AG	Substitution	95 -> 96	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	S -> T	ctrA CDS
GT	1042854	1042855	2 CC -> GT	Substitution	96 -> 97	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	G -> T	ctrA CDS
CGCT	1042858	1042961	3 TCCC -> CGCT	Substitution	86 -> 87	97.7%	8,6E-304	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	GS -> SG	ctrA CDS
T	1042863	1042863	1 C -> T	SNP (transition)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	S -> N	ctrA CDS
TG	1042866	1042867	2 GC -> TG	Substitution	82	100.0%	4E-303	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	A -> Q	ctrA CDS
A	1042880	1042880	1 G -> A	SNP (transition)	89	98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
C	1042885	1042885	1 T -> C	SNP (transition)	89	98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	N -> D	ctrA CDS
A	1042892	1042892	1 G -> A	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
T	1042900	1042900	1 C -> T	SNP (transition)	85	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	D -> N	ctrA CDS
G	1042922	1042922	1 A -> G	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
C	1042937	1042937	1 T -> C	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1042940	1042940	1 G -> A	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1042964	1042964	1 G -> A	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1042985	1042985	1 G -> A	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
C	1042994	1042994	1 T -> C	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
T	1043000	1043000	1 G -> T	SNP (transversion)	94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
C	1043087	1043087	1 T -> C	SNP (transition)	100	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1043093	1043093	1 G -> A	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1043099	1043099	1 G -> A	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1043258	1043258	1 G -> A	SNP (transition)	82	98.8%	1,6E-297	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
TC	1043267	1043268	2 CT -> TC	Substitution	86 -> 87	97.7%	1,5E-298	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	K -> R	ctrA CDS
G	1043271	1043271	1 A -> G	SNP (transition)	87	98.9%	2,2E-307	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	F -> S	ctrA CDS
C	1043584	1043584	1 G -> C	SNP (transversion)	98	98.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	L -> V	ctrA CDS
CAA	1043648	1043650	2 AAG -> CAA	Substitution	91	98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
GTT	1043657	1043659	2 ATC -> GTT	Substitution	94 -> 95	97.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	D -> N	ctrA CDS
G	1043669	1043669	1 A -> G	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1043672	1043672	1 A -> G	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
T	1043690	1043690	1 A -> T	SNP (transversion)	89	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1043717	1043717	1 A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
C	1043720	1043720	1 A -> C	SNP (transversion)	92	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
T	1043724	1043724	1 C -> T	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	S -> N	ctrA CDS
A	1043765	1043765	1 G -> A	SNP (transition)	118	99.2%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1043769	1043769	1 A -> G	SNP (transition)	116	98.3%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	V -> A	ctrA CDS
C	1043774	1043774	1 T -> C	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
CAA	1043792	1043794	2 TAG -> CAA	Substitution	107	99.1%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1043801	1043801	1 A -> G	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
T	1043861	1043861	1 C -> T	SNP (transition)	98	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
C	1043867	1043867	1 T -> C	SNP (transition)	98	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
TGC	1043870	1043872	2 AGA -> TGC	Substitution	96 -> 100	97.9% -> 98.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	S -> A	ctrA CDS
T	1043876	1043876	1 C -> T	SNP (transition)	103	98.1%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1043882	1043882	1 G -> A	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1043891	1043891	1 G -> A	SNP (transition)	96	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
T	1043896	1043896	1 C -> T	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	D -> N	ctrA CDS
T	1043903	1043903	1 C -> T	SNP (transition)	97	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1043912	1043917	1 A -> G	SNP (transition)	104	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
GTC	1043922	1043924	3 CCA -> GTC	Substitution	86 -> 87	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	SG -> ST	ctrA CDS
G	1043927	1043927	1 A -> G	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1043930	1043930	1 G -> A	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1043966	1043966	1 A -> G	SNP (transition)	72	98.6%	1,4E-260	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
C	1043999	1043999	1 T -> C	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1044005	1044005	1 A -> G	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
T	1044024	1044024	1 G -> T	SNP (transversion)	94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	P -> Q	ctrA CDS
A	1044029	1044029	1 T -> A	SNP (transversion)	95	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	R -> S	ctrA CDS
G	1044044	1044044	1 A -> G	SNP (transition)	94	98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1044047	1044047	1 A -> G	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1044074	1044074	1 G -> A	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1044110	1044110	1 A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
C	1044128	1044128	1 T -> C	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1044155	1044155	1 G -> A	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
T	1044191	1044191	1 C -> T	SNP (transition)	75	100.0%	3,2E-277	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
T	1044314	1044314	1 C -> T	SNP (transition)	94	98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1044662	1044662	1 A -> G	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1044720	1044720	1 C -> G	SNP (transversion)	106	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	S -> T	ctrA CDS
G	1044722	1044722	1 A -> G	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
GGT	1044761	1044763	2 AGC -> GGT	Substitution	82	98.8%	1,6E-297	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	A -> T	ctrA CDS
G	1044767	1044767	1 T -> G	SNP (transversion)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
C	1044781	1044781	1 T -> C	SNP (transition)	74	98.6%	5,9E-268	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	I -> V	ctrA CDS
T	1044785	1044785	1 C -> T	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1044788	1044788	1 A -> G	SNP (transition)	78	98.7%	4,9E-275	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1044791	1044791	1 G -> A	SNP (transition)	82	100.0%	6,3E-299	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
T	1044797	1044797	1 C -> T	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1044815	1044815	1 A -> G	SNP (transition)	81	100.0%	2E-299	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1044821	1044821	1 A -> G	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
GCTT	1044824	1044827	4 AGCC -> GCTT	Substitution	85 -> 88	90.8% -> 91.8%	7,8E-271	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	LA -> LS	ctrA CDS
G	1044830	1044830	1 A -> G	SNP (transition)	87	92.0%	5,8E-286	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1044833	1044833	1 G -> A	SNP (transition)	82	100.0%	6,3E-299	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
G	1044842	1044842	1 A -> G	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
T	1044848	1044848	1 C -> T	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
T	1044859	1044859	1 A -> T	SNP (transversion)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	L -> I	ctrA CDS
T	1044863	1044863	1 C -> T	SNP (transition)	66	100.0%	2,5E-237	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ctrA CDS
A	1044903	1044903	1 G -> A	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
	1048144	1048149	6 (TAAACA)3 -> (TAAACA)2	Deletion (tandem repeat)	257	100.0%	2E-25	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
G	1048119	1048119	1 A -> G	SNP (transition)	289	100.0%	2E-86	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
	1048539	1048539	1 (T)7 -> (T)6	Deletion (tandem repeat)	306	96.7%	6,7E-18	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
CT	1048758	1048759	2 TC -> CT	Substitution	320 -> 333	95.9% -> 96.1%	1,9E-74	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
A	1048762	1048762	1 C -> A	SNP (transversion)	314	99.4%	3,1E-89	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
C	1050073	1050073	1 A -> C	SNP (transversion)	302	99.7%	7,6E-88	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
	1052544	1052544	1 (A)3 -> (A)2	Deletion (tandem repeat)	257	96.1%	9,3E-14	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
C	1052849	1052849	1 T -> C	SNP (transition)	283	99.6%	3,6E-82	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		
C	1056828	1056828	1 T -> C	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	E -> G	ccmA CDS
C	1058557	1058557	1 T -> C	SNP (transition)	80	98.8%	3,2E-282	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	I -> V	Putative ABC transport system permease CDS
T	1058795	1058795	1 G -> T	SNP (transversion)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		Putative ABC transport system permease CDS
T	1058819	1058819	1 C -> T	SNP (transition)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	R -> K	ataC CDS
T	1058880	1058880	1 C -> T	SNP (transition)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	V -> I	ataC CDS
G	1058884	1058884	1 A -> G	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1058971	1058971	1 G -> A	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059022	1059022	1 A -> G	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059106	1059106	1 G -> A	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059154	1059154	1 G -> A	SNP (transition)	97	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059162	1059162	1 A -> G	SNP (transition)	105	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss	F -> L	ataC CDS
T	1059259	1059259	1 C -> T	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059283	1059283	1 A -> G	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059487	1059487	1 A -> G	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS

9 Appendix

C	1059541	1059541	1 T -> C	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			ataC CDS
CA	1059570	1059571	2 TG -> CA	Substitution	84	100.0%	4E-302	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		ST -> SA	ataC CDS
G	1059624	1059624	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Phytase-like domain-containing protein CDS
T	1059660	1059660	1 C -> T	SNP (transition)	98	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Phytase-like domain-containing protein CDS
T	1059675	1059675	1 C -> T	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Phytase-like domain-containing protein CDS
G	1059897	1059897	1 A -> G	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Phytase-like domain-containing protein CDS
G	1059915	1059915	1 A -> G	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Phytase-like domain-containing protein CDS
A	1059961	1059961	1 G -> A	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		A -> V	Phytase-like domain-containing protein CDS
G	1059973	1059973	1 A -> G	SNP (transition)	98	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		I -> T	Phytase-like domain-containing protein CDS
C	1060048	1060048	1 T -> C	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		N -> S	Phytase-like domain-containing protein CDS
G	1060134	1060134	1 A -> G	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Phytase-like domain-containing protein CDS
A	1060458	1060458	1 G -> A	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Phytase-like domain-containing protein CDS
T	1060491	1060491	1 G -> T	SNP (transversion)	95	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Phytase-like domain-containing protein CDS
G	1060503	1060503	1 A -> G	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Phytase-like domain-containing protein CDS
A	1060557	1060557	1 G -> A	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Phytase-like domain-containing protein CDS
G	1060596	1060596	1 A -> G	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Phytase-like domain-containing protein CDS
T	1060641	1060641	1 C -> T	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Phytase-like domain-containing protein CDS
C	1061191	1061191	1 T -> C	SNP (transition)	72	100.0%	1E-251	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			afuA CDS
A	1061194	1061194	1 G -> A	SNP (transition)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			afuA CDS
A	1061399	1061399	1 G -> A	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		A -> V	afuA CDS
A	1061809	1061809	1 G -> A	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			afuA CDS
A	1061821	1061821	1 G -> A	SNP (transition)	121	98.3%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			afuA CDS
C	1062737	1062737	1 T -> C	SNP (transition)	94	100.0%	2,5E-214	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		V -> A	corA CDS
G	1062305	1062305	1 A -> G	SNP (transition)	61	100.0%	2E-225	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			corA CDS
G	1063367	1063367	1 A -> G	SNP (transition)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		I -> V	moaB CDS
AGC	1065015	1065017	3 GCT -> AGC	Substitution	77 -> 78	93.5% -> 93.6%	3,3E-255	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		A -> S	Peptidase, M48 family protein CDS
C	1065021	1065021	1 G -> C	SNP (transversion)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		V -> L	Peptidase, M48 family protein CDS
G	1065032	1065032	1 A -> G	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Peptidase, M48 family protein CDS
G	1066684	1066684	1 A -> G	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		I -> V	flaC CDS
T	1066860	1066860	1 C -> T	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			flaC CDS
A	1067425	1067425	1 G -> A	SNP (transition)	85	98.8%	3,4E-300	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		A -> T	Pyridoxal phosphate homeostasis protein CDS
T	1068252	1068252	1 C -> T	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		G -> E	dnaE CDS
A	1068284	1068284	1 G -> A	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			dnaE CDS
A	1068497	1068497	1 G -> A	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			dnaE CDS
A	1069352	1069352	1 G -> A	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			dnaE CDS
A	1070008	1070008	1 G -> A	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			dnaE CDS
G	1075504	1075504	1 T -> G	SNP (transversion)	86	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		K -> Q	rimM CDS
G	1075743	1075743	1 A -> G	SNP (transition)	84	98.8%	1,3E-296	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			RNA-binding protein CDS
C	1076616	1076616	1 T -> C	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		I -> M	ffh CDS
T	1078818	1078818	1 C -> T	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		R -> Q	3-deoxy-D-manno-octulosonic acid transferase CDS
T	1080585	1080585	1 G -> T	SNP (transversion)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		L -> I	Nif3-like dinuclear metal center hexameric protein CDS
T	1081250	1081250	1 C -> T	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			glyQ CDS
T	1081253	1081253	1 C -> T	SNP (transition)	85	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			glyQ CDS
C	1081259	1081259	1 T -> C	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			glyQ CDS
C	1081469	1081469	1 T -> C	SNP (transition)	85	100.0%	3,2E-297	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			glyQ CDS
A	1081520	1081520	1 G -> A	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			glyQ CDS
C	1081573	1081573	1 T -> C	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			glyQ CDS
A	1081578	1081578	1 T -> A	SNP (transversion)	80	98.9%	8,9E-308	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			glyQ CDS
A	1081571	1081571	1 C -> A	SNP (transversion)	93	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			glyQ CDS
C	1081580	1081580	1 T -> C	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			glyQ CDS
T	1081589	1081589	1 A -> T	SNP (transversion)	99	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			glyQ CDS
T	1081971	1081971	1 C -> T	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			DUF3972 domain-containing protein CDS
G	1318207	1318207	1 A -> G	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			gpmI CDS
G	1318468	1318468	1 A -> G	SNP (transition)	110	99.1%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			gpmI CDS
T	1319026	1319026	1 C -> T	SNP (transition)	109	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			mraY CDS
C	1319170	1319170	1 T -> C	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			mraY CDS
T	1320129	1320129	1 C -> T	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			murD CDS
G	1320495	1320495	1 A -> G	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			murD CDS
A	1321065	1321602	0 (A)5 -> (A)6	Insertion (tandem repeat)	103	98.1%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
	1321702	1321707	6 (TAAACA)3 -> (TAAACA)2	Deletion (tandem repeat)	258	100.0%	1,6E-25	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
G	1321877	1321877	1 A -> G	SNP (transition)	287	100.0%	7,9E-86	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
	1322097	1322097	1 (T)7 -> (T)6	Deletion (tandem repeat)	306	96.7%	6,7E-18	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
CT	1322116	1322117	2 TC -> CT	Substitution	320 -> 333	95.9% -> 96.1%	1,9E-74	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
A	1322320	1322320	1 C -> A	SNP (transversion)	314	99.4%	3,1E-89	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
C	1323631	1323631	1 A -> C	SNP (transversion)	302	99.7%	7,6E-88	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
	1326102	1326102	1 (A)3 -> (A)2	Deletion (tandem repeat)	257	96.1%	9,3E-14	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
C	1326407	1326407	1 T -> C	SNP (transition)	283	99.6%	3,6E-82	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
G	1327851	1327851	1 A -> G	SNP (transition)	173	99.4%	2,2E-49	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
TT	1327864	1327863	0 +TT	Insertion	160	96.9%	6,6E-54	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
T	1327866	1327866	1 A -> T	SNP (transversion)	160	99.4%	1,6E-45	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
	1327871	1327871	1 (T)3 -> (T)2	Deletion (tandem repeat)	162	97.5%	8,7E-11	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
G	1327896	1327896	1 A -> G	SNP (transition)	116	100.0%	4E-46	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
T	1327911	1327911	1 C -> T	SNP (transition)	85	100.0%	3,2E-42	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
T	1327914	1327913	0 (T)2 -> (T)3	Insertion (tandem repeat)	76	92.1%	2,3E-27	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
T	1329416	1329416	1 G -> T	SNP (transversion)	94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		A -> D	Methyl-accepting chemotaxis protein CDS
A	1329642	1329642	1 G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Methyl-accepting chemotaxis protein CDS
T	1329774	1329774	1 C -> T	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		E -> K	Methyl-accepting chemotaxis protein CDS
A	1387760	1387760	1 T -> A	SNP (transversion)	87	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
A	1387775	1387775	1 T -> A	SNP (transversion)	96	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
G	1387784	1387784	1 A -> G	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
A	1387856	1387856	1 C -> A	SNP (transversion)	127	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
T	1387862	1387862	1 C -> T	SNP (transition)	128	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
G	1387865	1387865	1 A -> G	SNP (transition)	123	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
C	1387868	1387868	1 T -> C	SNP (transition)	126	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
G	1387871	1387871	1 A -> G	SNP (transition)	127	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
A	1387889	1387889	1 G -> A	SNP (transition)	121	99.2%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
C	1387898	1387898	1 T -> C	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
A	1387901	1387901	1 G -> A	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
A	1387907	1387907	1 T -> A	SNP (transversion)	109	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
A	1387916	1387916	1 T -> A	SNP (transversion)	98	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
G	1387925	1387925	1 A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
A	1387934	1387934	1 G -> A	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
AGG	1387943	1387945	3 GAA -> AGG	Substitution	95 -> 97	97.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		KK -> KG	cmoB CDS
GTT	1387947	1387949	2 ATA -> GTT	Substitution	95 -> 96	97.9% -> 98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		I -> V	cmoB CDS
A	1387955	1387955	1 T -> A	SNP (transversion)	96	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		D -> E	cmoB CDS
GTT	1387962	1387964	2 ATC -> GTT	Substitution	94 -> 95	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		I -> V	cmoB CDS
C	1387966	1387966	1 A -> C	SNP (transversion)	91	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		E -> A	cmoB CDS
A	1387970	1387970	1 T -> A	SNP (transversion)	91	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
T	1387982	1387982	1 C -> T	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
CGT	1387986	1387988	2 AGG -> CGT	Substitution	92 -> 93	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
T	1387991	1387991	1 G -> T	SNP (transversion)	86	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
CATA	1387994	1387997	3 AGT -> CATA	Substitution	92 -> 94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		IV -> EI	cmoB CDS
G	1388009	1388009	1 A -> G	SNP (transition)	83	100.0%	7,8E-307	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
A	1388012	1388012	1 T -> A	SNP (transversion)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
C	1388027	1388027	1 T -> C	SNP (transition)	77	100.0%	6,8E-277	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
G	1388080	1388080	1 A -> G	SNP (transition)	77	100.0%	1,3E-284	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
C	1388042	1388042	1 T -> C	SNP (transition)	77	100.0%	1,3E-284	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
A	1388048	1388048	1 T -> A	SNP (transversion)	75	100.0%	3,2E-277	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoB CDS
C	1388562	1388562	1 T -> C	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			cmoC CDS
G	1389734	1389734	1 A -> G	SNP (transition)	106	98.1%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			hypothetical protein CDS
G	1391851	1391851	1 A -> G	SNP (transition)	93	98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		F -> S	Protoporphyrinogen IX oxidase CDS
A	1392767	1392767	1 G -> A	SNP (transition)	129	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			glmM CDS
G	1393072	1393072	1 A -> G	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			glmM CDS
G	1393477	1393477	1 A -> G	SNP (transition)	96	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		F -> L	glmM CDS
G	1394002	1394002	1 A -> G	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			mauG CDS
G	1394125	1394125	1 A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			mauG CDS
C	1394662	1394662	1 A -> C	SNP (transversion)	97	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			mauG CDS
A	1394825	1394824	0 (A)3 -> (A)4	Insertion (tandem repeat)	96	92.7%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
G	1395116	1395116	1 T -> G	SNP (transversion)	103	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		Y -> D	glyY CDS
C	1395289	1395289	1 T -> C	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			glyY CDS
A	1395701	1395701	1 G -> A	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		R -> K	Dihydroneopterin aldolase CDS
G	1398096	1398096	1 T -> G	SNP (transversion)	103	99.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		S -> A	Exopolyphosphatase CDS
C	1399217	1399217	1 T -> C	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			putative transmembrane protein CJ0352 CDS
G	1399701	1399701	1 A -> G	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			CheX domain-containing protein CDS
A	1400354	1400354	1 G -> A	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		L -> F	trpA CDS
G	1400588	1400588	1 A -> G	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			trpA CDS
G	1401010	1401010	1 A -> G	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			trpB CDS
C	1401061	1401061	1 T -> C	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			trpB CDS
C	1401082	1401082	1 T -> C	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			trpB CDS
T	1401385	1401385	1 C -> T	SNP (transition)	130	99.2%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			trpB CDS
C	1401823	1401823	1 G -> C	SNP (transversion)	88	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			trpB CDS
A	1402407	1402407	1 G -> A	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			N-(5'-phosphoribosyl)anthranilate isomerase CDS
A	1402888	1402888	1 G -> A	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			trpD CDS
G	1403564	1403564	1 A -> G	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		V -> A	trpD CDS
G	1403657	1403657	1 A -> G	SNP (transition)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		I -> T	trpD CDS
G	1404075	1404075	1 A -> G	SNP (transition)	88	98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			trpD CDS
G	1404881	1404881	1 A -> G	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			Anthranilate synthase component I family protein CDS
A	1405424	1405423	0 (A)6 -> (A)7	Insertion (tandem repeat)	89	98.9%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
G	1405765	1405765	1 A -> G	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		T -> A	putative membrane transporter protein CDS
C	1408713	1408713	1 T -> C	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			uvrA CDS
T	1408787	1408787	1 C -> T	SNP (transition)	110	99.1%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		A -> V	uvrA CDS
T	1409457	1409457	1 C -> T	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		T -> I	hypothetical protein CDS
GGGCTTTTAGCT	1409765	1409764	0 +GGGCTTTTAGCT	Insertion	77 -> 88	96.1% -> 96.6%	1,9E-27	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		-> GLLA	hypothetical protein CDS
A	1410749	1410749	1 G -> A	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss		A -> T	hypothetical protein CDS
G	1411343	1411343	1 A -> G	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			DedA family protein CDS
C	1411616	1411616	1 T -> C	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			DedA family protein CDS
G	1411742	1411742	1 A -> G	SNP (transition)	78	100.0%	1E-272	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			
A	1411859	1411855	1 G -> A	SNP (transition)	63	100.0%	7,9E-233	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			polA CDS
T	1411865	1411865	1 C -> T	SNP (transition)	75	100.0%	3,2E-277	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			polA CDS
T	1411913	1411913	1 C -> T	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			polA CDS
T	1411919	1411919	1 C -> T	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			polA CDS
C	1411958	1411958	1 T -> C	SNP (transition)	115	99.1%	0	Variants: BfR-CA-11057-TF156873_R	Concatemer BfR-CA-11057 - UniAss			polA CDS

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G	1412009	1412009	1 A -> G	SNP (transition)	104	84.6%	1E-227	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
T	1412042	1412042	1 C -> T	SNP (transition)	93	91.4%	3,2E-252	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
G	1412171	1412171	1 A -> G	SNP (transition)	127	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
G	1412384	1412384	1 A -> G	SNP (transition)	130	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
A	1412390	1412390	1 G -> A	SNP (transition)	131	99.2%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
C	1412396	1412396	1 T -> C	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
CTA	1412421	1412423	2 TTG -> CTA	Substitution	121 -> 122	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
A	1412426	1412426	1 G -> A	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
T	1412462	1412462	1 C -> T	SNP (transition)	134	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
T	1412529	1412529	1 C -> T	SNP (transition)	131	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
A	1412571	1412571	1 G -> A	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	V -> I	polA CDS
A	1412607	1412607	1 G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
GGGT	1412852	1412855	3 AAGC -> GGGT	Substitution	116	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	VS -> VG	polA CDS
G	1412858	1412858	1 A -> G	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
A	1412906	1412906	1 G -> A	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
T	1412990	1412990	1 C -> T	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
C	1413070	1413070	1 T -> C	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
G	1413128	1413128	1 A -> G	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
G	1413266	1413266	1 A -> G	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	I -> M	polA CDS
T	1413517	1413517	1 C -> T	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	A -> V	polA CDS
C	1413578	1413578	1 T -> C	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
T	1413593	1413593	1 C -> T	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
C	1413610	1413610	1 T -> C	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	L -> S	polA CDS
A	1413668	1413668	1 G -> A	SNP (transition)	92	97.8%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
T	1413710	1413710	1 C -> T	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
C	1413725	1413725	1 T -> C	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
A	1413732	1413732	1 G -> A	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	V -> I	polA CDS
T	1414103	1414103	1 C -> T	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
G	1414165	1414165	1 A -> G	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		polA CDS
A	1414239	1414239	1 G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	D -> N	polA CDS
T	1414988	1414988	1 C -> T	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		motA CDS
G	1414991	1414991	1 A -> G	SNP (transition)	115	99.1%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		motA CDS
G	1414997	1414997	1 A -> G	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		motA CDS
A	1415003	1415003	1 G -> A	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		motA CDS
T	1415006	1415006	1 A -> T	SNP (transversion)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		motA CDS
C	1415012	1415012	1 T -> C	SNP (transition)	86	97.7%	3,7E-290	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		motA CDS
T	1415015	1415015	1 C -> T	SNP (transition)	82	98.8%	2,1E-289	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		motA CDS
A	1415018	1415018	1 T -> A	SNP (transversion)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		motA CDS
C	1415171	1415171	1 T -> C	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		motA CDS
T	1415174	1415174	1 C -> T	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		motA CDS
T	1415274	1415274	1 C -> T	SNP (transition)	82	100.0%	6,3E-295	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		Flagellar motor protein MotB CDS
C	1415230	1415230	1 T -> C	SNP (transition)	83	97.6%	8,5E-288	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		Flagellar motor protein MotB CDS
C	1417038	1417038	1 T -> C	SNP (transition)	69	100.0%	3,2E-241	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	S -> G	fhiB CDS
G	1417538	1417538	1 A -> G	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss		ahpC CDS
	1418404	1418404	1 (A)5 -> (A)4	Deletion (tandem repeat)	82	97.6%	3,3E-244	Variants: BfR-CA-11057-TF15687-3_R	Concatemer BfR-CA-11057 - UniAss	M ->	ndk CDS
G	7037	7037	1 A -> G	SNP (transition)	68	100.0%	2,5E-251	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	T -> A	dnaN CDS
T	7042	7042	1 C -> T	SNP (transition)	67	100.0%	1,3E-247	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dnaN CDS
T	2141	2141	1 G -> T	SNP (transversion)	63	100.0%	1,6E-228	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dnaN CDS
T	2330	2330	1 C -> T	SNP (transition)	63	100.0%	1,6E-228	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dnaN CDS
C	2790	2790	1 T -> C	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
C	2799	2799	1 T -> C	SNP (transition)	104	99.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
T	2835	2835	1 A -> T	SNP (transversion)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
A	2922	2922	1 G -> A	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
C	2949	2949	1 T -> C	SNP (transition)	87	98.9%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
A	2974	2974	1 G -> A	SNP (transition)	87	98.9%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	V -> I	gyrB CDS
G	2982	2982	1 A -> G	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
C	3063	3063	1 T -> C	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
G	3819	3819	1 A -> G	SNP (transition)	82	98.8%	2,1E-289	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
A	3825	3825	1 G -> A	SNP (transition)	81	100.0%	2E-299	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
A	4035	4035	1 T -> A	SNP (transversion)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
T	4074	4074	1 G -> T	SNP (transversion)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
A	4080	4080	1 T -> A	SNP (transversion)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
A	4083	4083	1 T -> A	SNP (transversion)	85	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
T	4086	4086	1 C -> T	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
CTTG	4095	4098	3 TCTA -> CTTG	Substitution	81 -> 82	98.8%	7,5E-291	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
T	4821	4821	1 C -> T	SNP (transition)	82	100.0%	6,3E-299	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		gyrB CDS
C	5052	5052	1 G -> C	SNP (transversion)	69	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	5090	5089	0 (T)5 -> (T)6	Insertion (tandem repeat)	67	91.0%	2E-217	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	5103	5103	1 A -> C	SNP (transversion)	78	98.7%	4,9E-275	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
G	5129	5129	1 A -> G	SNP (transition)	78	98.7%	4,9E-275	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	5296	5296	1 C -> T	SNP (transition)	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> V	Transcriptional initiation protein Tat CDS
A	5437	5437	1 G -> A	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Transcriptional initiation protein Tat CDS
A	5437	5437	1 G -> A	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		putative p-cresol methylhydroxylase subunit CDS
C	5444	5444	1 A -> C	SNP (transversion)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	T -> P	putative p-cresol methylhydroxylase subunit CDS
T	5637	5637	1 C -> T	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> V	putative p-cresol methylhydroxylase subunit CDS
A	6048	6048	1 C -> A	SNP (transversion)	45	100.0%	1E-163	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
CAC	6051	6053	3 AGA -> CAC	Substitution	48 -> 55	100.0%	1,8E-172	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	6399	6399	1 G -> A	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	G -> E	putative p-cresol methylhydroxylase subunit CDS
C	6704	6704	1 T -> C	SNP (transition)	82	97.6%	3,3E-292	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	F -> S	Chain B, Stru CDS
	6882	6882	1 (A)7 -> (A)6	Deletion (tandem repeat)	103	94.2%	1,4E-281	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Cytochrome c CDS
CT	22604	22605	2 TC -> CT	Substitution	76 -> 77	94.8% -> 98.7%	2,1E-256	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	D -> S	dsbI CDS
CG	22608	22609	2 TT -> CG	Substitution	76 -> 77	94.7% -> 94.8%	6,1E-253	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	GK -> EE	dsbI CDS
C	22834	22834	1 T -> C	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
ATC	22864	22866	2 GTT -> ATC	Substitution	84 -> 85	98.8%	6,7E-305	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> D	dsbI CDS
A	22870	22870	1 G -> A	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
T	22891	22891	1 C -> T	SNP (transversion)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
A	22897	22897	1 G -> A	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
GA	22921	22922	2 TG -> GA	Substitution	74 -> 78	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	T -> I	dsbI CDS
A	22924	22924	1 G -> A	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
GTCA	22939	22942	3 ATTG -> GTCA	Substitution	90 -> 93	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	IN -> ID	dsbI CDS
C	22947	22947	1 T -> C	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	K -> E	dsbI CDS
A	22959	22959	1 C -> A	SNP (transversion)	88	98.9%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> S	dsbI CDS
A	22963	22963	1 G -> A	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
TG	22966	22967	2 GA -> TG	Substitution	88 -> 89	97.7% -> 97.8%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	I -> T	dsbI CDS
T	22971	22971	1 C -> T	SNP (transition)	85	98.8%	5,4E-300	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	D -> N	dsbI CDS
A	22987	22987	1 G -> A	SNP (transition)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
CAA	22990	22992	2 AAG -> CAA	Substitution	80 -> 82	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
C	23002	23002	1 T -> C	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
A	23038	23038	1 G -> A	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
C	23041	23041	1 T -> C	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		dsbI CDS
T	24185	24185	1 A -> T	SNP (transversion)	79	100.0%	4E-284	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
C	24212	24212	1 G -> T	SNP (transition)	78	100.0%	1,8E-280	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
T	24218	24218	1 G -> T	SNP (transversion)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
G	24224	24224	1 A -> G	SNP (transition)	79	100.0%	4E-284	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
A	24500	24500	1 G -> A	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
GC	24673	24674	2 AT -> GC	Substitution	91 -> 92	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
C	24710	24710	1 T -> C	SNP (transition)	82	100.0%	1,6E-278	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ygjM CDS
G	25001	25001	1 A -> G	SNP (transition)	73	100.0%	3,2E-255	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	25286	25286	1 T -> C	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
T	25408	25408	1 C -> T	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> K	RNA pseudouridylate synthase CDS
C	25469	25469	1 A -> C	SNP (transversion)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
T	25474	25474	1 C -> T	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> K	RNA pseudouridylate synthase CDS
A	25478	25478	1 T -> A	SNP (transversion)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
A	25489	25489	1 G -> A	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	H -> Y	RNA pseudouridylate synthase CDS
A	25526	25526	1 G -> A	SNP (transition)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
G	25538	25538	1 A -> G	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
G	25610	25610	1 A -> G	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
C	25691	25691	1 T -> C	SNP (transition)	86	100.0%	1E-303	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		RNA pseudouridylate synthase CDS
T	26306	26306	1 C -> T	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
A	26321	26321	1 G -> A	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
ACTT	26342	26345	3 GTTA -> ACTT	Substitution	73 -> 78	98.7% -> 100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
G	26348	26348	1 T -> G	SNP (transversion)	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
A	26369	26369	1 G -> A	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		purB CDS
T	27838	27838	1 C -> T	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	27892	27892	1 C -> T	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
C	27949	27949	1 T -> C	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
C	28003	28003	1 T -> C	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28015	28015	1 C -> T	SNP (transition)	78	97.4%	7,5E-270	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
C	28018	28018	1 T -> C	SNP (transition)	76	98.7%	2,4E-260	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
A	28024	28024	1 G -> A	SNP (transition)	76	97.4%	2,8E-255	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
GG	28135	28136	2 AA -> GG	Substitution	89	96.6%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	VS -> VG	mrdA CDS
C	28213	28213	1 T -> C	SNP (transition)	88	97.7%	5,6E-306	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28216	28216	1 C -> T	SNP (transition)	88	97.7%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28237	28237	1 G -> T	SNP (transversion)	98	98.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
G	28780	28780	1 T -> G	SNP (transversion)	122	99.2%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28816	28816	1 C -> T	SNP (transition)	171	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28822	28822	1 C -> T	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	32037	32037	1 C -> T	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		pyrG CDS
A	33736	33736	1 G -> A	SNP (transition)	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33748	33748	1 T -> C	SNP (transition)	77	100.0%	3,2E-268	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33751	33751	1 T -> C	SNP (transition)	77	98.7%	7,7E-264	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
T	33757	33757	1 C -> T	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33769	33769	1 T -> C	SNP (transition)	87	98.9%	2,2E-307	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
AA	36609	36609	1 G -> AA	Insertion	137 -> 139	92.7% -> 92.8%	4,7E-201	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	36624	36624	1 T -> C	SNP (transition)	149	100.0%	4E-238	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	36669	36669	1 T -> C	SNP (transition)	120	98.3%	2,6E-149	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
G	38113	38113	1 A -> G	SNP (transition)	106	100.0%	1,6E-31	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
G	40889	40889	1 T -> G	SNP (transversion)	93	100.0%	1,3E-27	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
G	41815	41815	1 T -> G	SNP (transversion)	74	100.0%	6,3E-22	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	42200	42200	1 G -> T	SNP (transversion)	107	99.1%	8,5E-30	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
AG	42203	42204	2 GA -> AG	Substitution	105 -> 108	97.1% -> 97.2%	6E-26	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	43128	43126	1 G -> A	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	T -> I	hypothetical protein CDS

G	48162	48162	1	A -> G	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Class I SAM-dependent DNA methyltransferase CDS
TTTG	461516	461519	3	AGTT -> TTTG	Substitution	62	80.6%	2,1E-127	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	NS -> QT	DUF115 domain-containing protein CDS
T	461526	461526	1	A -> T	SNP (transversion)	61	82.0%	4,1E-128	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	D -> E	DUF115 domain-containing protein CDS
C	461537	461537	1	T -> C	SNP (transition)	68	98.5%	1,1E-158	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> D	DUF115 domain-containing protein CDS
T	461547	461547	1	A -> T	SNP (transversion)	67	82.1%	5,7E-119	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	F -> L	DUF115 domain-containing protein CDS
A	533903	533903	1	T -> A	SNP (transversion)	85	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
GCG	533910	533912	2	ACA -> GCG	Substitution	75 -> 81	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	T -> A	uvrC CDS
T	533930	533930	1	C -> T	SNP (transition)	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	533933	533933	1	T -> A	SNP (transversion)	67	100.0%	1,3E-247	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	533936	533936	1	T -> A	SNP (transversion)	67	100.0%	6,3E-241	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	533945	533945	1	G -> A	SNP (transition)	60	100.0%	1E-221	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
G	533981	533981	1	A -> G	SNP (transition)	49	100.0%	5E-181	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
T	533987	533987	1	G -> T	SNP (transversion)	48	100.0%	1,6E-172	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
C	533999	533999	1	T -> C	SNP (transition)	58	100.0%	1,6E-208	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
G	534023	534023	1	A -> G	SNP (transition)	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	534044	534044	1	G -> A	SNP (transition)	63	100.0%	7,9E-233	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
AAT	534051	534053	2	GAA -> AAT	Substitution	63 -> 64	100.0%	7,9E-233	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> N	uvrC CDS
G	534065	534065	1	A -> G	SNP (transition)	64	100.0%	1,6E-236	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
T	534068	534068	1	C -> T	SNP (transition)	63	100.0%	7,9E-233	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	534074	534074	1	G -> A	SNP (transition)	63	100.0%	7,9E-233	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
T	534092	534092	1	A -> T	SNP (transversion)	67	100.0%	1,3E-247	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
T	534101	534101	1	C -> T	SNP (transition)	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
C	534107	534107	1	T -> C	SNP (transition)	66	98.5%	6,6E-232	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
C	534122	534122	1	T -> C	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	534134	534134	1	C -> A	SNP (transversion)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
T	534200	534200	1	C -> T	SNP (transition)	72	98.6%	1,4E-260	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
G	535091	535091	1	A -> G	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uvrC CDS
A	535179	535179	1	G -> A	SNP (transition)	64	100.0%	4E-230	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	D -> N	uvrC CDS
C	535746	535746	1	T -> C	SNP (transition)	65	100.0%	3,2E-240	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Putative membrane protein CDS
C	536112	536112	1	T -> C	SNP (transition)	76	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Putative membrane protein CDS
C	538264	538264	1	T -> C	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> D	hemE CDS
T	538297	538297	1	G -> T	SNP (transversion)	77	100.0%	1,3E-284	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	Q -> K	hemE CDS
G	539033	539033	1	A -> G	SNP (transition)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
	539103	539103	1	(T)8 -> (T)7	Deletion (tandem repeat)	82	98.8%	6,5E-249	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	539153	539153	1	C -> A	SNP (transversion)	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
TTTAGAAAATTTTTGATCATTT	539158	539157	0	+TTTAGAAAATTTTTGAT	Insertion	62 -> 69	98.4% -> 98.6%	4E-229	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	539211	539211	1	C -> T	SNP (transition)	53	100.0%	1,6E-190	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	539300	539300	1	T -> C	SNP (transition)	74	100.0%	2,5E-251	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	539555	539555	1	A -> T	SNP (transversion)	60	100.0%	1E-215	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> I	hypothetical protein CDS
A	539628	539628	1	G -> A	SNP (transition)	49	100.0%	4E-176	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
	539667	539669	3	-TTT	Deletion	57	100.0%	1E-170	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	PF -> P	hypothetical protein CDS
A	546556	546556	1	G -> A	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	T -> I	glyS CDS
T	546863	546863	1	C -> T	SNP (transition)	85	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> T	glyS CDS
A	546876	546876	1	G -> A	SNP (transition)	85	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		glyS CDS
C	547139	547139	1	T -> C	SNP (transition)	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	K -> E	glyS CDS
C	547308	547308	1	T -> C	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	547427	547427	1	T -> C	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	Q -> R	HAD family hydrolase CDS
T	547701	547701	1	C -> T	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> K	HAD family hydrolase CDS
C	548420	548420	1	T -> C	SNP (transition)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	I -> M	kch CDS
C	549972	549972	1	T -> C	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	K -> R	hspR CDS
A	905810	905810	1	G -> A	SNP (transition)	72	98.6%	1,8E-253	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> V	FtsX domain-containing protein CDS
A	906100	906100	1	G -> A	SNP (transition)	81	100.0%	2E-299	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		FtsX domain-containing protein CDS
G	906565	906565	1	A -> G	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		FtsX domain-containing protein CDS
C	906576	906576	1	G -> C	SNP (transversion)	79	98.7%	1,3E-278	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	L -> V	FtsX domain-containing protein CDS
C	906588	906588	1	T -> C	SNP (transition)	79	100.0%	4E-284	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> D	FtsX domain-containing protein CDS
G	906667	906667	1	A -> G	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		FtsX domain-containing protein CDS
T	906688	906688	1	C -> T	SNP (transition)	64	100.0%	4E-230	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		FtsX domain-containing protein CDS
G	906700	906700	1	A -> G	SNP (transition)	68	100.0%	2,5E-251	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		FtsX domain-containing protein CDS
C	906730	906730	1	T -> C	SNP (transition)	69	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		FtsX domain-containing protein CDS
G	906840	906840	1	A -> G	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
G	906852	906852	1	A -> G	SNP (transition)	67	100.0%	1,3E-247	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
G	906879	906879	1	A -> G	SNP (transition)	58	100.0%	1,6E-208	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
G	906885	906885	1	A -> G	SNP (transition)	63	100.0%	1,6E-226	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
T	906893	906893	1	C -> T	SNP (transition)	62	96.8%	1,9E-212	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> T	secA CDS
C	906921	906921	1	T -> C	SNP (transition)	52	100.0%	6,3E-187	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
C	906954	906954	1	T -> C	SNP (transition)	61	98.4%	6,1E-214	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
G	907998	907998	1	A -> G	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
C	908004	908004	1	T -> C	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
GCGC	908037	908040	3	TCTT -> GCGC	Substitution	81 -> 86	98.8%	1E-287	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
T	908043	908043	1	A -> T	SNP (transversion)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908046	908046	1	G -> A	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
T	908049	908049	1	C -> T	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
G	908052	908052	1	A -> G	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
C	908070	908070	1	T -> C	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908073	908073	1	T -> A	SNP (transversion)	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908082	908082	1	G -> A	SNP (transition)	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
G	908085	908085	1	T -> G	SNP (transversion)	71	100.0%	2,5E-255	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908094	908094	1	G -> A	SNP (transition)	76	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
C	908097	908097	1	T -> C	SNP (transition)	76	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908103	908103	1	G -> A	SNP (transition)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
G	908115	908115	1	A -> G	SNP (transition)	70	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
G	908139	908139	1	A -> G	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
AAG	908142	908144	2	CAA -> AAG	Substitution	68 -> 69	98.5% -> 98.6%	1,3E-247	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
T	908151	908151	1	C -> T	SNP (transition)	70	100.0%	1E-251	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
T	908157	908157	1	C -> T	SNP (transition)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908166	908166	1	G -> A	SNP (transition)	61	100.0%	2E-225	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908172	908172	1	G -> A	SNP (transition)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
C	908181	908181	1	A -> C	SNP (transversion)	58	100.0%	2,5E-214	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
T	908192	908192	1	C -> T	SNP (transition)	58	100.0%	2,5E-214	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	V -> I	secA CDS
A	908202	908202	1	G -> A	SNP (transition)	53	100.0%	1,6E-190	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908205	908205	1	G -> A	SNP (transition)	51	100.0%	2,5E-183	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908214	908214	1	G -> A	SNP (transition)	49	100.0%	4E-176	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
C	908226	908226	1	T -> C	SNP (transition)	50	100.0%	1E-184	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
T	908340	908340	1	C -> T	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
T	908346	908346	1	C -> T	SNP (transition)	79	100.0%	4E-284	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
CAA	908361	908363	2	AAG -> CAA	Substitution	84 -> 85	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908376	908376	1	T -> A	SNP (transversion)	89	98.9%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908379	908379	1	G -> A	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
T	908382	908382	1	A -> T	SNP (transversion)	88	97.7%	9,6E-306	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
T	908385	908385	1	C -> T	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
C	908397	908397	1	A -> C	SNP (transversion)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
T	908400	908400	1	C -> T	SNP (transition)	81	100.0%	2E-299	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908415	908415	1	G -> A	SNP (transition)	79	98.7%	2E-286	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908421	908421	1	T -> A	SNP (transversion)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908427	908427	1	G -> A	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
A	908438	908438	1	G -> A	SNP (transition)	82	100.0%	6,3E-295	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		secA CDS
C	909286	909286	1	T -> C	SNP (transition)	56	100.0%	2,5E-201	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> S	secA CDS
A	909291	909291	1	T -> A	SNP (transversion)	57	98.2%	5,7E-194	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	K -> N	secA CDS
G	909618	909618	1	A -> G	SNP (transition)	62	98.4%	2E-211	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> D	Outer membrane lipoprotein chaperone LolA CDS
AACC	909623	909626	3	GGCG -> AACC	Substitution	65 -> 67	96.9% -> 97.0%	7E-224	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	SA -> ST	Outer membrane lipoprotein chaperone LolA CDS
A	909632	909632	1	C -> A	SNP (transversion)	73	97.3%	6,6E-252	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Outer membrane lipoprotein chaperone LolA CDS
TC	909649	909650	2	CT -> TC	Substitution	68 -> 69	94.1% -> 94.2%	8,6E-228	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	T -> I	Outer membrane lipoprotein chaperone LolA CDS
A	910035	910035	1	G -> A	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	S -> L	Flagellar basal body-associated FliL family protein CDS
G	912967	912967	1	A -> G	SNP (transition)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> S	NlpC/P60 family CDS
T	913031	913031	1	C -> T	SNP (transition)	57	100.0%	3,2E-199	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		NlpC/P60 family CDS
T	913304	913304	1	C -> T	SNP (transition)	57	96.5%	5E-200	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		NlpC/P60 family CDS
T	913334	913334	1	C -> T	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		NlpC/P60 family CDS
T	913346	913346	1	C -> T	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		NlpC/P60 family CDS
G	913352	913352	1	A -> G	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		NlpC/P60 family CDS
C	913686	913686	1	T -> C	SNP (transition)	52	98.1%	2,1E-171	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		N-carbamoylputrescine amidohydrolase CDS
A	913824	913824	1	G -> A	SNP (transition)	85	98.8%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		N-carbamoylputrescine amidohydrolase CDS
T	913833	913833	1	C -> T	SNP (transition)	87	97.7%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		N-carbamoylputrescine amidohydrolase CDS
T	914001	914001	1	C -> T	SNP (transition)	75	98.7%	1,2E-271	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		N-carbamoylputrescine amidohydrolase CDS
G	914046	914046	1	A -> G	SNP (transition)	85	98.8%	3,4E-300	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		N-carbamoylputrescine amidohydrolase CDS
T	914157	914157	1	C -> T	SNP (transition)	62	100.0%	4E-229	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		N-carbamoylputrescine amidohydrolase CDS
G	914483	914483	1	A -> G	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		fieF CDS
G	914600	914600	1	A -> G	SNP (transition)	55	100.0%	3,2E-203	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		fieF CDS
T	914663	914663	1	C -> T	SNP (transition)	49	100.0%	5E-181	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		fieF CDS
C	914678	914678	1	T -> C	SNP (transition)	44	100.0%	4E-158	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		fieF CDS
A	914744	914744	1	G -> A	SNP (transition)	50	100.0%	1E-184	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		fieF CDS
T	915137	915137	1	C -> T	SNP (transition)	65	100.0%	3,2E-240	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		fieF CDS
A	915403	915403	1	G -> A	SNP (transition)	60	100.0%	1E-215	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Agamatine deiminase CDS
A	915814	915814	1	G -> A	SNP (transition)	52	100.0%	4E-192	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Agamatine deiminase CDS
G	915820	915820	1	A -> G	SNP (transition)	44	100.0%	1,6E-162	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Agamatine deiminase CDS
G	915841	915841	1	A -> G	SNP (transition)	43	100.0%	7,9E-159	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Agamatine deiminase CDS
T	915844	915844	1	C -> T	SNP (transition)	43	100.0%	1,6E-154	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Agamatine deiminase CDS
TG	916141	916142	2	AT -> TG	Substitution	61	98.4%	6,1E-214	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	D -> A	Agamatine deiminase CDS
G	916186	916186	1	A -> G	SNP (transition)	48	100.0%	1E-167	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Agamatine deiminase CDS
G	916258	916258	1	A -> G	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	916346	916346	1	G -> A	SNP (transition)	73	98.6%	4,6E-257	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	916421	916421	1	C -> T	SNP (transition)	60	98.3%	1,9E-204	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	S -> N	META domain-containing protein CDS
A	916609	916609	1	G -> A	SNP (transition)	74	98.6%	1,2E-260	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		META domain-containing protein CDS
C	916761	916761	1	T -> C	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	T -> A	META domain-containing protein CDS
C	916927	916927	1	T -> C	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	I -> M	HAMP domain-containing protein CDS
C	917001	917001	1	T -> C	SNP (transition)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> D	HAMP domain-containing protein CDS
C	917092	917092	1	T -> C	SNP (transition)	64	98.4%	5,1E-231	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		HAMP domain-containing protein CDS
C	917100	917100	1	T -> C	SNP (transition)	76	100.0%	2,5E-273	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	T -> A	HAMP domain-containing protein CDS
G	917269	917269	1	A -> G	SNP (transition)	74	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		HAMP domain-containing protein CDS
A	917351	917351	1	G -> A	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> V	HAMP domain-containing protein CDS
A	917356	917356	1	G -> A	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		HAMP domain-containing protein CDS
C	917833	917833	1	T -> C	SNP (transition)	76	100.0%	2,5E-273	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		HAMP domain-containing protein CDS
T	918802	918802	1	C -> T	SNP (transition)	82	100.0%	6,3E-295	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> T	purH CDS

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G	918820	918820	1 T -> G	SNP (transversion)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	I -> L	purH CDS
T	919046	919046	1 G -> T	SNP (transversion)	78	100.0%	1.6E-280	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purH CDS
T	919309	919309	1 C -> T	SNP (transition)	68	100.0%	1.6E-244	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	E -> K	purH CDS
T	919896	919896	1 C -> T	SNP (transition)	62	100.0%	6.3E-223	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	G -> E	purH CDS
T	920093	920092	0 (T)6 -> (T)7	Insertion (tandem repeat)	70	98.6%	3.5E-253	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		
G	920142	920142	1 A -> G	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	L -> S	DnaJ family molecular chaperone CDS
A	920148	920148	1 G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	H -> Y	DnaJ family molecular chaperone CDS
G	920740	920740	1 A -> G	SNP (transition)	72	100.0%	6.3E-259	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	C -> R	DnaJ family molecular chaperone CDS
G	920753	920753	1 A -> G	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		DnaJ family molecular chaperone CDS
A	920786	920786	1 G -> A	SNP (transition)	81	100.0%	2.5E-291	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		DnaJ family molecular chaperone CDS
A	921199	921199	1 G -> A	SNP (transition)	51	100.0%	2E-188	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
CT	921263	921264	2 GC -> CT	Substitution	59	100.0%	5E-218	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	A -> R	purL CDS
G	921292	921292	1 A -> G	SNP (transition)	64	100.0%	4E-230	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
G	921460	921460	1 A -> G	SNP (transition)	54	100.0%	1E-188	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
G	921913	921913	1 A -> G	SNP (transition)	84	98.8%	1.3E-296	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
T	927780	927780	1 C -> T	SNP (transition)	75	98.7%	1.2E-271	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
C	927792	927792	1 T -> C	SNP (transition)	67	98.5%	1.7E-235	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
T	922804	922804	1 G -> T	SNP (transversion)	59	100.0%	5E-218	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
A	922810	922810	1 G -> A	SNP (transition)	63	98.4%	6.3E-215	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
T	922834	922834	1 C -> T	SNP (transition)	60	100.0%	1E-215	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
G	922843	922843	1 T -> G	SNP (transversion)	57	100.0%	3.2E-199	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
G	922852	922852	1 A -> G	SNP (transition)	61	100.0%	2.5E-219	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
A	922858	922858	1 C -> A	SNP (transversion)	65	100.0%	3.2E-227	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
T	922861	922861	1 A -> T	SNP (transversion)	63	100.0%	1.6E-228	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
TG	922866	922867	2 CA -> TG	Substitution	61	100.0%	2.5E-219	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	ID -> IN	purL CDS
A	922879	922879	1 G -> A	SNP (transition)	57	100.0%	6.3E-205	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
A	922885	922885	1 T -> A	SNP (transversion)	49	100.0%	5E-183	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
C	922891	922891	1 G -> C	SNP (transversion)	50	100.0%	1E-174	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
A	927909	927909	1 T -> A	SNP (transversion)	50	100.0%	1E-174	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
T	922915	922915	1 A -> T	SNP (transition)	50	100.0%	1E-174	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
G	922930	922930	1 A -> G	SNP (transition)	54	100.0%	4E-194	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
A	922957	922957	1 G -> A	SNP (transition)	58	100.0%	1E-202	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
G	922984	922984	1 A -> G	SNP (transition)	56	100.0%	6.3E-207	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
A	927987	927987	1 C -> A	SNP (transversion)	61	100.0%	2.5E-219	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
T	927990	927990	1 A -> T	SNP (transversion)	61	100.0%	2E-225	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
AAG	922998	922998	2 TAA -> AAG	Substitution	64	100.0%	1.8E-238	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
A	923011	923011	1 G -> A	SNP (transition)	55	100.0%	3.2E-203	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
C	923014	923014	1 T -> C	SNP (transition)	54	100.0%	1E-188	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
T	923029	923029	1 A -> T	SNP (transversion)	53	100.0%	7.9E-196	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
T	923036	923036	1 G -> T	SNP (transversion)	59	100.0%	5E-218	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	A -> E	purL CDS
C	923044	923044	1 T -> C	SNP (transition)	62	100.0%	4E-275	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
G	923050	923050	1 A -> G	SNP (transition)	60	100.0%	1E-221	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
T	923071	923071	1 G -> T	SNP (transversion)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		purL CDS
G	923135	923135	1 A -> G	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	923183	923183	1 G -> A	SNP (transition)	70	98.6%	2.8E-246	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
G	923194	923194	1 A -> G	SNP (transition)	62	100.0%	6.3E-223	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
T	923503	923503	1 C -> T	SNP (transition)	76	98.1%	5.6E-265	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	D -> N	trmE CDS
G	923516	923516	1 A -> G	SNP (transition)	77	100.0%	6.3E-277	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	923564	923564	1 G -> A	SNP (transition)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
G	923588	923588	1 A -> G	SNP (transition)	70	98.6%	3.5E-253	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
T	923591	923591	1 C -> T	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
G	923602	923602	1 A -> G	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
C	923676	923676	1 T -> C	SNP (transition)	79	100.0%	4E-284	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	I -> V	trmE CDS
A	923638	923638	1 G -> A	SNP (transition)	81	98.8%	8.1E-294	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
CAAC	923648	923651	3 TAGT -> CAAC	Substitution	82 -> 86	98.8%	3.2E-283	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
C	923663	923663	1 T -> C	SNP (transition)	87	98.9%	2.2E-307	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	923669	923669	1 G -> A	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
T	923723	923723	1 C -> T	SNP (transition)	73	100.0%	7.9E-270	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	923726	923726	1 G -> A	SNP (transition)	70	100.0%	3E-253	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
C	923839	923839	1 T -> C	SNP (transition)	78	100.0%	1.6E-280	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	K -> E	trmE CDS
G	923852	923852	1 A -> G	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
AC	923875	923875	2 GT -> AC	Substitution	70 -> 71	100.0%	1E-258	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
T	923888	923888	1 C -> T	SNP (transition)	68	100.0%	2.5E-251	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
G	923912	923912	1 A -> G	SNP (transition)	55	100.0%	1E-197	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
C	923939	923939	1 T -> C	SNP (transition)	52	100.0%	4E-192	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	923951	923951	1 G -> A	SNP (transition)	52	100.0%	4E-192	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	923972	923972	1 T -> A	SNP (transversion)	57	100.0%	6.3E-205	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
T	923975	923975	1 C -> T	SNP (transition)	55	100.0%	3.2E-203	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
T	924056	924056	1 C -> T	SNP (transition)	59	100.0%	4E-212	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	924062	924062	1 G -> A	SNP (transition)	59	100.0%	3.2E-208	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
TT	924077	924078	2 CC -> TT	Substitution	57	100.0%	1.3E-210	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	R -> K	trmE CDS
G	924083	924083	1 A -> G	SNP (transition)	57	100.0%	1.3E-210	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
G	924095	924095	1 A -> G	SNP (transition)	53	100.0%	1.6E-190	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	924098	924098	1 G -> A	SNP (transition)	54	100.0%	1.6E-198	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	924113	924113	1 T -> A	SNP (transversion)	56	100.0%	6.3E-207	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
CAA	924116	924118	2 TAG -> CAA	Substitution	54 -> 56	100.0%	4E-194	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
T	924140	924140	1 C -> T	SNP (transition)	50	100.0%	1E-179	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
T	924149	924149	1 C -> T	SNP (transition)	55	100.0%	3.2E-203	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	924221	924221	1 G -> A	SNP (transition)	49	100.0%	5E-183	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	924233	924233	1 G -> A	SNP (transition)	54	98.1%	4.3E-194	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	924239	924239	1 T -> A	SNP (transversion)	58	100.0%	4E-212	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	924242	924242	1 G -> A	SNP (transition)	59	100.0%	4E-212	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
A	924254	924254	1 G -> A	SNP (transition)	57	98.2%	1.4E-199	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
C	924281	924281	1 T -> C	SNP (transition)	67	100.0%	6.3E-241	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
T	924287	924287	1 A -> T	SNP (transversion)	68	100.0%	1.6E-244	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		trmE CDS
G	926021	926021	1 A -> G	SNP (transition)	67	98.5%	4.2E-242	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	V -> A	ydC CDS
C	926040	926040	1 T -> C	SNP (transition)	76	100.0%	2.5E-273	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	N -> D	ydC CDS
C	926351	926351	1 T -> C	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	D -> G	ydC CDS
T	927784	927784	1 C -> T	SNP (transition)	55	100.0%	3.2E-203	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		
A	1028995	1028995	1 G -> A	SNP (transition)	65	100.0%	3.2E-240	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	S -> N	DL-methionine ABC transporter: MetINQ, substrate-binding p
G	1029015	1029015	1 A -> G	SNP (transition)	58	100.0%	1.6E-208	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	N -> D	DL-methionine ABC transporter: MetINQ, substrate-binding p
T	1029122	1029122	1 C -> T	SNP (transition)	57	100.0%	6.3E-205	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		DL-methionine ABC transporter: MetINQ, substrate-binding p
A	1029394	1029394	1 G -> A	SNP (transition)	60	100.0%	1E-221	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		
T	1029442	1029442	1 C -> T	SNP (transition)	59	100.0%	5E-218	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1029517	1029517	1 T -> C	SNP (transition)	58	100.0%	2.5E-214	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
CC	1029541	1029545	2 TT -> CC	Substitution	52 -> 57	100.0%	4E-192	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1029550	1029550	1 T -> C	SNP (transition)	56	100.0%	2.5E-201	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1029556	1029556	1 T -> C	SNP (transition)	55	100.0%	1E-197	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029559	1029559	1 C -> T	SNP (transition)	52	100.0%	6.3E-187	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
A	1029627	1029627	1 G -> A	SNP (transition)	50	98.0%	2E-174	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029748	1029748	1 C -> T	SNP (transition)	67	100.0%	6.3E-241	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029757	1029757	1 C -> T	SNP (transition)	62	100.0%	4E-220	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
G	1029760	1029760	1 A -> G	SNP (transition)	62	100.0%	4E-229	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029769	1029769	1 C -> T	SNP (transition)	62	98.4%	1.2E-223	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
GG	1029777	1029778	2 AA -> GG	Substitution	64	100.0%	4E-230	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	K -> R	flgA CDS
T	1029790	1029790	1 C -> T	SNP (transition)	66	100.0%	6.3E-244	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1029901	1029901	1 C -> T	SNP (transition)	75	97.3%	4.4E-253	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
ATC	1029914	1029916	2 GTT -> ATC	Substitution	78	98.7%	7.6E-268	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	V -> I	flgA CDS
C	1029922	1029922	1 T -> C	SNP (transition)	74	98.6%	1.2E-260	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
G	1029943	1029943	1 A -> G	SNP (transition)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
C	1030030	1030030	1 T -> C	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		flgA CDS
T	1030264	1030264	1 G -> T	SNP (transversion)	129	100.0%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	A -> S	3-octaprenyl-4-hydroxybenzoate carboxy-lyase CDS
A	1030581	1030581	1 G -> A	SNP (transition)	76	100.0%	6.3E-281	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		3-octaprenyl-4-hydroxybenzoate carboxy-lyase CDS
G	1030821	1030821	1 A -> G	SNP (transition)	85	97.6%	2.8E-303	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		coaD CDS
G	1032161	1032161	1 A -> G	SNP (transition)	77	100.0%	3.2E-269	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	S -> G	hisS CDS
T	1032172	1032172	1 C -> T	SNP (transition)	76	100.0%	6.3E-281	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
AG	1032227	1032228	2 GA -> AG	Substitution	81	100.0%	2.5E-291	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	E -> R	hisS CDS
G	1032244	1032244	1 A -> G	SNP (transition)	85	100.0%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032250	1032250	1 T -> C	SNP (transition)	83	100.0%	1.8E-298	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032265	1032265	1 C -> T	SNP (transition)	91	98.9%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032304	1032304	1 C -> T	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032307	1032307	1 T -> C	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
A	1032310	1032310	1 G -> A	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
GC	1032375	1032376	2 AT -> GC	Substitution	80	100.0%	1E-287	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	EY -> EH	hisS CDS
G	1032355	1032355	1 A -> G	SNP (transition)	71	100.0%	2.5E-255	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1032361	1032361	1 A -> G	SNP (transition)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032376	1032376	1 T -> C	SNP (transition)	72	100.0%	6.3E-259	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1032400	1032400	1 A -> G	SNP (transition)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032466	1032466	1 C -> T	SNP (transition)	81	97.5%	1.3E-280	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1032523	1032523	1 A -> G	SNP (transition)	62	100.0%	6.3E-223	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032526	1032526	1 C -> T	SNP (transition)	59	100.0%	5E-218	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
T	1032529	1032529	1 C -> T	SNP (transition)	57	100.0%	1.3E-210	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
C	1032532	1032532	1 T -> C	SNP (transition)	59	100.0%	4E-212	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hisS CDS
G	1038237	1038237	1 A -> G	SNP (transition)	58	100.0%	4E-212	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	I -> T	MBL fold metallo-hydrolase CDS
G	1038273	1038273	1 A -> G	SNP (transition)	53	100.0%	7.9E-196	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		
A	1040375	1040375	1 G -> A	SNP (transition)	70	98.6%	3.5E-253	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		dnaK CDS
T	1042179	1042179	1 C -> T	SNP (transition)	81	98.8%	8.1E-294	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042182	1042182	1 G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
AC	1042187	1042188	2 GT -> AC	Substitution	88	98.9%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
T	1042191	1042191	1 C -> T	SNP (transition)	88	98.9%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
C	1042194	1042194	1 T -> C	SNP (transition)	88	98.9%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042208	1042208	1 A -> G	SNP (transition)	83	100.0%	7.9E-307	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042218	1042218	1 A -> G	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042221	1042221	1 G -> A	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
T	1042233	1042233	1 C -> T	SNP (transition)	97	99.0%	0	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
C	1042249	1042249	1 T -> C	SNP (transition)	78	100.0%	2.5E-288	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss	N -> S	hrcA CDS
A	1042293	1042293	1 G -> A	SNP (transition)	73	100.0%	1.6E-262	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042371	1042371	1 G -> A	SNP (transition)	71	100.0%	2.5E-255	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042431	1042431	1 A -> G	SNP (transition)	70	100.0%	1E-251	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042479	1042479	1 A -> G	SNP (transition)	57	100.0%	1.3E-210	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		
T	1042488	1042488	1 C -> T	SNP (transition)	61	100.0%	2E-225	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		
A	1042490	1042490	1 T -> A	SNP (transversion)	64	100.0%	1.6E-236	Variants: BfR-CA-11057-TF156874-A_R	Concatemer BfR-CA-11057 - UniAss		

G	1042492	1042492	1	T -> G	SNP (transversion)	67	100.0%	6,3E-241	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
AG	1042520	1042521	2	TA -> AG	Substitution	61 -> 71	100.0%	2E-225	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	1042591	1042591	1	A -> T	SNP (transversion)	77	100.0%	1,3E-284	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	1042596	1042596	1	G -> A	SNP (transition)	79	98.7%	2E-286	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	1042608	1042608	1	G -> A	SNP (transition)	77	100.0%	1,3E-284	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
G	1042632	1042632	1	A -> G	SNP (transition)	76	98.7%	7,6E-268	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	1042634	1042634	1	C -> A	SNP (transversion)	76	98.7%	7,6E-268	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	1042638	1042638	1	C -> A	SNP (transversion)	67	98.5%	4,2E-242	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1042642	1042642	1	T -> C	SNP (transition)	59	98.3%	1,5E-212	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
GT	1042650	1042651	2	AA -> GT	Substitution	59	98.3%	9,3E-207	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
ACAG	1042654	1042657	4	TGCA -> ACAG	Substitution	55 -> 58	96.4% -> 96.6%	2,4E-187	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
G	1042659	1042658	0	+G	Insertion	48	95.8%	7,1E-167	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	1042687	1042687	1	T -> A	SNP (transversion)	47	97.9%	3E-168	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	1042690	1042690	1	A -> T	SNP (transversion)	51	80.4%	4E-133	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1042692	1042692	1	T -> C	SNP (transition)	50	80.0%	1E-133	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1042729	1042729	1	T -> C	SNP (transition)	56	94.6%	2,2E-191	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
AC	1042750	1042751	2	GA -> AC	Substitution	55	98.2%	8,7E-198	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1042763	1042763	1	T -> C	SNP (transition)	58	96.6%	1E-203	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	1042765	1042765	1	C -> T	SNP (transition)	58	98.3%	7,3E-209	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
AC	1042784	1042785	2	GT -> AC	Substitution	62	100.0%	4E-229	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> S	cfrA CDS
A	1042793	1042793	1	G -> A	SNP (transition)	65	100.0%	3,2E-240	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042796	1042796	1	A -> G	SNP (transition)	65	98.5%	1E-234	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1042805	1042805	1	C -> T	SNP (transition)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	M -> I	cfrA CDS
A	1042829	1042829	1	G -> A	SNP (transition)	67	100.0%	1,3E-247	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042832	1042832	1	A -> G	SNP (transition)	67	100.0%	1,3E-247	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042835	1042835	1	G -> A	SNP (transition)	67	100.0%	6,3E-241	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042841	1042841	1	T -> G	SNP (transversion)	63	100.0%	1,6E-226	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
AG	1042850	1042851	2	GC -> AG	Substitution	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	S -> T	cfrA CDS
GT	1042854	1042855	2	CC -> GT	Substitution	70 -> 72	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	G -> T	cfrA CDS
CGCT	1042858	1042861	3	TCCC -> CGCT	Substitution	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	GS -> SG	cfrA CDS
T	1042863	1042863	1	C -> T	SNP (transition)	67	100.0%	1,3E-247	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	S -> N	cfrA CDS
TG	1042866	1042867	2	GC -> TG	Substitution	66 -> 67	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> Q	cfrA CDS
A	1042880	1042880	1	G -> A	SNP (transition)	83	98.8%	5,2E-293	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042885	1042885	1	T -> C	SNP (transition)	84	98.8%	6,7E-305	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> D	cfrA CDS
A	1042892	1042892	1	G -> A	SNP (transition)	84	98.8%	1,3E-296	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1042900	1042900	1	C -> T	SNP (transition)	82	98.8%	1,6E-297	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	D -> N	cfrA CDS
G	1042922	1042922	1	A -> G	SNP (transition)	92	98.9%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042937	1042937	1	T -> C	SNP (transition)	101	99.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042940	1042940	1	G -> A	SNP (transition)	99	99.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042964	1042964	1	G -> A	SNP (transition)	105	99.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042985	1042985	1	G -> A	SNP (transition)	110	99.1%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042994	1042994	1	T -> C	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043000	1043000	1	G -> T	SNP (transversion)	95	98.9%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043087	1043087	1	T -> C	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043093	1043093	1	G -> A	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043099	1043099	1	G -> A	SNP (transition)	76	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043258	1043258	1	G -> A	SNP (transition)	79	98.7%	2E-286	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
TC	1043267	1043268	2	CT -> TC	Substitution	82	98.8%	1,6E-297	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	K -> R	cfrA CDS
G	1043271	1043271	1	A -> G	SNP (transition)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	F -> S	cfrA CDS
C	1043584	1043584	1	G -> C	SNP (transversion)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	L -> V	cfrA CDS
CAA	1043648	1043650	2	AAG -> CAA	Substitution	71 -> 73	100.0%	2E-262	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GTT	1043657	1043659	2	ATC -> GTT	Substitution	74 -> 76	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	D -> N	cfrA CDS
G	1043669	1043669	1	A -> G	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043672	1043672	1	A -> G	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043690	1043690	1	A -> T	SNP (transversion)	68	100.0%	2,5E-251	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043717	1043717	1	A -> G	SNP (transition)	77	100.0%	1,3E-284	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043720	1043720	1	A -> C	SNP (transversion)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043724	1043724	1	C -> T	SNP (transition)	75	98.7%	3E-264	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	S -> N	cfrA CDS
A	1043765	1043765	1	G -> A	SNP (transition)	82	98.8%	2,6E-281	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043769	1043769	1	A -> G	SNP (transition)	82	98.8%	1,6E-297	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	V -> A	cfrA CDS
C	1043774	1043774	1	T -> C	SNP (transition)	82	100.0%	6,3E-295	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
CAA	1043792	1043794	2	TAG -> CAA	Substitution	79	98.7%	7,9E-271	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043801	1043801	1	A -> G	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043861	1043861	1	C -> T	SNP (transition)	69	100.0%	5E-255	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043867	1043867	1	T -> C	SNP (transition)	70	100.0%	1E-251	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
TGC	1043870	1043872	2	AGA -> TGC	Substitution	60 -> 71	98.6%	1,6E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	S -> A	cfrA CDS
T	1043876	1043876	1	C -> T	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043882	1043882	1	G -> A	SNP (transition)	78	100.0%	1E-272	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043891	1043891	1	G -> A	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043896	1043896	1	C -> T	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	D -> N	cfrA CDS
T	1043903	1043903	1	C -> T	SNP (transition)	82	100.0%	6,3E-295	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043912	1043912	1	A -> G	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GTC	1043922	1043924	3	CCA -> GTC	Substitution	78	98.7%	1,6E-280	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	SG -> ST	cfrA CDS
G	1043927	1043927	1	A -> G	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043930	1043930	1	G -> A	SNP (transition)	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043966	1043966	1	A -> G	SNP (transition)	70	98.6%	3,5E-253	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043999	1043999	1	T -> C	SNP (transition)	63	100.0%	3,2E-220	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044005	1044005	1	A -> G	SNP (transition)	64	98.4%	1E-224	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044024	1044024	1	G -> T	SNP (transversion)	69	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	P -> Q	cfrA CDS
A	1044029	1044029	1	T -> A	SNP (transversion)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	R -> S	cfrA CDS
G	1044044	1044044	1	A -> G	SNP (transition)	64	100.0%	1,6E-236	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044047	1044047	1	A -> G	SNP (transition)	64	98.4%	5,1E-231	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044074	1044074	1	G -> A	SNP (transition)	70	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044110	1044110	1	A -> G	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1044128	1044128	1	T -> C	SNP (transition)	74	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044155	1044155	1	G -> A	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044191	1044191	1	C -> T	SNP (transition)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044314	1044314	1	C -> T	SNP (transition)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044662	1044662	1	A -> G	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044720	1044720	1	C -> G	SNP (transversion)	59	100.0%	5E-218	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	S -> T	cfrA CDS
G	1044722	1044722	1	A -> G	SNP (transition)	58	100.0%	1,6E-208	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GGT	1044761	1044763	2	AGC -> GGT	Substitution	52	100.0%	6,3E-187	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> T	cfrA CDS
G	1044767	1044767	1	T -> G	SNP (transversion)	53	100.0%	3,2E-185	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1044781	1044781	1	T -> C	SNP (transition)	49	98.0%	1,2E-175	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	I -> V	cfrA CDS
T	1044785	1044785	1	C -> T	SNP (transition)	46	97.8%	4,6E-160	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044788	1044788	1	A -> G	SNP (transition)	47	97.9%	3E-168	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044791	1044791	1	G -> A	SNP (transition)	48	97.9%	3E-167	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044797	1044797	1	C -> T	SNP (transition)	47	97.9%	4,7E-159	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044815	1044815	1	A -> G	SNP (transition)	41	100.0%	2,5E-147	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044821	1044821	1	A -> G	SNP (transition)	41	100.0%	3,2E-143	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GCTT	1044824	1044827	4	AGCC -> GCTT	Substitution	47 -> 49	91.5% -> 91.8%	5,6E-145	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	LA -> LS	cfrA CDS
G	1044830	1044830	1	A -> G	SNP (transition)	48	93.8%	5,5E-162	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044833	1044833	1	G -> A	SNP (transition)	47	100.0%	6,3E-169	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044842	1044842	1	A -> G	SNP (transition)	40	100.0%	1E-143	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044848	1044848	1	C -> T	SNP (transition)	41	100.0%	2E-151	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044859	1044859	1	A -> T	SNP (transversion)	42	100.0%	4E-155	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	L -> I	cfrA CDS
T	1044863	1044863	1	C -> T	SNP (transition)	41	100.0%	2E-151	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044903	1044903	1	G -> A	SNP (transition)	43	100.0%	1,6E-154	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
G	1048319	1048319	1	A -> G	SNP (transition)	103	100.0%	1,3E-30	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
	1048539	1048539	1	(T)7 -> (T)6	Deletion (tandem repeat)	95	100.0%	3,2E-09	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
CT	1048758	1048759	2	TC -> CT	Substitution	95 -> 101	99.0% -> 100.0%	3,2E-28	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	1048762	1048762	1	C -> A	SNP (transversion)	100	100.0%	1E-29	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1049147	1049147	1	A -> C	SNP (transversion)	81	100.0%	5E-24	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1050073	1050073	1	A -> C	SNP (transversion)	83	100.0%	1,3E-24	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1052849	1052849	1	T -> C	SNP (transition)	89	100.0%	2E-26	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1056828	1056828	1	T -> C	SNP (transition)	58	98.3%	3,7E-203	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> G	ccmA CDS
C	1058557	1058557	1	T -> C	SNP (transition)	60	100.0%	1E-215	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	I -> V	Putative ABC transport system permease CDS
T	1058795	1058795	1	G -> T	SNP (transversion)	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Putative ABC transport system permease CDS
T	1058819	1058819	1	C -> T	SNP (transition)	63	100.0%	7,9E-233	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	R -> K	ataC CDS
T	1058880	1058880	1	C -> T	SNP (transition)	66	100.0%	2,5E-237	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	V -> I	ataC CDS
G	1058884	1058884	1	A -> G	SNP (transition)	64	100.0%	4E-230	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1058971	1058971	1	G -> A	SNP (transition)	71	100.0%	2E-262	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059022	1059022	1	A -> G	SNP (transition)	70	100.0%	1E-251	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059106	1059106	1	G -> A	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059154	1059154	1	G -> A	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059162	1059162	1	A -> G	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	F -> L	ataC CDS
T	1059259	1059259	1	C -> T	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059283	1059283	1	A -> G	SNP (transition)	84	98.8%	2,7E-288	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059487	1059487	1	A -> G	SNP (transition)	71	100.0%	2,5E-255	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
C	1059541	1059541	1	T -> C	SNP (transition)	65	100.0%	3,2E-240	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
CA	1059570	1059571	2	TG -> CA	Substitution	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	ST -> SA	ataC CDS
G	1059624	1059624	1	A -> G	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1059660	1059660	1	C -> T	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1059675	1059675	1	C -> T	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1059897	1059897	1	A -> G	SNP (transition)	68	98.5%	4,3E-239	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1059915	1059915	1	A -> G	SNP (transition)	62	96.8%	1,9E-212	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1059961	1059961	1	G -> A	SNP (transition)	59	100.0%	4E-212	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> V	Phytase-like domain-containing protein CDS
G	1059973	1059973	1	A -> G	SNP (transition)	60	100.0%	1E-215	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	I -> T	Phytase-like domain-containing protein CDS
C	1060048	1060048	1	T -> C	SNP (transition)	66	98.5%	6,6E-232	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> S	Phytase-like domain-containing protein CDS
G	1060134	1060134	1	A -> G	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1060458	1060458	1	G -> A	SNP (transition)	71	100.0%	2,5E-255	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1060491	1060491	1	G -> T	SNP (transversion)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1060503	1060503	1	A -> G	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1060557	1060557	1	G -> A	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1060596	1060596	1	A -> G	SNP (transition)	86	100.0%	1E-300	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1060641	1060641	1	C -> T	SNP (transition)	75	98.7%	3E-264	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1132278	1132278	1	C -> T	SNP (transition)	61	100.0%	2E-225	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> K	Ribosomal RNA small subunit methyltransferase B CDS
C	1136546	1136546	1	T -> C	SNP (transition)	88	98.9%	2,8E-302	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		vacB CDS
A	1136552	1136552	1	T -> A	SNP (transversion)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		vacB CDS
A	1136564	1136564	1	T -> A	SNP (transversion)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		vacB CDS
GC	1142477	1142478	2	AG -> GC	Substitution	62	98.4%	1,6E-217	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	T -> S	hypF CDS
C	1144646	1144646	1	T -> C	SNP (transition)	70	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	T -> A	hypothetical protein CDS

T	1145178	1145178	1	C -> T	SNP (transition)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1321877	1321877	1	A -> G	SNP (transition)	98	100.0%	4E-29	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
	1322097	1322097	1	(T)7 -> (T)6	Deletion (tandem repeat)	102	98.0%	0,00000024	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
CT	1322316	1322317	2	TC -> CT	Substitution	77 -> 82	94.8% -> 95.1%	1,1E-16	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	1322320	1322320	1	C -> A	SNP (transversion)	75	100.0%	3,2E-22	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1322705	1322705	1	A -> C	SNP (transversion)	81	100.0%	5E-24	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1323631	1323631	1	A -> C	SNP (transversion)	97	100.0%	7,9E-29	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1326407	1326407	1	T -> C	SNP (transition)	68	98.5%	2,7E-18	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
G	1327851	1327851	1	A -> G	SNP (transition)	88	100.0%	6,3E-35	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
G	1327896	1327896	1	A -> G	SNP (transition)	54	96.3%	5,1E-28	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	1327911	1327911	1	C -> T	SNP (transition)	40	97.5%	1,6E-25	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	1329416	1329416	1	G -> T	SNP (transversion)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> D	Methyl-accepting chemotaxis protein CDS
A	1329562	1329562	1	G -> A	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Methyl-accepting chemotaxis protein CDS
T	1329774	1329774	1	C -> T	SNP (transition)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> K	Methyl-accepting chemotaxis protein CDS
A	1330823	1330823	1	G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		PMT-2 domain-containing protein CDS
G	1330927	1330927	1	A -> G	SNP (transition)	76	100.0%	2,5E-273	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	F -> L	PMT-2 domain-containing protein CDS
G	1334002	1334002	1	A -> G	SNP (transition)	87	98.9%	8,7E-299	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334026	1334026	1	C -> T	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
C	1334029	1334029	1	T -> C	SNP (transition)	78	96.2%	2,4E-257	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
A	1334035	1334035	1	G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334044	1334044	1	A -> T	SNP (transversion)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
A	1334047	1334047	1	G -> A	SNP (transition)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334053	1334053	1	A -> T	SNP (transversion)	84	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
CTT	1334057	1334059	3	GCA -> CTT	Substitution	90 -> 91	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	IA -> IS	uup CDS
G	1334067	1334067	1	T -> G	SNP (transversion)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> H	uup CDS
G	1334071	1334071	1	A -> G	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334080	1334080	1	A -> T	SNP (transversion)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334083	1334083	1	C -> T	SNP (transition)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
ACTT	1334089	1334092	4	TGAC -> ACTT	Substitution	83 -> 86	96.4% -> 96.5%	1,5E-298	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
C	1334098	1334098	1	T -> C	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
C	1334110	1334110	1	A -> C	SNP (transversion)	86	100.0%	1E-300	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
C	1334116	1334116	1	T -> C	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
G	1334122	1334122	1	A -> G	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
A	1334128	1334128	1	G -> A	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334140	1334140	1	G -> T	SNP (transversion)	81	100.0%	2E-299	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334254	1334254	1	C -> T	SNP (transition)	57	100.0%	6,3E-205	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
A	1334257	1334257	1	G -> A	SNP (transition)	58	100.0%	2,5E-214	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
G	1334260	1334260	1	A -> G	SNP (transition)	55	100.0%	3,2E-203	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
TAG	1334287	1334289	2	CAA -> TAG	Substitution	55	100.0%	1E-197	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334293	1334293	1	C -> T	SNP (transition)	64	100.0%	1,6E-236	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
AAGC	1334296	1334299	3	CAAA -> AAGC	Substitution	65 -> 68	98.5%	1E-233	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
A	1334305	1334305	1	T -> A	SNP (transversion)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
G	1334311	1334311	1	A -> G	SNP (transition)	69	100.0%	4E-248	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
G	1334317	1334317	1	A -> G	SNP (transition)	68	100.0%	1E-237	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334341	1334341	1	C -> T	SNP (transition)	54	100.0%	1,6E-199	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
A	1334356	1334356	1	G -> A	SNP (transition)	53	100.0%	1,6E-190	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
G	1334359	1334359	1	A -> G	SNP (transition)	54	100.0%	4E-194	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
G	1334389	1334389	1	A -> G	SNP (transition)	54	100.0%	1,6E-199	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334401	1334401	1	C -> T	SNP (transition)	58	100.0%	1,6E-208	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
C	1334407	1334407	1	T -> C	SNP (transition)	64	100.0%	1,6E-236	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
C	1334488	1334488	1	T -> C	SNP (transition)	66	100.0%	1E-230	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
G	1334506	1334506	1	A -> G	SNP (transition)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
G	1334539	1334539	1	A -> G	SNP (transition)	77	100.0%	3,2E-269	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
G	1334542	1334542	1	C -> G	SNP (transversion)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
A	1334545	1334545	1	C -> A	SNP (transversion)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
A	1334551	1334551	1	G -> A	SNP (transition)	77	100.0%	3,2E-269	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334557	1334557	1	C -> T	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
C	1334593	1334593	1	T -> C	SNP (transition)	50	100.0%	1E-184	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
C	1334641	1334641	1	G -> C	SNP (transversion)	49	100.0%	4E-176	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
C	1334647	1334647	1	T -> C	SNP (transition)	47	100.0%	3,2E-164	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
GT	1334667	1334668	2	AC -> GT	Substitution	49 -> 56	100.0%	5E-181	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
G	1334671	1334671	1	A -> G	SNP (transition)	56	100.0%	2,5E-201	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
CG	1334758	1334759	2	TA -> CG	Substitution	64	100.0%	4E-230	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	I -> T	uup CDS
C	1334782	1334782	1	T -> C	SNP (transition)	63	100.0%	3,2E-220	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334842	1334842	1	C -> T	SNP (transition)	65	98.5%	6,5E-222	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334857	1334857	1	C -> T	SNP (transition)	61	100.0%	2E-225	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
A	1334875	1334875	1	G -> A	SNP (transition)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
A	1334878	1334878	1	C -> A	SNP (transversion)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> D	uup CDS
G	1334899	1334899	1	A -> G	SNP (transition)	57	100.0%	6,3E-205	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334905	1334905	1	C -> T	SNP (transition)	65	100.0%	1E-233	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
C	1334908	1334908	1	T -> C	SNP (transition)	63	100.0%	3,2E-220	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1334968	1334968	1	C -> T	SNP (transition)	54	100.0%	4E-194	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
A	1334971	1334971	1	G -> A	SNP (transition)	52	100.0%	6,3E-187	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
C	1335028	1335028	1	T -> C	SNP (transition)	63	100.0%	7,9E-233	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
C	1335046	1335046	1	T -> C	SNP (transition)	61	100.0%	2,5E-219	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
A	1335058	1335058	1	T -> A	SNP (transversion)	66	100.0%	2,5E-237	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
G	1335061	1335061	1	T -> G	SNP (transversion)	62	100.0%	6,3E-223	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
A	1335064	1335064	1	T -> A	SNP (transversion)	61	100.0%	2,5E-219	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1335091	1335091	1	C -> T	SNP (transition)	63	100.0%	1,6E-226	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		uup CDS
T	1335206	1335206	1	G -> T	SNP (transversion)	45	100.0%	3,2E-166	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	1335208	1335208	1	G -> A	SNP (transition)	45	100.0%	3,2E-166	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	1335215	1335215	1	G -> A	SNP (transition)	41	100.0%	2E-151	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1336486	1336486	1	A -> C	SNP (transversion)	42	97.6%	1,1E-145	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1336489	1336489	1	C -> T	SNP (transition)	42	97.6%	1,1E-145	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
GG	1336500	1336501	2	CA -> GG	Substitution	56 -> 60	100.0%	2,5E-201	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	GA -> GP	hypothetical protein CDS
T	1336516	1336516	1	C -> T	SNP (transition)	60	98.3%	2,4E-210	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
CATC	1336528	1336531	3	TACT -> CATC	Substitution	60	96.7%	1,6E-208	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	LV -> LM	hypothetical protein CDS
A	1336537	1336537	1	G -> A	SNP (transition)	60	100.0%	1E-221	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1336540	1336540	1	A -> G	SNP (transition)	60	100.0%	1E-221	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
AAG	1336552	1336554	2	TAT -> AAG	Substitution	57 -> 58	100.0%	6,3E-205	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	I -> L	hypothetical protein CDS
A	1336558	1336558	1	T -> A	SNP (transversion)	51	100.0%	2E-188	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
T	1336564	1336564	1	C -> T	SNP (transition)	48	100.0%	1,6E-172	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
ATT	1336567	1336569	3	TGC -> ATT	Substitution	48	100.0%	1,6E-172	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> N	hypothetical protein CDS
AC	1336572	1336573	2	CT -> AC	Substitution	47 -> 48	100.0%	6,3E-169	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	VV -> VL	hypothetical protein CDS
A	1336576	1336576	1	T -> A	SNP (transversion)	46	97.8%	1,5E-164	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> D	hypothetical protein CDS
TC	1336584			G -> TC	Insertion	41 -> 42	95.1% -> 95.2%	4,1E-141	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
CTT	1336588	1336590	2	ATC -> CTT	Substitution	41	97.6%	4,1E-142	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	D -> K	hypothetical protein CDS
G	1336592	1336592	1	T -> G	SNP (transversion)	41	97.6%	4,1E-146	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> A	hypothetical protein CDS
	1336594	1336595	2	-AT	Deletion	41	100.0%	1E-122	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
AC	1336636	1336637	2	TG -> AC	Substitution	40	97.5%	1,6E-138	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> G	hypothetical protein CDS
C	1336691	1336690	0	+C	Insertion	42	85.7%	3,3E-126	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	1336692	1336692	1	C -> T	SNP (transition)	42	95.2%	8,6E-145	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	1336694	1336694	1	A -> T	SNP (transversion)	41	97.6%	4,1E-146	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
A	1336701	1336701	1	G -> A	SNP (transition)	43	97.7%	1,7E-153	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	1336713	1336713	1	A -> T	SNP (transversion)	45	95.6%	7,9E-156	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
TC	1336715	1336716	2	AT -> TC	Substitution	45	95.6%	7,9E-156	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	1336719	1336719	1	C -> T	SNP (transition)	45	97.8%	7,1E-161	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1336731	1336731	1	T -> C	SNP (transition)	52	96.2%	1,3E-181	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1336786	1336786	1	T -> C	SNP (transition)	72	98.6%	1,8E-253	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	1337410	1337410	1	C -> T	SNP (transition)	84	97.6%	2,2E-291	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		GGDEF domain-containing protein CDS
T	1337806	1337806	1	C -> T	SNP (transition)	94	98.9%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		GGDEF domain-containing protein CDS
T	1338155	1338155	1	C -> T	SNP (transition)	63	100.0%	1,6E-226	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	G -> S	Polyisoprenoid-binding protein CDS
TT	1338158	1338159	2	GC -> TT	Substitution	61 -> 62	98.4%	6,1E-220	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	AP -> AT	Polyisoprenoid-binding protein CDS
T	1338165	1338165	1	G -> T	SNP (transversion)	63	100.0%	1,6E-226	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> K	Polyisoprenoid-binding protein CDS
T	1338189	1338189	1	A -> T	SNP (transversion)	59	100.0%	4E-212	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Polyisoprenoid-binding protein CDS
T	1338204	1338204	1	A -> T	SNP (transversion)	59	100.0%	4E-212	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Polyisoprenoid-binding protein CDS
T	1338209	1338209	1	C -> T	SNP (transition)	46	100.0%	6,3E-170	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	V -> I	Polyisoprenoid-binding protein CDS
G	1338228	1338228	1	A -> G	SNP (transition)	54	100.0%	1E-188	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Polyisoprenoid-binding protein CDS
T	1338231	1338231	1	C -> T	SNP (transition)	51	100.0%	2,5E-183	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Polyisoprenoid-binding protein CDS
C	1338254	1338254	1	T -> C	SNP (transition)	54	100.0%	1,6E-199	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	T -> A	Polyisoprenoid-binding protein CDS
GAT	1338264	1338266	2	CAC -> GAT	Substitution	62 -> 63	100.0%	4E-229	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	V -> I	Polyisoprenoid-binding protein CDS
T	1338778	1338778	1	C -> T	SNP (transition)	63	100.0%	1,6E-226	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	G -> S	HIT domain-containing protein CDS
C	1340025	1340025	1	A -> C	SNP (transversion)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	D -> E	Beta-lactamase CDS
T	1340360	1340360	1	C -> T	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	A -> T	Beta-lactamase CDS
C	1340395	1340395	1	T -> C	SNP (transition)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	Y -> C	Beta-lactamase CDS
T	1340477	1340477	1	C -> T	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> K	Beta-lactamase CDS
T	1340558	1340558	1	C -> T	SNP (transition)	72	100.0%	6,3E-259	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	D -> N	Beta-lactamase CDS
C	1340601	1340601	1	T -> C	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	I -> M	Beta-lactamase CDS
T	1341164	1341164	1	C -> T	SNP (transition)	58	100.0%	1,6E-208	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ATP-binding protein CDS
C	1341359	1341359	1	T -> C	SNP (transition)	60	100.0%	1E-203	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ATP-binding protein CDS
T	1341827	1341827	1	C -> T	SNP (transition)	76	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ATP-binding protein CDS
C	1341836	1341836	1	T -> C	SNP (transition)	77	100.0%	3,2E-269	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ATP-binding protein CDS
C	1343256	1343256	1	T -> C	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ATP /GTP binding protein CDS
A	1343648	1343648	1	G -> A	SNP (transition)	71	100.0%	2,5E-255	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		ATP /GTP binding protein CDS
T	1344696	1344696	1	C -> T	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		frdB CDS
C	1344732	1344732	1	T -> C	SNP (transition)	70	98.6%	2,8E-246	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		frdB CDS
A	1345017	1345017	1	G -> A	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		frdB CDS
A	1345023	1345023	1	G -> A	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		frdB CDS
A	1345115	1345115	1	G -> A	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	P -> S	frdB CDS
T	1345242	1345242	1	C -> T	SNP (transition)	74	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		frdB CDS
C	1345393	1345393	1	T -> C	SNP (transition)	83	98.8%	5,2E-293	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
A	1345519	1345519	1	G -> A	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
G	1345621	1345621	1	A -> G	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
G	1345633	1345633	1	A -> G	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
A	1345641	1345641	1	G -> A	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
C	1345648	1345648	1	T -> C	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
C	1345660	1345660	1	T -> C	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
C	1345699	1345699	1	T -> C	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
G	1345702	1345702	1	A -> G	SNP (transition)	91	98.9%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
T	1345720	1345720	1	C -> T	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
C	1345723	1345723	1	T -> C	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
A	1345738	1345738	1	G -> A	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS

G	1345792	1345792	1	A -> G	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
T	1346476	1346476	1	C -> T	SNP (transition)	72	97.2%	2,6E-248	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
A	1346656	1346656	1	G -> A	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
A	1347217	1347217	1	T -> A	SNP (transversion)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
C	1347226	1347226	1	A -> C	SNP (transversion)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		sdhA CDS
T	1348881	1348881	1	C -> T	SNP (transition)	82	98.8%	2,1E-289	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lgt CDS
C	1349019	1349019	1	T -> C	SNP (transition)	84	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	1349691	1349691	1	C -> T	SNP (transition)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Lipoprotein, putative CDS
G	1350036	1350036	1	A -> G	SNP (transition)	74	100.0%	1,6E-273	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
C	1350277	1350277	1	T -> C	SNP (transition)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	N -> S	aroE CDS
G	1350306	1350306	1	A -> G	SNP (transition)	62	100.0%	4E-229	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		aroE CDS
TAG	1350312	1350314	2	CAA -> TAG	Substitution	74 -> 75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		aroE CDS
G	1351505	1351505	1	A -> G	SNP (transition)	78	100.0%	1E-272	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		SPOR domain-containing protein CDS
T	1353101	1353101	1	C -> T	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	S -> N	glyA CDS
A	1353268	1353268	1	G -> A	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		glyA CDS
C	1353370	1353370	1	T -> C	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	I -> M	glyA CDS
C	1353579	1353579	1	T -> C	SNP (transition)	91	98.9%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lysS CDS
G	1353632	1353632	1	A -> G	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lysS CDS
T	1353723	1353723	1	C -> T	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lysS CDS
T	1353882	1353882	1	C -> T	SNP (transition)	81	100.0%	2E-299	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lysS CDS
T	1354105	1354105	1	C -> T	SNP (transition)	64	100.0%	1,6E-236	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	R -> Q	lysS CDS
C	1354115	1354115	1	T -> C	SNP (transition)	63	100.0%	7,9E-233	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	K -> E	lysS CDS
A	1354215	1354215	1	G -> A	SNP (transition)	63	100.0%	1,6E-226	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lysS CDS
T	1354305	1354305	1	C -> T	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lysS CDS
A	1354356	1354356	1	G -> A	SNP (transition)	75	100.0%	3,2E-277	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lysS CDS
T	1354359	1354359	1	C -> T	SNP (transition)	76	98.7%	2,4E-275	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lysS CDS
A	1354371	1354371	1	T -> A	SNP (transversion)	76	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lysS CDS
A	1354374	1354374	1	G -> A	SNP (transition)	76	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lysS CDS
GT	1354465	1354466	2	AC -> GT	Substitution	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	V -> T	lysS CDS
G	1354551	1354551	1	A -> G	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lysS CDS
A	1354794	1354794	1	G -> A	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lysS CDS
T	1354814	1354814	1	C -> T	SNP (transition)	59	100.0%	5E-218	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	V -> I	lysS CDS
C	1354817	1354817	1	T -> C	SNP (transition)	58	100.0%	1,6E-208	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	I -> V	lysS CDS
G	1354824	1354824	1	A -> G	SNP (transition)	57	98.2%	1,4E-199	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		lysS CDS
C	1354928	1354928	1	A -> C	SNP (transversion)	67	98.5%	1,7E-235	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	L -> V	lysS CDS
A	1355174	1355174	1	G -> A	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		fur CDS
G	1355177	1355177	1	T -> G	SNP (transversion)	100	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		fur CDS
T	1355210	1355210	1	C -> T	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		fur CDS
G	1359254	1359254	1	A -> G	SNP (transition)	73	100.0%	1,6E-262	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	T -> A	Malate dehydrogenase (quinone) CDS
T	1359457	1359457	1	C -> T	SNP (transition)	65	100.0%	3,2E-240	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Malate dehydrogenase (quinone) CDS
A	1359538	1359538	1	G -> A	SNP (transition)	59	100.0%	4E-212	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Malate dehydrogenase (quinone) CDS
T	1359682	1359682	1	C -> T	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Malate dehydrogenase (quinone) CDS
G	1359925	1359925	1	A -> G	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Malate dehydrogenase (quinone) CDS
G	1359979	1359979	1	A -> G	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Malate dehydrogenase (quinone) CDS
AGC	1360184	1360186	2	GGT -> AGC	Substitution	64 -> 65	100.0%	4E-230	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	G -> S	Malate dehydrogenase (quinone) CDS
G	1360642	1360642	1	A -> G	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Pyruvate kinase CDS
A	1360646	1360646	1	G -> A	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> K	Pyruvate kinase CDS
A	1361476	1361476	1	G -> A	SNP (transition)	79	100.0%	4E-284	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Pyruvate kinase CDS
A	1361507	1361507	1	G -> A	SNP (transition)	75	100.0%	3,2E-277	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	V -> I	Pyruvate kinase CDS
A	1361564	1361564	1	G -> A	SNP (transition)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> K	Pyruvate kinase CDS
C	1361725	1361725	1	T -> C	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Pyruvate kinase CDS
C	1362042	1362042	1	T -> C	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	1362284	1362284	1	C -> T	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1362368	1362368	1	A -> G	SNP (transition)	80	98.8%	3,2E-282	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
G	1362530	1362530	1	A -> G	SNP (transition)	75	100.0%	3,2E-262	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	1362802	1362802	1	T -> C	SNP (transition)	76	98.7%	7,6E-268	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
G	1362925	1362925	1	A -> G	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
T	1363189	1363189	1	C -> T	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
G	1363312	1363312	1	A -> G	SNP (transition)	57	100.0%	1,3E-210	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
G	1363404	1363404	1	C -> G	SNP (transversion)	76	100.0%	2,5E-273	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	D -> H	Tetratricopeptide repeat protein CDS
A	1363570	1363570	1	G -> A	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
C	1363696	1363696	1	T -> C	SNP (transition)	71	100.0%	2,5E-255	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
T	1364170	1364170	1	A -> T	SNP (transversion)	76	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
A	1364236	1364236	1	G -> A	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
A	1364628	1364628	1	G -> A	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
T	1364641	1364641	1	C -> T	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
C	1364647	1364647	1	T -> C	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
T	1364677	1364677	1	C -> T	SNP (transition)	73	100.0%	6,3E-248	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
C	1364743	1364743	1	T -> C	SNP (transition)	79	100.0%	3,2E-276	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
A	1364940	1364940	1	G -> A	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	P -> S	Tetratricopeptide repeat protein CDS
T	1364946	1364946	1	C -> T	SNP (transition)	82	98.8%	2,1E-289	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	D -> N	Tetratricopeptide repeat protein CDS
T	1364953	1364953	1	C -> T	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
AC	1364972	1364973	2	GA -> AC	Substitution	81 -> 83	97.5% -> 97.6%	8,1E-286	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	S -> V	Tetratricopeptide repeat protein CDS
T	1364977	1364977	1	C -> T	SNP (transition)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
T	1364980	1364980	1	C -> T	SNP (transition)	80	98.8%	4E-290	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
A	1364986	1364986	1	G -> A	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
G	1364998	1364998	1	A -> G	SNP (transition)	74	98.6%	5,9E-268	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Tetratricopeptide repeat protein CDS
T	1365012	1365012	1	C -> T	SNP (transition)	75	100.0%	1E-269	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	G -> S	Tetratricopeptide repeat protein CDS
C	1365178	1365178	1	T -> C	SNP (transition)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		
T	1365221	1365221	1	C -> T	SNP (transition)	70	100.0%	1E-251	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	R -> K	serS CDS
T	1365226	1365226	1	C -> T	SNP (transition)	68	100.0%	1,6E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
C	1365277	1365277	1	T -> C	SNP (transition)	71	100.0%	3,2E-248	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
A	1365286	1365286	1	G -> A	SNP (transition)	74	98.6%	1,2E-260	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
C	1365301	1365301	1	A -> C	SNP (transversion)	81	100.0%	2,5E-291	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
T	1365316	1365316	1	C -> T	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
G	1365373	1365373	1	A -> G	SNP (transition)	83	100.0%	3,2E-290	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
A	1365391	1365391	1	G -> A	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
T	1365406	1365406	1	C -> T	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
A	1365418	1365418	1	T -> A	SNP (transversion)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
T	1365421	1365421	1	C -> T	SNP (transition)	78	100.0%	1,6E-280	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
G	1365433	1365433	1	A -> G	SNP (transition)	81	98.8%	8,1E-286	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
T	1365436	1365436	1	C -> T	SNP (transition)	77	100.0%	6,3E-277	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
T	1365442	1365442	1	C -> T	SNP (transition)	64	100.0%	1,6E-236	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
G	1365451	1365451	1	A -> G	SNP (transition)	67	100.0%	3,2E-234	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
A	1365456	1365456	1	G -> A	SNP (transition)	64	100.0%	1,6E-236	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
A	1365463	1365463	1	G -> A	SNP (transition)	66	100.0%	6,3E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
G	1365466	1365466	1	A -> G	SNP (transition)	73	98.6%	4,6E-257	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
C	1365487	1365487	1	A -> C	SNP (transversion)	76	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
A	1365502	1365502	1	G -> A	SNP (transition)	83	100.0%	3,2E-290	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
A	1365505	1365505	1	G -> A	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
C	1365508	1365508	1	T -> C	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
C	1365532	1365532	1	T -> C	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
C	1365543	1365543	1	T -> C	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	I -> V	serS CDS
A	1365547	1365547	1	G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
G	1365550	1365550	1	A -> G	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
C	1365583	1365583	1	T -> C	SNP (transition)	81	100.0%	3,2E-283	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
A	1365613	1365613	1	G -> A	SNP (transition)	82	98.8%	2,1E-289	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
C	1365616	1365616	1	T -> C	SNP (transition)	80	98.8%	2E-266	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
A	1365622	1365622	1	G -> A	SNP (transition)	79	100.0%	5E-292	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
G	1365670	1365670	1	A -> G	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
T	1365685	1365685	1	C -> T	SNP (transition)	85	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
T	1365697	1365697	1	C -> T	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
C	1365811	1365811	1	T -> C	SNP (transition)	87	100.0%	3,2E-304	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
A	1365814	1365814	1	G -> A	SNP (transition)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
T	1366074	1366074	1	C -> T	SNP (transition)	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	E -> K	serS CDS
C	1366374	1366374	1	T -> C	SNP (transition)	70	100.0%	1E-244	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss	K -> E	serS CDS
G	1366378	1366378	1	A -> G	SNP (transition)	68	100.0%	1E-237	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		serS CDS
A	1367778	1367778	1	G -> A	SNP (transition)	73	98.6%	4,6E-257	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		Shikimate kinase CDS
T	1368772	1368772	1	C -> T	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		der CDS
A	1370898	1370898	1	G -> A	SNP (transition)	74	100.0%	1E-258	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		kdsA CDS
T	1372793	1372793	1	C -> T	SNP (transition)	81	98.8%	8,1E-294	Variants: BfR-CA-11057-TF15687-4_R	Concatemer BfR-CA-11057 - UniAss		pyrF CDS
C	13411	13411	1	T -> C	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	13501	13501	1	C -> T	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	13819	13819	1	C -> T	SNP (transition)	121	99.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	14023	14023	1	T -> G	SNP (transversion)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	14029	14029	1	C -> T	SNP (transition)	123	99.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14032	14032	1	G -> A	SNP (transition)	112	99.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14035	14035	1	T -> A	SNP (transversion)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14059	14059	1	T -> A	SNP (transversion)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14062	14062	1	G -> A	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	14170	14170	1	A -> T	SNP (transversion)	122	99.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	14173	14173	1	A -> G	SNP (transition)	119	99.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	14179	14179	1	A -> C	SNP (transversion)	99	99.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
C	14431	14431	1	T -> C	SNP (transition)	134	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	14662	14662	1	T -> A	SNP (transversion)	92	97.8%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
GCTA	14665	14668	3	AGTG -> GCTA	Substitution	93 -> 94	97.8% -> 97.9%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	KV -> KL	gltB3 CDS
G	14674	14674	1	A -> G	SNP (transition)	90	98.9%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
A	15274	15274	1	G -> A	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
G	15526	15526	1	A -> G	SNP (transition)	83	100.0%	7,9E-307	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
T	15538	15538	1	C -> T	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltB3 CDS
GAT	16211	16213	2	CAA -> GAT	Substitution	126	99.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	Q -> D	gltD CDS
C	16219	16219	1	G -> C	SNP (transversion)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
T	16222	16222	1	G -> T	SNP (transversion)	123	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
A	16228	16228	1	G -> A	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
C	16231	16231	1	T -> C	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
G	16235	16235	1	A -> G	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	K -> E	gltD CDS
C	16240	16240	1	T -> C	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
T	16243	16243	1	G -> T	SNP (transversion)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
A	16246	16246	1	T -> A	SNP (transversion)	126	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
G	16255	16255	1	A -> G	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
A	16258	16258	1	G -> A	SNP (transition)	118	99.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		gltD CDS
G	17240	17240	1	A -> G	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		rnhB CDS

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C	17383	17383	1 T -> C	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			rnhB CDS
G	17889	17889	1 A -> G	SNP (transition)	134	99.3%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			Desulfoferrodoxin Fe(4 iron-binding domain-containing pro
T	18297	18297	1 C -> T	SNP (transition)	134	97.8%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			Desulfoferrodoxin Fe(4 iron-binding domain-containing pro
T	18372	18372	1 C -> T	SNP (transition)	137	98.5%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			
A	19670	19670	1 G -> A	SNP (transition)	115	99.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			ilv3 CDS
A	20611	20611	1 G -> A	SNP (transition)	120	99.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	20614	20614	1 T -> A	SNP (transversion)	123	98.4%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
G	20635	20635	1 T -> G	SNP (transversion)	128	99.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	20638	20638	1 G -> A	SNP (transition)	128	99.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	20644	20644	1 G -> A	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	20656	20656	1 T -> C	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	20659	20659	1 A -> T	SNP (transversion)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
CAA	20662	20664	2 TAG -> CAA	Substitution	106 -> 107	99.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	20674	20674	1 T -> C	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	20680	20680	1 G -> A	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	20682	20682	1 G -> A	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	20695	20695	1 T -> C	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	20709	20709	1 T -> C	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	N -> D		comGF CDS
C	20716	20716	1 T -> C	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	20725	20725	1 A -> T	SNP (transversion)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
G	20731	20731	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	20755	20755	1 T -> C	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	20776	20776	1 A -> C	SNP (transversion)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
G	20779	20779	1 A -> G	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	20785	20785	1 A -> T	SNP (transversion)	100	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	20797	20797	1 G -> A	SNP (transition)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	20812	20812	1 C -> T	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
G	20821	20821	1 A -> G	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	20830	20830	1 C -> T	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
AAG	20836	20836	2 TAA -> AAG	Substitution	104 -> 105	97.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	20842	20842	1 G -> A	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	20845	20845	1 G -> A	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
G	20851	20851	1 T -> G	SNP (transversion)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	20854	20854	1 G -> T	SNP (transversion)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
TAA	20866	20868	2 AAG -> TAA	Substitution	106	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	20872	20872	1 G -> A	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	20890	20890	1 G -> A	SNP (transition)	131	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	20893	20893	1 T -> C	SNP (transition)	138	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
G	20899	20899	1 A -> G	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	20908	20908	1 C -> T	SNP (transition)	127	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	20917	20917	1 A -> T	SNP (transversion)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	D -> E		comGF CDS
A	20920	20920	1 G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
G	20926	20926	1 A -> G	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	20932	20932	1 G -> A	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	20941	20941	1 G -> A	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	21001	21001	1 G -> A	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	21004	21004	1 G -> T	SNP (transversion)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	21007	21007	1 T -> A	SNP (transversion)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	21010	21010	1 A -> T	SNP (transversion)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	21034	21034	1 G -> A	SNP (transition)	129	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
AGC	21040	21042	2 GGT -> AGC	Substitution	109 -> 119	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	T -> A		comGF CDS
A	21046	21046	1 G -> A	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
G	21049	21049	1 A -> G	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	21054	21054	1 G -> A	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	21058	21058	1 T -> C	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
G	21075	21075	1 A -> G	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	21079	21079	1 C -> T	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	21082	21082	1 T -> C	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	21106	21106	1 G -> A	SNP (transition)	122	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
G	21118	21118	1 A -> G	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	21136	21136	1 C -> A	SNP (transversion)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	21139	21139	1 C -> T	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	21142	21142	1 T -> A	SNP (transversion)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	21154	21154	1 G -> A	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	21157	21157	1 T -> C	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	21172	21172	1 T -> C	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	21193	21193	1 A -> T	SNP (transversion)	105	99.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	21196	21196	1 T -> C	SNP (transition)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	21202	21202	1 G -> A	SNP (transition)	101	98.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	21205	21205	1 G -> A	SNP (transition)	97	99.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	21214	21214	1 T -> C	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	21226	21226	1 A -> C	SNP (transversion)	94	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
CA	21238	21239	2 AG -> CA	Substitution	102 -> 106	99.1% -> 100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	A -> V		comGF CDS
T	21244	21244	1 C -> T	SNP (transition)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	M -> I		comGF CDS
A	21268	21268	1 T -> A	SNP (transversion)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
G	21271	21271	1 A -> G	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	21274	21274	1 G -> A	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	21280	21280	1 A -> T	SNP (transversion)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
G	21283	21283	1 T -> G	SNP (transversion)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	21298	21298	1 C -> A	SNP (transversion)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	21313	21313	1 C -> T	SNP (transition)	114	99.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
A	21316	21316	1 G -> A	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
C	21319	21319	1 T -> C	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			comGF CDS
T	21418	21417	0 (T)6 -> (T)7	Insertion (tandem repeat)	122	93.4%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			
T	21682	21682	1 C -> T	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			queC CDS
A	22093	22093	1 G -> A	SNP (transition)	137	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			queC CDS
C	22173	22173	1 T -> C	SNP (transition)	144	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			
A	22276	22276	1 G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
T	22282	22282	1 G -> T	SNP (transversion)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
T	22291	22291	1 C -> T	SNP (transition)	108	98.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
C	22294	22294	1 T -> C	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
AG	22306	22307	2 GT -> AG	Substitution	109	98.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	D -> A		dsbI CDS
G	22315	22315	1 A -> G	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
TA	22320	22321	2 CG -> TA	Substitution	111	98.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	AV -> AI		dsbI CDS
G	22324	22324	1 A -> G	SNP (transition)	109	99.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
CT	22604	22605	2 TC -> CT	Substitution	104 -> 105	98.1% -> 99.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	D -> S		dsbI CDS
CG	22608	22609	2 TT -> CG	Substitution	102 -> 103	97.1% -> 98.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	GK -> GE		dsbI CDS
C	22834	22834	1 T -> C	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
ATC	22864	22866	2 GTT -> ATC	Substitution	82 -> 87	100.0%	46-363	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	N -> D		dsbI CDS
A	22870	22870	1 G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
T	22891	22891	1 G -> T	SNP (transversion)	106	99.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
A	22897	22897	1 G -> A	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
GA	22921	22922	2 TG -> GA	Substitution	76 -> 79	100.0%	6,3E-281	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	T -> I		dsbI CDS
A	22924	22924	1 G -> A	SNP (transition)	78	100.0%	2,5E-288	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
GTCA	22939	22942	4 ATTG -> GTCA	Substitution	90 -> 93	98.9%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	IN -> ID		dsbI CDS
C	22947	22947	1 T -> C	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	K -> E		dsbI CDS
A	22959	22959	1 C -> A	SNP (transversion)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	A -> S		dsbI CDS
A	22963	22963	1 G -> A	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
TG	22966	22967	2 GA -> TG	Substitution	92 -> 95	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	I -> T		dsbI CDS
T	22971	22971	1 C -> T	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	D -> N		dsbI CDS
A	22987	22987	1 G -> A	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
CAA	22990	22992	2 AAG -> CAA	Substitution	102 -> 104	99.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
C	23002	23002	1 T -> C	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
A	23038	23038	1 G -> A	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
C	23041	23041	1 T -> C	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			dsbI CDS
T	24185	24185	1 A -> T	SNP (transversion)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			ygfM CDS
T	24212	24212	1 C -> T	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			ygfM CDS
T	24218	24218	1 G -> T	SNP (transversion)	173	99.3%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			ygfM CDS
G	24224	24224	1 A -> G	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			ygfM CDS
A	24500	24500	1 G -> A	SNP (transition)	97	97.9%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			ygfM CDS
GC	24673	24674	2 AT -> GC	Substitution	95	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			ygfM CDS
C	24710	24710	1 T -> C	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			ygfM CDS
G	25001	25001	1 A -> G	SNP (transition)	110	99.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			RNA pseudouridylate synthase CDS
C	25286	25286	1 T -> C	SNP (transition)	166	99.4%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			RNA pseudouridylate synthase CDS
T	25408	25408	1 C -> T	SNP (transition)	156	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	E -> K		RNA pseudouridylate synthase CDS
C	25469	25469	1 A -> C	SNP (transversion)	121	99.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			RNA pseudouridylate synthase CDS
T	25474	25474	1 C -> T	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	E -> K		RNA pseudouridylate synthase CDS
A	25478	25478	1 T -> A	SNP (transversion)	125	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			RNA pseudouridylate synthase CDS
A	25489	25489	1 G -> A	SNP (transition)	130	99.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	H -> Y		RNA pseudouridylate synthase CDS
A	25576	25576	1 G -> A	SNP (transition)	126	99.2%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			RNA pseudouridylate synthase CDS
G	25638	25638	1 A -> G	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			RNA pseudouridylate synthase CDS
G	25610	25610	1 A -> G	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			RNA pseudouridylate synthase CDS
C	25691	25691	1 T -> C	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			RNA pseudouridylate synthase CDS
C	26306	26306	1 T -> C	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			purB CDS
A	26321	26321	1 G -> A	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			purB CDS
ACTT	26342	26345	5 GTTA -> ACTT	Substitution	94 -> 98	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			purB CDS
G	26348	26348	1 T -> G	SNP (transversion)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			purB CDS
A	26369	26369	1 G -> A	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			purB CDS
T	27838	27838	1 C -> T	SNP (transition)	148	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			mrdA CDS
T	27892	27892	1 C -> T	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			mrdA CDS
C	27949	27949	1 T -> C	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			mrdA CDS
C	28003	28003	1 T -> C	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			mrdA CDS
T	28015	28015	1 C -> T	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			mrdA CDS
C	28018	28018	1 T -> C	SNP (transition)	85	100.0%	3,2E-297	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			mrdA CDS
A	28024	28024	1 G -> A	SNP (transition)	88	100.0%	1E-307	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			mrdA CDS
GG	28135	28136	2 AA -> GG	Substitution	94	98.9%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	VS -> VG		mrdA CDS
C	28213	28213	1 T -> C	SNP (transition)	95	97.9%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			mrdA CDS
T	28216	28216	1 C -> T	SNP (transition)	95	98.9%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			mrdA CDS
T	28237	28237	1 G -> T	SNP (transversion)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			mrdA CDS
G	28780	28780	1 T -> G	SNP (transversion)	124	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			mrdA CDS
T	28816	28816	1 C -> T	SNP (transition)	117	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			mrdA CDS
T	28822	28823	1 C -> T	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss			mrdA CDS

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T	32037	32037	1 C -> T	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		pyrG CDS
A	33736	33736	1 G -> A	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33748	33748	1 T -> C	SNP (transition)	111	99.1%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33751	33751	1 T -> C	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
T	33757	33757	1 C -> T	SNP (transition)	126	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33769	33769	1 T -> C	SNP (transition)	130	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
G	38113	38113	1 A -> G	SNP (transition)	293	99.3%	5,4E-83	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
	38420	38420	1 (T)3 -> (T)2	Deletion (tandem repeat)	306	95.4%	1E-14	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
G	401153	401153	1 A -> G	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	F -> L	ncS2 CDS
C	401178	401178	1 T -> C	SNP (transition)	122	99.2%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		ncS2 CDS
T	402011	402011	1 C -> T	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	G -> S	ncS2 CDS
T	402130	402129	0 (T)5 -> (T)6	Insertion (tandem repeat)	108	93.5%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
G	402146	402146	1 T -> G	SNP (transversion)	113	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	K -> Q	thiH CDS
T	402171	402171	1 C -> T	SNP (transition)	109	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		thiH CDS
G	402424	402424	1 A -> G	SNP (transition)	147	99.3%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	M -> T	thiH CDS
C	461537	461537	1 T -> C	SNP (transition)	97	94.8%	1E-212	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	N -> D	DUF115 domain-containing protein CDS
A	1040375	1040375	1 G -> A	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		dnaK CDS
T	1042179	1042179	1 C -> T	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042182	1042182	1 G -> A	SNP (transition)	90	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
AC	1042187	1042188	2 GT -> AC	Substitution	87	98.9%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
T	1042191	1042191	1 C -> T	SNP (transition)	84	100.0%	4E-302	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
C	1042194	1042194	1 T -> C	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042206	1042206	1 A -> G	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042218	1042218	1 A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042221	1042221	1 G -> A	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
T	1042233	1042233	1 C -> T	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
C	1042249	1042249	1 T -> C	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	N -> S	hrcA CDS
A	1042293	1042293	1 G -> A	SNP (transition)	72	100.0%	4E-266	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
A	1042371	1042371	1 G -> A	SNP (transition)	83	98.8%	5,2E-293	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042431	1042431	1 A -> G	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		hrcA CDS
G	1042479	1042479	1 A -> G	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
T	1042488	1042488	1 C -> T	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
A	1042490	1042490	1 T -> A	SNP (transversion)	94	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
G	1042492	1042492	1 T -> G	SNP (transversion)	102	99.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
AG	1042520	1042521	2 TA -> AG	Substitution	99 -> 110	99.0% -> 99.1%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
T	1042591	1042591	1 A -> T	SNP (transversion)	95	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
A	1042596	1042596	1 G -> A	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
A	1042608	1042608	1 G -> A	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
G	1042632	1042632	1 A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
A	1042634	1042634	1 C -> A	SNP (transversion)	94	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
A	1042638	1042638	1 C -> A	SNP (transversion)	86	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
C	1042642	1042642	1 T -> C	SNP (transition)	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
GT	1042650	1042651	2 AA -> GT	Substitution	70	98.6%	1,1E-218	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
ACAG	1042654	1042657	4 TGCA -> ACAG	Substitution	65 -> 69	96.9% -> 98.6%	1,7E-229	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
G	1042659	1042658	0 +G	Insertion	61	91.8%	3,7E-200	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
A	1042687	1042687	1 T -> A	SNP (transversion)	57	100.0%	1,3E-210	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
T	1042690	1042690	1 A -> T	SNP (transversion)	55	92.7%	6,8E-183	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
C	1042692	1042692	1 T -> C	SNP (transition)	55	92.7%	6,8E-183	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
AA	1042696	1042697	2 TG -> AA	Substitution	60	83.3%	7,5E-174	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
T	1042699	1042699	1 C -> T	SNP (transition)	61	82.0%	4,2E-173	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
C	1042729	1042729	1 T -> C	SNP (transition)	68	94.1%	1,3E-230	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
AC	1042750	1042751	2 GA -> AC	Substitution	63 -> 65	100.0%	1,6E-226	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
C	1042763	1042763	1 T -> C	SNP (transition)	71	100.0%	1E-253	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
T	1042765	1042765	1 C -> T	SNP (transition)	67	100.0%	6,3E-241	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
AC	1042784	1042785	2 GT -> AC	Substitution	73	100.0%	7,9E-270	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	N -> S	cfrA CDS
A	1042793	1042793	1 G -> A	SNP (transition)	80	100.0%	1E-287	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042796	1042796	1 A -> G	SNP (transition)	83	96.4%	9,2E-291	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1042805	1042805	1 C -> T	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	M -> I	cfrA CDS
A	1042829	1042829	1 G -> A	SNP (transition)	64	100.0%	4E-302	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042832	1042832	1 A -> G	SNP (transition)	86	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042835	1042835	1 G -> A	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1042841	1042841	1 T -> G	SNP (transversion)	91	96.7%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
AG	1042850	1042851	2 GC -> AG	Substitution	98 -> 99	99.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	S -> T	cfrA CDS
GT	1042854	1042855	2 CC -> GT	Substitution	92 -> 95	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	G -> T	cfrA CDS
CGCT	1042858	1042861	3 TCCC -> CGCT	Substitution	87	100.0%	3,2E-304	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	CS -> SG	cfrA CDS
T	1042863	1042863	1 C -> T	SNP (transition)	84	98.8%	1,3E-296	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	S -> N	cfrA CDS
TG	1042866	1042867	2 GC -> TG	Substitution	82	98.8%	2,1E-289	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	A -> Q	cfrA CDS
A	1042880	1042880	1 G -> A	SNP (transition)	99	99.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042885	1042885	1 T -> C	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	N -> D	cfrA CDS
A	1042892	1042892	1 G -> A	SNP (transition)	99	99.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1042900	1042900	1 C -> T	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	D -> N	cfrA CDS
G	1042922	1042922	1 A -> G	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1042937	1042937	1 T -> C	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042940	1042940	1 G -> A	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042964	1042964	1 G -> A	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1042985	1042985	1 G -> A	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043087	1043087	1 T -> C	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043093	1043093	1 G -> A	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043099	1043099	1 G -> A	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043258	1043258	1 G -> A	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
TC	1043267	1043268	2 CT -> TC	Substitution	99 -> 100	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	K -> R	cfrA CDS
G	1043271	1043271	1 A -> G	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	P -> S	cfrA CDS
C	1043584	1043584	1 G -> C	SNP (transversion)	105	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	L -> V	cfrA CDS
T	1043724	1043724	1 C -> T	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	S -> N	cfrA CDS
A	1043765	1043765	1 G -> A	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043769	1043769	1 A -> G	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	V -> A	cfrA CDS
C	1043774	1043774	1 T -> C	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
CAA	1043792	1043794	2 TAG -> CAA	Substitution	120	98.3%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043801	1043801	1 A -> G	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043861	1043861	1 C -> T	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043867	1043867	1 T -> C	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
TGC	1043870	1043872	2 AGA -> TGC	Substitution	93	98.9%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	S -> A	cfrA CDS
T	1043876	1043876	1 C -> T	SNP (transition)	101	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043882	1043882	1 G -> A	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043891	1043891	1 G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1043896	1043896	1 C -> T	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	D -> N	cfrA CDS
T	1043903	1043903	1 C -> T	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043912	1043912	1 A -> G	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GTC	1043922	1043924	3 CCA -> GTC	Substitution	98 -> 103	99.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	SG -> ST	cfrA CDS
G	1043927	1043927	1 A -> G	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1043930	1043930	1 G -> A	SNP (transition)	99	99.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1043966	1043966	1 A -> G	SNP (transition)	94	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1043999	1043999	1 T -> C	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044005	1044005	1 A -> G	SNP (transition)	84	98.8%	6,7E-305	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044024	1044024	1 G -> T	SNP (transversion)	89	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	P -> Q	cfrA CDS
A	1044079	1044079	1 T -> A	SNP (transversion)	87	98.9%	2,2E-307	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	R -> S	cfrA CDS
G	1044064	1044064	1 A -> G	SNP (transition)	76	98.7%	2,4E-275	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044047	1044047	1 A -> G	SNP (transition)	75	98.7%	7,5E-257	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044074	1044074	1 G -> A	SNP (transition)	80	98.8%	3,2E-282	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044110	1044110	1 A -> G	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1044128	1044128	1 T -> C	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044155	1044155	1 G -> A	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044191	1044191	1 C -> T	SNP (transition)	97	99.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044314	1044314	1 C -> T	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044662	1044662	1 A -> G	SNP (transition)	85	98.8%	8,5E-292	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044720	1044720	1 C -> G	SNP (transversion)	77	97.4%	9,2E-274	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	T -> R	cfrA CDS
G	1044722	1044722	1 A -> G	SNP (transition)	75	97.3%	2,2E-266	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GGT	1044761	1044763	2 AGC -> GGT	Substitution	73	98.6%	4,8E-257	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	A -> T	cfrA CDS
G	1044767	1044767	1 T -> G	SNP (transversion)	78	98.7%	4,9E-275	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1044781	1044781	1 T -> C	SNP (transition)	80	100.0%	1E-295	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	I -> V	cfrA CDS
T	1044785	1044785	1 C -> T	SNP (transition)	76	100.0%	1E-265	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044788	1044788	1 A -> G	SNP (transition)	77	100.0%	6,8E-277	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044791	1044791	1 G -> A	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044797	1044797	1 C -> T	SNP (transition)	87	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044815	1044815	1 A -> G	SNP (transition)	85	97.8%	5,7E-299	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044821	1044821	1 A -> G	SNP (transition)	86	100.0%	1E-309	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
GCTT	1044824	1044827	4 AGCC -> GCTT	Substitution	92 -> 93	88.0% -> 89.1%	1,3E-277	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	LA -> LS	cfrA CDS
G	1044830	1044830	1 A -> G	SNP (transition)	92	91.3%	1,5E-299	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044833	1044833	1 G -> A	SNP (transition)	85	98.8%	3,4E-300	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
G	1044842	1044842	1 A -> G	SNP (transition)	80	100.0%	1E-279	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
T	1044848	1044848	1 C -> T	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
C	1044859	1044859	1 A -> T	SNP (transversion)	85	98.8%	3,4E-300	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	L -> I	cfrA CDS
T	1044863	1044863	1 C -> T	SNP (transition)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		cfrA CDS
A	1044903	1044903	1 G -> A	SNP (transition)	86	98.8%	8,6E-304	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
	1052544	1052544	1 (A)3 -> (A)2	Deletion (tandem repeat)	113	93.9%	8,1E-12	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
C	1052849	1052849	1 T -> C	SNP (transition)	293	99.3%	5,4E-83	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		
C	1056828	1056828	1 T -> C	SNP (transition)	92	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	E -> G	ccmA CDS
C	1058557	1058557	1 T -> C	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	I -> V	Putative ABC transport system permease CDS
T	1058795	1058795	1 G -> T	SNP (transversion)	96	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		Putative ABC transport system permease CDS
T	1058819	1058819	1 C -> T	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	R -> K	ataC CDS
T	1058880	1058880	1 C -> T	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	V -> I	ataC CDS
G	1058884	1058884	1 A -> G	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1058971	1058971	1 G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059022	1059022	1 A -> G	SNP (transition)	101	99.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059106	1059106	1 G -> A	SNP (transition)	93	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059154	1059154	1 G -> A	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059162	1059162	1 A -> G	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	F -> L	ataC CDS
T	1059259	1059259	1 C -> T	SNP (transition)	99	99.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059283	1059283	1 A -> G	SNP (transition)	100	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059487	1059487	1 A -> G	SNP (transition)	115	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
C	1059541	1059541	1 T -> C	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
CA	1059570	1059571	2 TG -> CA	Substitution	95	100.0%	0	Variants: BfR-CA-11057-TF156B7-S_R	Concatemer BfR-CA-11057 - UniAss	ST -> SA	ataC CDS

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G	1059824	1059824	1 A -> G	SNP (transition)	116	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1059660	1059660	1 C -> T	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1059675	1059675	1 C -> T	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1059897	1059897	1 A -> G	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1059915	1059915	1 A -> G	SNP (transition)	91	98.9%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1059961	1059961	1 G -> A	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	A -> V	Phytase-like domain-containing protein CDS
G	1059973	1059973	1 A -> G	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	I -> T	Phytase-like domain-containing protein CDS
C	1060048	1060048	1 T -> C	SNP (transition)	91	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	N -> S	Phytase-like domain-containing protein CDS
G	1060134	1060134	1 A -> G	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1060458	1060458	1 G -> A	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1060491	1060491	1 G -> T	SNP (transversion)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1060503	1060503	1 A -> G	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1060557	1060557	1 G -> A	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1060596	1060596	1 A -> G	SNP (transition)	102	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1060641	1060641	1 C -> T	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
C	1061191	1061191	1 T -> C	SNP (transition)	75	100.0%	1[-269	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
A	1061194	1061194	1 G -> A	SNP (transition)	76	100.0%	6,8[-281	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
A	1061399	1061399	1 G -> A	SNP (transition)	88	98.9%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	A -> V	afuA CDS
A	1061809	1061809	1 G -> A	SNP (transition)	103	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
A	1061821	1061821	1 G -> A	SNP (transition)	112	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		afuA CDS
C	1062232	1062232	1 T -> C	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	V -> A	corA CDS
G	1062305	1062305	1 A -> G	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		corA CDS
G	1063967	1063967	1 A -> G	SNP (transition)	70	100.0%	1[-235	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	I -> V	mraR CDS
AGC	1065015	1065017	3 GCT -> AGC	Substitution	76 -> 80	97.4% -> 97.5%	4,5[-270	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	A -> S	Peptidase, M48 family protein CDS
C	1065021	1065021	1 G -> C	SNP (transversion)	82	100.0%	6,3[-209	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	V -> L	Peptidase, M48 family protein CDS
G	1065032	1065032	1 A -> G	SNP (transition)	82	100.0%	4[-363	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		Peptidase, M48 family protein CDS
G	1066684	1066684	1 A -> G	SNP (transition)	89	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	I -> V	ftsC CDS
T	1066860	1066860	1 C -> T	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		ftsC CDS
A	1067425	1067425	1 G -> A	SNP (transition)	93	100.0%	4[-248	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	A -> T	Pyridoxal phosphate homeostasis protein CDS
T	1068252	1068252	1 C -> T	SNP (transition)	84	100.0%	4[-362	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss	G -> E	dnaE CDS
A	1068284	1068284	1 G -> A	SNP (transition)	81	100.0%	2,5[-291	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1068497	1068497	1 G -> A	SNP (transition)	105	97.1%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
A	1069352	1069352	1 G -> A	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		dnaE CDS
	1326102	1326102	1 (A)3 -> (A)2	Deletion (tandem repeat)	311	93.9%	8,11[-12	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		
C	1326407	1326407	1 T -> C	SNP (transition)	293	99.3%	5,4[-83	Variants: BfR-CA-11057-TF15687-5_R	Concatemer BfR-CA-11057 - UniAss		
GG	28135	28136	2 AA -> GG	Substitution	119	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	VS -> VG	mrdA CDS
C	28213	28213	1 T -> C	SNP (transition)	131	98.5%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28216	28216	1 C -> T	SNP (transition)	132	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28237	28237	1 G -> T	SNP (transversion)	140	99.3%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
G	28780	28780	1 T -> G	SNP (transversion)	121	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28816	28816	1 C -> T	SNP (transition)	129	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	28822	28822	1 C -> T	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		mrdA CDS
T	32037	32037	1 C -> T	SNP (transition)	139	99.3%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		pyrG CDS
A	33736	33736	1 G -> A	SNP (transition)	126	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33748	33748	1 T -> C	SNP (transition)	122	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33751	33751	1 T -> C	SNP (transition)	121	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
T	33757	33757	1 C -> T	SNP (transition)	128	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
C	33769	33769	1 T -> C	SNP (transition)	134	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		recJ CDS
A	36609	36609	1 G -> A	SNP (transition)	274	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
A	36610	36609	0 +A	Insertion	273	85.7%	1,5[-280	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
C	36624	36624	1 T -> C	SNP (transition)	297	99.7%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
	36651	36651	1 (A)3 -> (A)2	Deletion (tandem repeat)	308	92.2%	4,6[-83	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
A	36654	36654	1 T -> A	SNP (transversion)	296	95.6%	5,7[-233	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
AA	36660	36659	0 +AA	Insertion	290	90.0%	1,8[-196	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
C	36669	36669	1 T -> C	SNP (transition)	307	99.3%	1,1[-269	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
G	38113	38113	1 A -> G	SNP (transition)	153	99.7%	4,4[-103	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
	70630	70630	1 (C)10 -> (C)9	Deletion (tandem repeat)	123	82.9%	6[-262	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Iron-binding protein CDS
T	461516	461516	1 A -> T	SNP (transversion)	94	80.9%	2,3[-178	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	S -> T	DUF115 domain-containing protein CDS
T	461528	461528	1 C -> T	SNP (transition)	95	80.0%	1,3[-177	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	D -> N	DUF115 domain-containing protein CDS
C	461537	461537	1 T -> C	SNP (transition)	97	94.8%	6,3[-222	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	N -> D	DUF115 domain-containing protein CDS
T	461547	461547	1 A -> T	SNP (transversion)	98	80.6%	2,6[-177	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	F -> L	DUF115 domain-containing protein CDS
	566899	566899	1 (G)10 -> (G)9	Deletion (tandem repeat)	101	86.1%	2,5[-233	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		hypothetical protein CDS
C	590366	590366	1 G -> C	SNP (transversion)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		metE CDS
T	590288	590288	1 C -> T	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		metE CDS
G	590669	590669	1 A -> G	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		metE CDS
G	591435	591435	1 A -> G	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	V -> A	metE CDS
A	591751	591751	1 G -> A	SNP (transition)	125	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	A -> V	MetQ/NlpA family ABC transporter substrate-binding protei
G	592020	592020	1 A -> G	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		MetQ/NlpA family ABC transporter substrate-binding protei
C	593035	593035	1 T -> C	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Oxidoreductase, ZDG-Fe(II) oxygenase family protein CDS
A	593863	593863	1 G -> A	SNP (transition)	116	99.1%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		luxS CDS
G	595686	595686	1 A -> G	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		gatB CDS
G	595755	595755	1 A -> G	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		gatB CDS
T	596264	596264	1 C -> T	SNP (transition)	96	99.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Glycerol-3-phosphate dehydrogenase [NAD(P)+] CDS
C	596757	596757	1 G -> C	SNP (transversion)	115	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	G -> A	Amidohydrolase CDS
G	596806	596806	1 A -> G	SNP (transition)	128	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Amidohydrolase CDS
G	597340	597340	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Amidohydrolase CDS
T	598008	598008	1 C -> T	SNP (transition)	123	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	V -> I	pilA CDS
G	598108	598108	1 A -> G	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		pilA CDS
C	598204	598204	1 T -> C	SNP (transition)	134	98.5%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		pilA CDS
T	932843	932843	1 A -> T	SNP (transversion)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	I -> N	Lysozyme CDS
C	1052849	1052849	1 T -> C	SNP (transition)	153	99.7%	4,4[-103	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
C	1056829	1056829	1 T -> C	SNP (transition)	110	99.1%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	E -> G	ccmA CDS
C	1058557	1058557	1 T -> C	SNP (transition)	104	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	I -> V	Putative ABC transport system permease CDS
T	1058795	1058795	1 G -> T	SNP (transversion)	103	97.1%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Putative ABC transport system permease CDS
T	1058819	1058819	1 C -> T	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	R -> K	ataC CDS
T	1058880	1058880	1 C -> T	SNP (transition)	99	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	V -> I	ataC CDS
G	1058884	1058884	1 A -> G	SNP (transition)	98	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1058971	1058971	1 G -> A	SNP (transition)	122	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059022	1059022	1 A -> G	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059108	1059108	1 G -> A	SNP (transition)	130	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
A	1059154	1059154	1 G -> A	SNP (transition)	119	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059162	1059162	1 A -> G	SNP (transition)	128	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	F -> L	ataC CDS
T	1059259	1059259	1 C -> T	SNP (transition)	123	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059283	1059283	1 A -> G	SNP (transition)	127	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059487	1059487	1 A -> G	SNP (transition)	126	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
C	1059541	1059541	1 T -> C	SNP (transition)	111	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		ataC CDS
G	1059624	1059624	1 A -> G	SNP (transition)	156	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
T	1059660	1059660	1 C -> T	SNP (transition)	136	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
C	1059675	1059675	1 C -> T	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1059897	1059897	1 A -> G	SNP (transition)	107	99.1%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
G	1059915	1059915	1 A -> G	SNP (transition)	106	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
A	1059961	1059961	1 G -> A	SNP (transition)	111	99.1%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	A -> V	Phytase-like domain-containing protein CDS
G	1059973	1059973	1 A -> G	SNP (transition)	111	98.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	I -> T	Phytase-like domain-containing protein CDS
C	1060048	1060048	1 T -> C	SNP (transition)	107	98.1%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	N -> S	Phytase-like domain-containing protein CDS
G	1060134	1060134	1 A -> G	SNP (transition)	102	99.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Phytase-like domain-containing protein CDS
C	1793565	1793565	1 T -> C	SNP (transition)	134	97.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	T -> A	cofH_nupC CDS
C	1294638	1294638	1 T -> C	SNP (transition)	136	99.3%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		MFS transporter CDS
T	1294793	1294793	1 C -> T	SNP (transition)	120	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	T -> I	MFS transporter CDS
A	1295652	1295652	1 G -> A	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		nusA CDS
T	1295733	1295733	1 C -> T	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		nusA CDS
C	1296710	1296710	1 T -> C	SNP (transition)	179	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		miaB CDS
A	1300327	1300327	1 G -> A	SNP (transition)	142	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	T -> I	tNC CDS
A	1303903	1303902	0 (A)7 -> (A)8	Insertion (tandem repeat)	106	89.6%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
A	1304441	1304441	1 G -> A	SNP (transition)	133	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	E -> K	Chemotaxis protein CDS
G	1306198	1306198	1 A -> G	SNP (transition)	114	99.1%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Ferric enterobactin receptor CDS
T	1307149	1307149	1 C -> T	SNP (transition)	123	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		Ferric enterobactin receptor CDS
G	1308269	1308269	1 A -> G	SNP (transition)	141	98.6%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	S -> P	CoA ester lyase CDS
T	1308298	1308298	1 C -> T	SNP (transition)	140	99.3%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	S -> N	CoA ester lyase CDS
C	1308320	1308320	1 T -> C	SNP (transition)	137	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	I -> V	CoA ester lyase CDS
G	1308428	1308428	1 A -> G	SNP (transition)	159	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	S -> P	CoA ester lyase CDS
A	1308485	1308485	1 T -> A	SNP (transversion)	141	99.3%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	I -> L	CoA ester lyase CDS
G	1308525	1308525	1 A -> G	SNP (transition)	139	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		CoA ester lyase CDS
A	1310383	1310383	1 G -> A	SNP (transition)	126	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	A -> V	hypothetical protein CDS
G	1311022	1311022	1 T -> G	SNP (transversion)	127	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
C	1311340	1311340	1 T -> C	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
T	1312069	1312069	1 C -> T	SNP (transition)	134	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
A	1312081	1312081	1 G -> A	SNP (transition)	138	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
C	1312087	1312087	1 T -> C	SNP (transition)	131	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		MatC-N domain-containing protein CDS
A	1312095	1312095	1 G -> A	SNP (transition)	128	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	L -> F	MatC-N domain-containing protein CDS
A	1312289	1312289	1 T -> A	SNP (transversion)	108	98.1%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
C	1312291	1312291	1 T -> C	SNP (transition)	108	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
AA	1312296	1312298	3 TTT -> AA	Deletion	101 -> 105	92.4% -> 96.1%	6,9[-260	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
TTT	1312313	1312315	3 AAG -> TTT	Substitution	100	99.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
GT	1312330	1312331	2 TC -> GT	Substitution	103	99.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
AG	1312333	1312334	2 TA -> AG	Substitution	103 -> 105	99.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
C	1312340	1312340	1 A -> C	SNP (transversion)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
C	1312342	1312342	1 T -> C	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
C	1312352	1312352	1 T -> C	SNP (transition)	127	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
G	1312383	1312383	1 A -> G	SNP (transition)	110	99.1%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
G	1312394	1312394	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
T	1312407	1312407	1 C -> T	SNP (transition)	99	98.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
A	1312413	1312413	1 G -> A	SNP (transition)	88	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
T	1312415	1312415	1 C -> T	SNP (transition)	88	98.9%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
	1312427	1312427	1 (T)6 -> (T)5	Deletion (tandem repeat)	78	97.4%	3[-224	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
C	1312433	1312433	1 T -> C	SNP (transition)	75	100.0%	3,2[-277	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
AG	1312440	1312441	2 GT -> AG	Substitution	73	98.6%	4,6[-257	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
A	1312448	1312448	1 G -> A	SNP (transition)	71	100.0%	2[-262	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
TGTG	1312456	1312455	4 GCAT -> TGTG	Substitution	65 -> 67	90.8% -> 91.0%	2,1[-207	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
GC	1312461	1312460	0 +GC	Insertion	71	81.7%	0,2[-199	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
G	1312465	1312465	1 A -> G	SNP (transition)	76	97.4%	1,1[-262	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
A	1312470	1312470	1 G -> A	SNP (transition)	77	98.7%	1,8[-271	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
A	1312481	1312481	1 G -> A	SNP (transition)	72	100.0%	6,3[-258	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		

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C	1312485	1312485	1 T -> C	SNP (transition)	72	98.6%	1,8E-253	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
C	1312487	1312487	1 A -> C	SNP (transversion)	73	82.2%	8,6E-196	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
A	1312489	1312489	1 G -> A	SNP (transition)	71	84.5%	2,6E-203	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
C	1312505	1312505	1 T -> C	SNP (transition)	58	98.3%	7,3E-209	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
C	1312507	1312507	1 A -> C	SNP (transversion)	56	96.4%	2,4E-196	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
	1312512	1312512	1 -T	Deletion	57	96.5%	5E-167	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
GG	1312516	1312517	2 TT -> GG	Substitution	58 -> 65	100.0%	1,8E-208	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
AT	1312519	1312520	2 TA -> AT	Substitution	65	100.0%	3,2E-227	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
TA	1312529	1312530	2 AC -> TA	Substitution	73 -> 74	100.0%	7,9E-270	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
C	1312538	1312538	1 T -> C	SNP (transition)	76	98.7%	2,4E-275	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
ATG	1312540	1312542	3 TGT -> ATG	Substitution	76	98.7%	2,4E-275	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
A	1312544	1312545	2 GG -> A	Deletion	77 -> 80	93.8% -> 97.4%	2,4E-217	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
	1312551	1312551	1 -C	Deletion	80	100.0%	1E-235	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
A	1312558	1312558	1 G -> A	SNP (transition)	81	98.8%	8,1E-294	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
T	1312560	1312560	1 C -> T	SNP (transition)	81	100.0%	2E-299	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
A	1312565	1312565	1 T -> A	SNP (transversion)	82	100.0%	6,8E-295	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
G	1312568	1312568	1 T -> G	SNP (transversion)	82	100.0%	4E-303	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
G	1312570	1312570	1 A -> G	SNP (transition)	83	100.0%	1,6E-298	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
G	1312577	1312577	1 A -> G	SNP (transition)	85	100.0%	3,2E-297	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
T	1312580	1312580	1 A -> T	SNP (transversion)	85	100.0%	1E-305	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
A	1312591	1312590	0 (A)3 -> (A)4	Insertion (tandem repeat)	100	88.0%	1,7E-301	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
GGG	1312610	1312612	3 TAA -> GGG	Substitution	104 -> 116	99.0% -> 99.1%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
A	1312664	1312664	1 G -> A	SNP (transition)	97	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
A	1312674	1312674	1 G -> A	SNP (transition)	96	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	A -> V	accA CDS
C	1312676	1312676	1 A -> C	SNP (transversion)	94	97.9%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
T	1312685	1312685	1 C -> T	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
T	1313231	1313231	1 C -> T	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		accA CDS
G	1314216	1314216	1 A -> G	SNP (transition)	127	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		fabF CDS
A	1314306	1314306	1 G -> A	SNP (transition)	110	99.1%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		fabF CDS
C	1314653	1314653	1 T -> C	SNP (transition)	146	99.3%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	T -> A	fabF CDS
A	1316808	1316808	1 G -> A	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
G	1316877	1316877	1 A -> G	SNP (transition)	103	99.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
C	1316976	1316976	1 T -> C	SNP (transition)	110	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		fabG CDS
A	1317402	1317402	1 G -> A	SNP (transition)	129	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	L -> F	gpmI CDS
A	1317449	1317449	1 G -> A	SNP (transition)	96	99.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	A -> V	gpmI CDS
A	1317469	1317469	1 G -> A	SNP (transition)	113	99.1%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317562	1317562	1 G -> A	SNP (transition)	95	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317958	1317958	1 A -> C	SNP (transversion)	140	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	D -> E	gpmI CDS
T	1317970	1317970	1 C -> T	SNP (transition)	141	99.3%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317973	1317973	1 A -> C	SNP (transversion)	143	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1317976	1317976	1 T -> C	SNP (transition)	144	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
A	1317979	1317979	1 T -> A	SNP (transversion)	142	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss	E -> D	gpmI CDS
G	1318006	1318006	1 A -> G	SNP (transition)	105	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
C	1318015	1318015	1 G -> C	SNP (transversion)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318018	1318018	1 A -> G	SNP (transition)	107	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318207	1318207	1 A -> G	SNP (transition)	126	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
G	1318468	1318468	1 A -> G	SNP (transition)	114	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		gpmI CDS
T	1319026	1319026	1 C -> T	SNP (transition)	128	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		mraY CDS
C	1319170	1319170	1 T -> C	SNP (transition)	118	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		mraY CDS
T	1320129	1320129	1 C -> T	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		murD CDS
G	1320495	1320495	1 A -> G	SNP (transition)	113	100.0%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		murD CDS
A	1321003	1321002	0 (A)5 -> (A)6	Insertion (tandem repeat)	170	99.2%	0	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
C	1326407	1326407	1 T -> C	SNP (transition)	353	99.7%	4,4E-103	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
G	1327851	1327851	1 A -> G	SNP (transition)	232	100.0%	1,6E-92	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
TT	1327864	1327863	0 +TT	Insertion	216	98.1%	1,4E-56	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
T	1327866	1327866	1 A -> T	SNP (transversion)	216	99.1%	3,7E-60	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
	1327871	1327871	1 (T)3 -> (T)2	Deletion (tandem repeat)	220	95.9%	1,8E-11	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
G	1327896	1327896	1 A -> G	SNP (transition)	154	99.4%	5,9E-59	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
T	1327911	1327911	1 C -> T	SNP (transition)	109	100.0%	3,2E-54	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		
T	1327914	1327913	0 (T)2 -> (T)3	Insertion (tandem repeat)	100	90.0%	4,1E-33	Variants: BfR-CA-11057-TF15687-6_R	Concatemer BfR-CA-11057 - UniAss		

Summary of exported data from SNP analysis								
Transformant	Deletion	Deletion (tandem repeat)	Insertion	Insertion (tandem repeat)	SNP (transition)	SNP (transversion)	Substitution	sum of SNPs
BfR-CA-11057-TF15687-11	7	8	6	9	844	228	133	1235
BfR-CA-11057-TF15687-12		5	3	2	156	18	6	190
BfR-CA-11057-TF15687-13	5	10	6	5	390	103	80	599
BfR-CA-11057-TF15687-1	5	6	3	7	307	49	18	395
BfR-CA-11057-TF15687-2	9	5	7	3	399	111	78	612
BfR-CA-11057-TF15687-3		14	5	5	468	102	59	653
BfR-CA-11057-TF15687-4	2	4	5	2	620	127	76	836
BfR-CA-11057-TF15687-5		3	1	2	268	58	38	370
BfR-CA-11057-TF15687-6	4	5	4	4	125	24	11	177
Consensus of all transformants					3			3

Read coverage <5 of transformants relative to recipient				
Transformant	Coverage	Minimum [bp]	Maximum [bp]	Length [bp]
BfR-CA-11057-TF15687-12	0->4	1687100	1687202	103
BfR-CA-11057-TF15687-11	0->1	1687099	1687202	104
BfR-CA-11057-TF15687-1	0	1687099	1687202	104
BfR-CA-11057-TF15687-2	0	1687099	1687202	104
BfR-CA-11057-TF15687-3	0	1687099	1687202	104
BfR-CA-11057-TF15687-5	0	1687099	1687202	104
BfR-CA-11057-TF15687-4	0->1	1687099	1687202	104
BfR-CA-11057-TF15687-13	0	1687099	1687202	104
BfR-CA-11057-TF15687-6	0->2	1687099	1687202	104
BfR-CA-11057-TF15687-4	0->4	1335289	1336405	1117
BfR-CA-11057-TF15687-2	4	1327923	1327929	7
BfR-CA-11057-TF15687-13	0->4.8	1322086	1322103	18
BfR-CA-11057-TF15687-2	4	1054273	1054279	7
BfR-CA-11057-TF15687-13	0->4.8	1048528	1048545	18
BfR-CA-11057-TF15687-13	0->4	1021333	1021662	330
BfR-CA-11057-TF15687-2	0->4	1021325	1021668	344
BfR-CA-11057-TF15687-11	0->4	190076	195222	5147
BfR-CA-11057-TF15687-4	1	47012	47022	11
BfR-CA-11057-TF15687-11	0->4	5773	6005	233
BfR-CA-11057-TF15687-4	0->4	5761	6008	248

Unused reads mapped to the donor BfR-CA-15687 with coverage >=20				
Transformant	Coverage	Minimum [bp]	Maximum [bp]	Length [bp]
BfR-CA-11057-TF15687-4	20->38	1305474	1305622	149
BfR-CA-11057-TF15687-4	20	1305427	1305427	1
BfR-CA-11057-TF15687-4	20->23	1305399	1305416	18
BfR-CA-11057-TF15687-4	20->102	1304276	1305396	1121
BfR-CA-11057-TF15687-2	20->38	1001583	1001917	335
BfR-CA-11057-TF15687-13	20->60	1001551	1001952	402
BfR-CA-11057-TF15687-11	20->24	5768	5903	136
BfR-CA-11057-TF15687-4	20->48	5697	5907	211