# The Molecular Epidemiology and Ecology of *Neisseria* Species in the African Meningitis Belt

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# Abstract

*Neisseria meningitidis* (*Nm*) is one of the major causes of bacterial meningitis in the African meningitis belt (AMB). This organism is part of the genus *Neisseria*, which includes ten human restricted species, mostly harmless commensals of the nasopharynx; however, *Nm* is capable of causing invasive meningococcal disease. The transition from carriage to pathogenic state remains perplexing, and strict virulece factors have yet to be identified.

It has been hypothesised that non-pathogenic *Neisseria* (NPN) carried asymptomatically in the oroopharynx could play a role in modulating carriage of *Nm*, and therefore, its likelihood of invasion. In chapter 3, the diversity of the genus was characterised within a collection of 46 034 nasopharyngeal samples obtained across the AMB: five different species were identified, with *Nm* and NPNs displaying inversely related risk factors fo carriage. Chapter 5 presents the whole genome sequence (WGS) analysis of 107 *Neisseria* isolates unclassified by other methods. This higher genetic resolution, complemented with the use of a novel speciation approach, revealed seven novel *Neisseria* species, mostly collected in African countries.

The invasive potential may also be due to the presence of particular genetic factors in the meningococcal genome. Chapter 4 presents the WGS comparison of 23 carried and invasive serogroup A *Nm* collected in Chad during the 2011 meningitis epidemic. Isolates from both phenotypic groups were found to be part of the same bacterial populations; however, discrete clusters were identified, associated with distinct age groups.

These results indicate that genomic analyses are essential to appropriately study *Neisseria* diversity, and that lower resolution methods have greatly underestimated the diversity of the genus in Africa. The identification of *Nm* clusters associated with certain niches and of the differences in carriage risk factors suggests that variation in the environment, including the presence of NPNs, may be key in modulating carriage of *Nm*.

# Acknowledgments

I would like to first express my gratitude to my supervisor Professor Martin Maiden for his constant guidance and support throughout the completion of my DPhil project. He has provided me with an excellent learning environment, and his suggestions and encouragements have pushed me to grow and better myself both academically and individually.

I would like to thank the Wellcome Trust for funding my project and providing me the financial peace of mind necessary to be trained and conduct state of the art research in my area of interest, infectious diseases.

I would also like to thank the CVD-Mali family for giving me my first professional experience without which I would not be here today, especially Professor Samba Sow, Dr Boubou Tamboura, Dr Awa Traore, Mrs Araba Maradou and all members of the laboratory division.

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Praise goes to Allah, for always guiding and protecting me and giving me the strength to undertake yet another challenge!

# Statement of contributions

This thesis has been made possible by the collection of isolates by international projects involving multiples research centres in Africa. However, the work and analyses presented herein are my own, except where explicitly stated in the relevant chapters or in the relevant sections below. No part of this work has been submitted for any other degree or professional qualification.

Chapter 3, published in *Journal of Infection* in June 2016; doi: 10.1016/j.jinf.2016.03.010 made use of DNA samples from isolates collected as part of the MenAfriCar project which took place in 7 countries of the African Meningitis Belt: Chad, Ethiopia, Ghana, Mali, Niger, Nigeria and Senegal, and involved the work of many people in each centres, to collect the nasopharyngeal swabs, characterise the isolates and prepare the DNA. The sequencing of the *f_rplF* loci was made in collaboration with Lisa S. Rebbetts. I was the lead and corresponding author upon submission of the paper.

Chapter 4 was published in *BMC Genomics* in May 2017; doi: 10.1186/s12864-017-3789-0. The isolates were collected as part of the MenAfriCar project and the routine meningitis surveillance in Chad by a team led by Kadija Gamougam from the "Centre de Support en Santé International" of N'Djamena (Chad). DNA was extracted by Dr Jay Lucidarme at the Public Health England Meningococcal Reference Unit (PHE-MRU, Manchester, UK) and by Pr Dominique A. Caugant's team at the Norwegian Institute of Public Health (Oslo, Norway), where isolates were stored. The genomes were sequenced at the Oxford Genomics Centre and were assembled and uploaded to the PubMLST

database by Dr James Bray from the Maiden group. I was the lead and corresponding author upon submission of the paper.

Chapter 5 made use of isolates collected in Mali and Chad (MenAfriCar project), in Malawi and The Gambia (by Dr Jenny MacLennan from the Maiden group), and in the UK (UKMenCar4 project). DNA was extracted by the PHE-MRU for the Chadian isolates, by Dr Jenny MacLennan for the Gambian isolates and by the respective UKMenCar4 groups for the UK isolates. The *de novo* sequenced genomes were done at the Wellcome Trust Sanger Institute (Hinxton, UK), under the supervision of Pr Julian Parkhill, and were assembled and uploaded to the PubMLST database by Dr James Bray. Additional genomes, available on the PubMLST database, were also used in the analysis. The morphological assessments were done with help from Dr Odile Harrison from the Maiden roup, and the scanning electron microscopy with help from Dr Errin Johnson, the Electron Microscopy Facility Manager of the Sir William Dunn School of Pathology (University of Oxford).

PDF formatted versions of the published manuscripts are available in Appendix 4.

# List of abbreviations

| | |
|---|---|
| ACT | Artemis Comparison tool |
| AMB | African Meningitis Belt |
| ANI | Average Nucleotide identity |
| aRRR | Adjusted Relative Risk Ratio |
| ASM | Acid sphingomyelinase |
| BAP | Blood agar plates |
| BCE | Before Coming Era |
| BIGSdb | Bacterial Isolate Genome Sequence Database |
| bp | base pairs |
| cc | clonal complex |
| cc5 | ST-5 clonal complex |
| CDS | Coding DNA Sequences |
| CEACAM | Carcinoembryonic antigen-related cell adhesion molecule |
| cgMLST | Core genome MLST |
| CI | Confidence Interval |
| *cnl* | *Capsule null* locus |
| CNS | Central Nervous System |
| *cps* | *Capsule synthesis* locus |
| CSF | Cerebrospinal fluids |
| DDH | DNA-DNA Hybridisation |
| ddNTPs | dideoxynucleotide triphosphates |
| DNA | Deoxyribonucleic Acid |
| DSS | Demographic Surveillance System |
| DUS | DNA Uptake Sequences |
| ECM | Extracellular matrix |
| ENA | European Nucleotide Archive |
| ETs | Electrophoretic Types |
| *f_rplF* | *RplF* fragment |
| *fetA_VR* | Variable region of the *fetA* gene |
| *fnl* | *FetA null* locus |
| GBDP | Genome Blast Distance Phylogeny |
| *gDNA* | Genomic DNA |
| GGA | Gamma Glutamil Aminopeptidase |
| *GGT* | Gamma-glutamyl transferase |
| Gubbins | Genealogies Unbiased By recomBinations In Nucleotide Sequences |
| GWAS | Genome Wide Association Studies |
| HGT | Horizontal Gene Transfer |

| | |
|---|---|
| *Hib* | *Haemophilus influenza* type b |
| HIV | Human Immunodeficiency Virus |
| HMDS | Hexamethyldisilazane |
| HSPG | Heparin sulphate proteoglycan |
| IMD | Invasive meningococcal diseases |
| Mb | Megabases |
| MDA | Meningococcal Disease Associated |
| MLEE | Multi Locus Enzyme Electrophoresis |
| MLSA | Multi-Locus Sequence Analysis |
| MLST | Multi-Locus Sequence Typing |
| MRF-MGL | Meningitis Research Foundation Meningococcus Genome Library |
| MRSA | Multi resistant *Staphylococcus aureus* |
| *Nb* | *Neisseria bergeri* |
| *Nb1* | *N. bergeri* subcluster 1 |
| *Nb2* | *N. bergeri* subcluster 2 |
| *Nb3* | *N. bergeri* subcluster 2 |
| *Nba* | *Neisseria bacilliformis* |
| *Nc* | *Neisseria cinerea* |
| *Ne* | *Neisseria elongate* |
| *Ng* | *Neisseria gonorrhoeae* |
| NGS | Next Generation Sequencing |
| NJT | Neighbor-joining tree |
| NJP | Neighbor-joining phylogeny |
| *Nl* | *Neisseria lactamica* |
| *Nm* | *Neisseria meningitidis* |
| *NmA* | serogroup A *Nm* |
| *NmB* | serogroup B *Nm* |
| *NmC* | serogroup C *Nm* |
| *NmE* | serogroup E *Nm* |
| *NmH* | serogroup H *Nm* |
| *NmI* | serogroup I *Nm* |
| *NmK* | serogroup K *Nm* |
| *NmL* | serogroup L *Nm* |
| *Nmu* | *Neisseria mucosa* |
| *NmW* | serogroup W *Nm* |
| *NmX* | serogroup X *Nm* |
| *NmY* | serogroup Y *Nm* |
| *NmZ* | serogroup Z *Nm* |
| *No* | *Neisseria oralis* |
| *Np* | *Neisseria polysaccharea* |
| NPN | Non-pathogenic *Neisseria* |

| | |
|---|---|
| *Ns* | *Neisseria subflava* |
| NSMs | Non-synonymous mutations |
| *Nspp* | *Neisseria spp.* |
| OMP | Outer Membranes Proteins |
| OMV | Outer Membrane Vesicles |
| ONPG | Orthonitrophényl-β-galactoside |
| OPGND | Oxidase positive, Gram negative diplococci |
| ORFs | Open reading frames |
| OsO4 | Osmium tetroxide |
| PCR | Polymerase chain reactions |
| rMLST | Ribosomal MLST |
| rt-PCR | Real time polymerase chain reactions |
| SBA | Serum bactericidal antibody |
| SEM | Scanning Electron Microscopy |
| SGS | Second Generation Sequencing |
| *Sp* | *Streptococcus pneumonia* |
| STs | Sequence Types |
| TGS | Third Generation Sequencing |
| TM | Thayer martin |
| UK | United Kingdom |
| wgMSLT | Whole genome MLST |
| WGS | Whole Genome Sequence |
| wgSNP | Whole genome single nucleotide polymorphism |
| WHO | World Health Organisation |

# Table of Contents

# I- Introduction

## A- Chapter 1: *Neisseria meningitidis*, the accidental pathogen

### Invasive meningococcal disease

Meningitis is a severe disease affecting the central nervous system (CNS) following inflammation of the spinal cord and meninges, the protective layers of the brain. Many different pathogens have been implicated but the most common are viruses that generally have non-life-threatening manifestations (1). On the other hand, bacterial meningitis is more dangerous and necessitates early diagnosis and immediate clinical intervention in order to prevent death or severe sequelae such as loss of hearing or sight, neurological damage and limb loss (2). The most common bacteria implicated in this disease are *Neisseria meningitidis* (*Nm)*, *Streptococcus pneumoniae* (*Sp*) and *Haemophilus influenzae* type b (*Hib).*

Invasive meningococcal diseases (IMD) refers to any affliction caused by an infection with the Gram-negative bacterium *Nm,* also called the meningococcus. Meningococcal meningitis and the blood infection called meningococcal septicaemia (or meningococcemia) are the typical manifestations and both have the potential to lead to life-threatening conditions.

## *Host-pathogen interactions*

The meningococcus is often referred to as an accidental pathogen, because its ability to cause disease confers no known evolutionary advantages to bacteria; on the contrary it is known to interrupt its chain of transmission and represents an ecological dead end (3). *Nm* is usually carried asymptomatically at the back of the throat of healthy individuals, a phenomenon called carriage. During this process, the meningococcus binds to the mucosal epithelial cells through interactions between its adhesin molecules, type IV pili, opacity associated proteins (Opa and Opc) (4) and the newly characterized minor adhesin proteins (5), and protein on the extracellular surfaces of the host epithelial cells leading to a strong attachment. For reasons that are still not clearly understood, bacteria are then able to cross the nasopharyngeal epithelial cells and either enter the blood stream causing meningococcemia (6) and/or disseminate to the spinal cord and meninges leading to meningitis. Despite extensive research, specific "virulence" factors that could explain the pathogenic potential of meningococci and help understand underlying mechanisms leading to invasive disease have yet to be identified; however, bacterial factors that most likely play a role in allowing the necessary invasion step have been described and studied (7-9). One of the most important is the capsule, a polysaccharide coating enclosing the bacterial cell, which is thought to be protective in the blood stream by allowing the bacteria to evade the immune system through different mechanisms leading to the inhibition of serum bactericidal antibody (SBA) induced complement–mediated lysis (10). All invasive meningococci are usually capsulated which indicates an important role for the capsule in the progression of the disease; however, many capsulated bacteria are also identified in asymptomatic carriage and

there have been reports of a few invasive disease cases caused by non-capsulated strains (11-13). These findings indicate that the capsule is probably part of a more complex system and is not sufficient for the organism to become pathogenic; it may also have another role in the bacterial life cycle that is yet to be discovered. Other mechanisms used by the meningococcus to evade the immune system have also been described, including host cell mimicry; one of the most prominent example is the binding of the factor H binding protein, a bacterial outer membrane lipoprotein (14) to human factor H leading to the down regulation of the complement mediated immune activity directed against the bacteria (15, 16). Once bacteria reach the blood brain barrier, they must breach that otherwise very impermeable membrane. Recent work has suggested that it is upon disruption of the tight junctions of the meninges and "hijacking" of the beta2-adrenoceptor/beta-arrestin pathway that the bacteria can gain access to the brain (17, 18). In the blood and the brain, most of the damage is caused by the strong inflammatory response, a consequence of the activation of the innate and adaptive responses orchestrated by immune cells such as neutrophils, and T and B lymphocytes.

Because *Nm* is a human restricted commensal and pathogen, no adequate animal models have been developed yet to allow appropriate *in vivo* studies. The recent discovery of a *Neisseria musculi sp. nov*, a new species found in a wild house mouse now provides the possibility to develop a good mouse model for the study of pathogen-host interaction (19). Nevertheless, *in vitro* studies have identified some of the human binding receptors targeted by the bacteria. The platelet activating factor and a member of the immunoglobulin superfamily (CD147) have been characterised as the pilus target on the airways epithelial cells and on the brain endothelial cells, respectively (20, 21). Opa

mostly bind to epithelial cells via members of the human carcinoembryonic antigen-related cell adhesion molecule (CEACAM) family (22); they can also bind to heparin sulphate proteoglycan (HSPG) or integrins (23); however, their targets on brain endothelial cells are yet to be fully defined (24). On the other hand, Opc is known to be involved in invasion of the brain endothelial cells through binding to their extracellular matrix (ECM) and serum proteins like vitronectin or fibronectin (25, 26). Recent studies have also demonstrated that the interaction of *Nm* with lipids such as acid sphingomyelinase (ASM) on the cell membrane of brain microvessels, could facilitate the invasion of the bacteria into the brain endothelial cells (27).

Individuals with complement deficiencies (15, 28-30) as well as immunocompromised hosts, including people living with human immunodeficiency virus (HIV) infection (31), have been associated with higher risk of developing meningococcal disease.

### *Clinical Diagnosis*

Clinical diagnosis is the first step in the identification of suspected cases of meningococcal disease. It is based on the identification of classic symptoms such as high fever, headache and stiff neck; clinicians are advised to look for additional symptoms such as nausea or vomiting, sensitivity to light or signs of neurological problems (confusion, dizziness or convulsion) (32). Depending on the age of the patient, these symptoms can be difficult to appropriately assess, especially in very young children (infants or neonates). Additionally, the principal symptoms are often not specific enough to distinguish meningitis from other common diseases, such as influenza or malaria,

which makes diagnosis very difficult especially in countries where a high burden of fever-inducing diseases are also major public health issues.

Because of the fast progression of IMD, rapid patient care is needed to prevent life-threatening consequences, such as death and/or permanent disabilities. This often leads to empirical treatment based solely on clinical diagnosis while awaiting laboratory confirmation.

### *Laboratory Diagnosis*

Early diagnosis is key to the effective management of IMD. The most commonly used laboratory diagnostic methods consist of the analysis and culture of cerebrospinal fluid (CSF) on selective growth media to obtain bacterial colonies for further characterization by microscopy as well as biochemical and serological tests. As CSF is a normally sterile body fluid, many parameters can indicate a probable case of infection such as: (i) the visual aspect of the liquid, which should be clear, any deviation from which indicates an abnormality and a cloudy aspect often associated with infection; (ii) the presence of any bacteria following Gram staining of CSF is indicative of a probable infection; and (iii) the number of white blood cells in the CSF can also indicate infection. The World Health Organization (WHO) guidelines recommend treating any patient with a CSF with a white blood cell count higher than 10 cells/$mm^3$ as a probable case of meningitis (33).

A case can only be confirmed when the presence of a specific bacterium has been identified by a laboratory following tests indexing the bacterial-specific properties. The application of molecular methods like polymerase chain reaction (PCR) for a culture-independent diagnosis has allowed a more sensitive detection of pathogens in the body

flui of patients (e.g.: blood, CSF) (34) but these methods do not provide important phenotypic information such as antibiotic resistance profiles and can only be used as an additional tool for efficient diagnosis. Culture methods still remain essential in many settings.

### *Treatment*

IMD patients are usually hospitalized and treated using a range of antibiotics such as penicillin, ampicillin, chloramphenicol and ceftriaxone (35). When possible, it is recommended that treatment is administered after collection of CSF for laboratory confirmation and bacterial characterisation; however, laboratory confirmation, which can take up to few days, cannot be awaited before the start of chemotherapy. Broad spectrum antibiotics are initially used and can be adjusted later on according to the laboratory results. The WHO recommends that household contacts of every case of IMD be offered antibiotic chemoprophylaxis as an important public health intervention, preventing transmission and potentially more cases among close contacts, a group at higher risk of contracting meningococcal disease. Nevertheless, many countries of the African meningitis Belt (AMB) have not been following that recommendation because of the associated cost , despite new studies reemphasizing the importance of such measures. (36).

### *Vaccination*

*Nm* is an encapsulated bacterium and the capsule protecting the cell has been the target of the first vaccines developed (37). Twelve different polysaccharide capsules have been characterised, differing by their biochemical properties and historically referred to as

serogroup (38), but only six of them are mostly implicated in IMD; serogroup A, B, C, W, X and Y (39). The most dominant serogroups associated with IMD have changed over time and their epidemiology varies geographically. It is therefore important to maintain disease surveillance, to allow an evidence-based choice of vaccines to be administered depending on the geographical location.

Serogroup-specific polysaccharide vaccines were the first vaccines available against meningococcal disease. These specifically target the polysaccharide capsule and are efficient in reducing the prevalence of IMD. However, they elicit short-term immunity in vaccinated individuals because of their T cell-independent immune response and require frequent booster vaccinations to maintain the level of protection. They therefore are a costly public health measure and are often not affordable for many developing countries, particularly as they do not elicit sufficient immune responses in infants and young children, the age groups most affected by the disease. Finally, polysaccharide vaccines do not affect carriage of meningococci and so do not reduce their transmission, which would allow indirect protection of unvaccinated individuals through herd immunity (37). Three polysaccharide vaccines are however still available: (i) bivalent A/C; (ii) trivalent A/C/W; and (iii) quadrivalent A/C/Y/W but none are routinely recommended in industrialised countries (40).

Newer conjugate vaccines have been more frequently used since their development in the 1990s. Such vaccines are able to deliver the poorly immunogenic polysaccharide antigens attached by covalent bonds to a carrier protein and are thus capable of inducing immunological memory in a T-cell-dependent response thereby generating long-term immunity (37). These new types of vaccines, known as polysaccharide-conjugate

vaccines, have been shown to be immunogenic in infants and young children (41). They have also been found to reduce the carriage rate of the targeted serogroups and thus decrease the risk of transmission. Different conjugate vaccines have been developed targeting one or multiple serogroups at a time and have been used in industrialized countries depending on the most common organism implicated. A serogroup C conjugate vaccine (MCC) was introduced in the UK in 1999 and had a significant impact on the reduction of both disease (42) and carriage of serogroup C *Nm* (*NmC*) (43). Several conjugate vaccines have since been developed targeting different combinations of serogroup: (i) monovalent serogroup C conjugate vaccine (44); (ii) bivalent serogroup A and C (45); and (iii) quadrivalent vaccines targeting seroroups A (*NmA*), W (*NmW*), Y (*NmY*) *Nm* and *NmC*, such as the MCV-4® (46), Menveo® (47) or Nimenrix® (48).

African countries, which were not able to buy these vaccines for mass vaccination campaigns, continue to use polysaccharide vaccines as reactive tools for responses to epidemics. In 2001 the Meningitis Vaccine Project was established as a collaboration between WHO and PATH, with financial support from the Bill and Melinda Gates Foundation. Their primary objective was to produce an affordable Serogroup A meningococcal conjugate vaccine suitable for countries of the AMB (49) where *NmA* IMD was responsible for prolonged outbreaks spanning several years. In fewer than 10 years, a serogroup A meningococcal conjugate vaccine, PSA-TT (MenAfriVac®), was produced at the Serum Institute of India, tested by clinical trials for safety and immunogenicity in multiples countries including India (50, 51), Ghana (52), The Gambia, Senegal and Mali (53). MenAfriVac® was first introduced in 2010 in Burkina Faso (54), Mali and Niger (55) and has been rolled out progressively in the other AMB countries, reaching 26 countries

and more than 270 million individuals by the end of 2016 (56). Serogroup X *Nm* (*NmX*) had not been included in any vaccine at the time of writing, but the development of a pentavalent A/C/W/X/Y conjugate vaccine by the Serum Institute of India has been on-going and opens opportunities for a better control of IMD in regions affected by these serogroups (57).

Conjugate vaccines were not tested for efficacy prior to their introduction, because of the low incidence of meningococcal disease, making efficacy studies unpractical (58). This stressed the importance of rigorous impact assessments on disease incidence following introduction of the vaccine but also on the carriage rates in order to evaluate the potential for the MenC conjugate vaccine in the UK (43) and for MenAfriVac® in the AMB countries to generate herd immunity (59).

There has been no successful attempt at producing a polysaccharide vaccine against serogroup B *Nm* (*NmB*), because of the homology between its polysaccharide molecule and the human neural cell adhesion molecules and the fear of creating an autoimmune response (60). New methods had to be designed to create a vaccine against *NmB* which is the major cause of IMD in occidental countries. Two approaches have been used: the first is based on outer membrane vesicles (OMV vaccines) containing proteins of interest that are present in the majority of characterised *NmB* isolates; these have been mostly efficient against specific strains circulating in a particular country and could not be licensed globally due to the diversity of the protein used (61). The second approach is based on the reverse vaccinology method, using genetic information to identify conserved proteins to be included in a "cocktail vaccine" (62). Two such vaccines have recently been licensed in Australia, Europe and North America, MenB-4C (Bexsero)(63)

and MenB-FHbp (Trumenba)(64). Although these vaccines have the potential to cover a larger part of the global diversity of serogroup B, it is not entirely clear how efficient they would be and whether they would also affect carriage, as seen with the polysaccharide-conjugate vaccines, allowing a larger population protection through herd immunity (65). Development of a universal vaccine, that would protect against all *Nm* serogroups, still remains an important part of the vaccine research field in meningococcal disease.

## Meningitis in Africa

### *History of meningitis in Africa*

Many CNS infections have been evident from anthropological specimens such as Egyptian skeletons dating from 3500 BCE and earlier; however, the unavailability of descriptions of symptoms or infectious agents makes it impossible to determine whether meningitis was already present at that time (66). The first known meningitis outbreak was reported in 1805 in Geneva followed by other accounts of the disease in Europe and North America during the nineteenth century (67). The first known African outbreak was reported in Algiers in 1840 among French militaries (68), followed in the late 1880's and early 1890's by outbreaks in South Africa (69) and later on in Egypt and Sudan as reported by members of the British Royal Army Medical Corps (70). It was not until 1912 that the first meningitis epidemic was documented in East Africa, with a large one recorded in the Rift Valley region of Kenya, causing thousands of deaths (69). There are

reasons to believe that the first epidemic also reached West Africa in the late 1890s, based on the recounts of local leaders in Nigeria during a meningitis epidemic in 1921, who described a disease with similar symptoms encountered 30 years earlier; however with no proper description or official reports it is difficult to determine whether it was indeed meningitis or another fever inducing epidemic disease which was not uncommon in the region at the time. Recounts from Ghana and other francophone countries reported that they had not encountered a similar disease before (69), and there are no mentions of any disease resembling meningitis outbreaks, which are quite dramatic and difficult to miss, in the diaries and writing of European explorers that had documented their travels in West Africa during colonial times.

### *The African meningitis belt*

The African meningitis belt (AMB) has been described by Lapeyssonnie as the region with the highest burden of meningitis with 7000 to 180 000 cases annually (71). From Senegal in the west to Ethiopia in the east, it covers parts of 26 countries of the sub Saharan part of Africa (Figure 1).

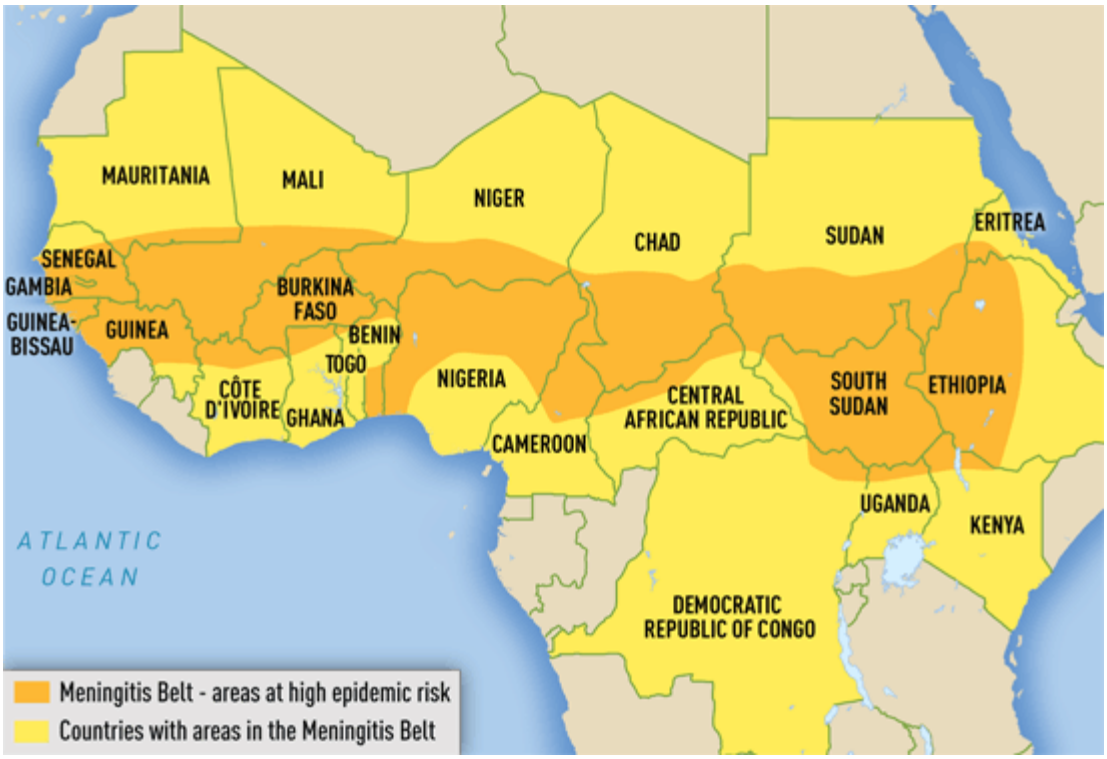



**Figure 1: Countries of the meningitis belt**
This map shows the countries that have part of their territory in the area called the Meningitis belt. It was obtained from the Centers for Disease Control and Prevention website

By the end of the 20th century, records of epidemics in Sudan were well established and a large epidemic was reported in Omdurman in 1899 (70). However, the first official account of an epidemic in west Africa occurred in 1905 in the north of Nigeria (72), which then spread to northern Ghana in 1906 (73). The meningococcus was suspected to have come from Sudan, with the pilgrims coming back from the Hajj (69). The epidemics in Nigeria and Ghana were impressive in their scale, causing thousands of deaths and leading to further investigations by the colonial authorities and to formal reports such as for the 1921 epidemic in Nigeria when more than 45 000 persons died or in 1949-1950, with 14 273 deaths (69, 74). In more recent years, the belt has suffered recurrent and unpredictable meningitis epidemics, observed every few years, with

annual attack rates as high as 1000 cases per 100 000 individuals. The largest epidemic was registered in 1996 with more than 250 000 suspected cases recorded (75). Since 1950, this region has also been subject to seasonal meningitis outbreaks occurring every year, starting around January at the beginning of the dry and dusty season and ending with the start of the rainy season in May (71). Most countries of the region have developed an enhanced national system for surveillance of the disease and detection of outbreaks. Data for all countries are centralised in the WHO reference laboratory in Ouagadougou Burkina Faso; reports are published weekly during the "meningitis season" and monthly during the rest of the year (76) (Figure 2).

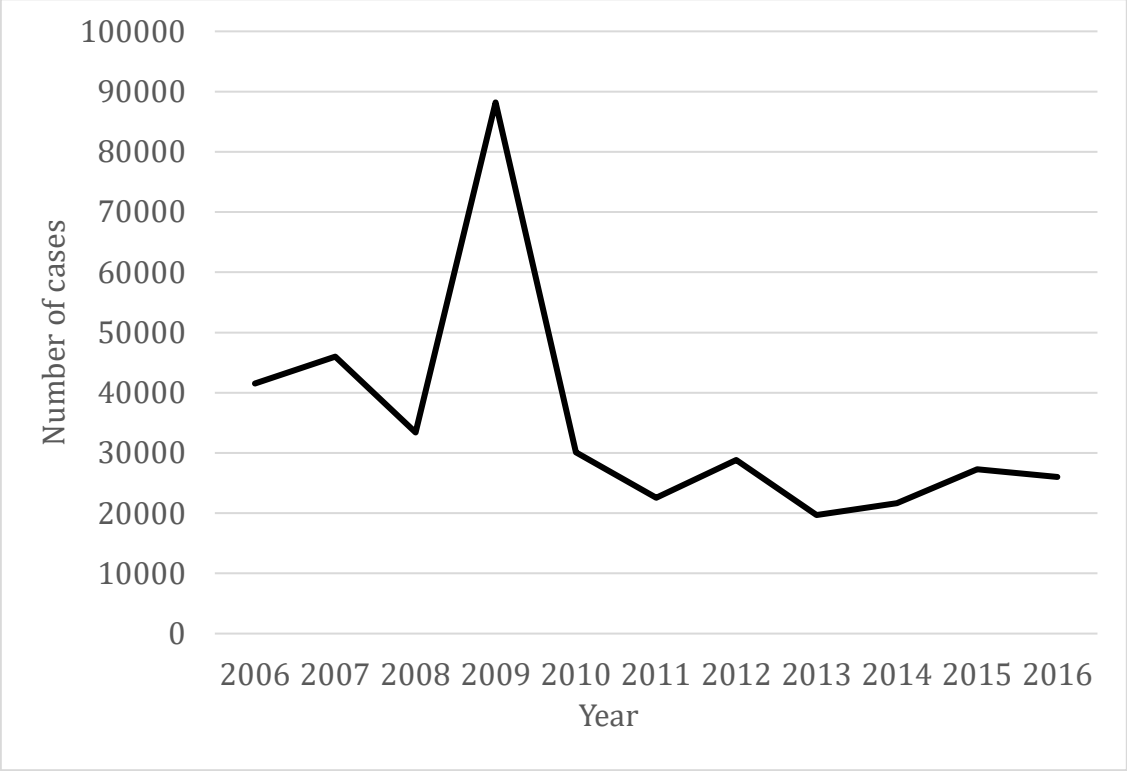



**Figure 2: Number of meningitis cases recorded in the African meningitis belt**
The data obtained from the Regional Meningitis surveillance weekly reports published by the WHO-Multi-Disease Surveillance Centre based in Ouagadougou, Burkina Faso and is available on the WHO website (http://www.who.int/csr/disease/meningococcal/epidemiological/en/). Countries under surveillance are: Benin, Burkina Faso, Cameroun, Centrafrique, Côte d'Ivoire, Ethiopia, Ghana, Guinea, Guinee Bissau, Gambia, Kenya, Mali, Mauritania, Niger, Nigeria, RD Congo, Senegal, Sierra Leone, South Sudan, Sudan, Tanzania, Chad, Togo and Uganda.

In 2016, 26 029 suspected IMD cases and 2080 deaths were recorded in 19 countries of the belt giving an average mortality rate of 8% (77). The most common pathogens identified in 2016 were *Nm* (1487cases out of the 11 118 samples collected, 13.4%) followed by *Sp* (1062 cases, 9.6%); only 87 cases (0.8%) of *Hib* were detected during the whole year.

Timely diagnosis in the AMB is challenging as very few laboratories are equipped to perform the necessary bacterial detection and characterisation. Laboratory strengthening programs sponsored by the WHO and other projects such as the recent MenAfriNet program have emphasized the importance of laboratory confirmation in the diagnosis of meningitis, but the laboratories targeted are often located in capital cities, which can be difficult to access from rural areas. Culture methods are still the most commonly used, although rapid diagnostic tests like Pastorex Meningitis (Bio-Rad) (78) or dipsticks (79-82) are also used, when available, to complement culture results.

The widespread uncontrolled access to antibiotics in some countries of the AMB and the use of self-medication or traditional medicine prior to presentation at hospital can make diagnosis of IMD difficult by reducing the ability to recover viable isolates for culture diagnosis. PCR methods are becoming more readily available especially in most national reference laboratories which are usually able to fully confirm their results by molecular methods (54, 83, 84). However, diagnosis in remote regions remains heavily dependent on clinical diagnosis and investments in sustainable laboratory capacity in those regions is still lacking.

Vaccination remains the most efficient public health intervention in the control of meningococcal meningitis; in the AMB, polysaccharide vaccines are still being

predominantly used, especially serogroup A and A/C, in numerous reactive immunization campaigns during meningitis epidemics across the belt (85-88). Other existing polysaccharide vaccines including additional serogroups, such as W and Y, have been used depending on the major epidemic strains identified by the surveillance (89-91). Until affordable pentavalent conjugate vaccines become available, these polysaccharide vaccines will remain crucial in a country response to epidemics; despite their known limitations.

Very few data are available for other regions of the African continent. North of the AMB, in countries such as Algeria and Morocco, surveillance is enhanced during periods of mass gatherings, especially during the Hajj pilgrimage, and vaccination is required for every pilgrim. The disease burden appears to be lower with an incidence rate of 2 to 3.6 per 100 and a case fatality ratio of 7 to 13% in Morocco, and an incidence of 0.48 per 100 000 in children <5 years old reported in Algeria in 2012 (92). Serogroups in circulation are closer to those found in European countries with *NmB* predominantly identified (92). Similarly, surveillance data in countries south of the belt are limited, except for South Africa which has a strong surveillance system and where IMD is endemic with a peak between May and October; the South African incidence rate reported in 2014 was 0.36 per 100 000 and the predominant serogroups causing disease were *NmW* and *NmB* (92, 93). Meningitis cases are occasionally reported from Malawi, but they are rarely caused by *Nm* and are usually attributed to *Sp* (94). Mozambique had recorded 63 cases of meningococcal disease between 1998 and 2008 and these were mostly caused by *NmA, NmW* and *NmY* (93). In other countries of the southern and northern regions, no global system is currently in place to capture that information as has been done for the

region of the meningitis belt. There has been a general tendency for the belt to expand towards the south, with cases identified between 1989 and 1994 in Kenya, Uganda, Rwanda, Central African Republic, Cameroon, Burundi, Zambia and Tanzania (95) and more recently with outbreaks occurring more regularly in the southern regions of Togo and Ghana (76); regions that are not strictly speaking in the meningitis belt described by Lapeyssonie.

### *Risk factors*

Risk factors have been investigated in relation to meningococcal disease in the AMB, and include: age, with children younger than 5 years being the most affected by the disease; exposure to smoke through cooking fires (96, 97) and tobacco/cigarette smoking albeit this was only true for *NmW* and *NmY* but not *NmA* (98); and proximity to a meningitis case (96, 97). Concomitant respiratory infections have also been found to increase the risk of IMD, through weakening of the immune system (97-99).

The following individual risk factors for asymptomatic infections were identified as increasing the odds of meningococcal carriage: being aged between 5-14 years old; being male; living in a rural site; sharing a room with more than two people; and smoking or cooking indoors. Surprisingly, recent respiratory symptoms were not a significant risk factor for carriage (100).

### *Seasonality*

Meningitis in the AMB has a clear seasonality pattern as the number of cases increases from January to May, with a peak occurring in March or April, the dry and hottest period in the region, corresponding to a hyper-endemic period often referred to as the

meningitis season (76). It is during this period that most IMD epidemics have been recorded. The number of cases dramatically decline with the start of the rainy season, from June to November, entering an endemic period with low incidence rates similar to what is usually seen in European countries (101).

In most countries of the Sahelian region, the meningitis season is often associated with the Harmattan, a dry wind coming from the desert, heavy with dust and sand particles, which alternates between very hot temperatures during the day and colder nights. The period during which that phenomenon happens, December to March, corresponds to the meningitis season, and the harsh weather conditions that are associated with it are likely to play a role in weakening the throat and/or respiratory tract mucosa and promoting respiratory infections of all sorts including IMD (71, 102, 103).

### *Pre and post MenAfriVac epidemiology*

Before the introduction of the *NmA* conjugate vaccine (MenAfriVac®) in 2010, *NmA* was the major cause of disease in the AMB leading to the largest epidemic recorded in 1996 (49, 104). In 2002 the first *NmW* epidemic occurred in Burkina Faso, associated with the return of pilgrims from the Hajj in Saudi Arabia (105). Both serogroups then coexisted with the ratio varying over the years (76) and other serogroups were rarely observed. Since the introduction of MenAfriVac®, the epidemiology of meningococcal disease has greatly changed. The numbers of cases of *NmA* reported in the WHO surveillance reports have drastically decreased in countries where vaccination has been implemented. A handful of cases have been reported in completely vaccinated countries, Burkina Faso in 2015 and Mali in 2016 (76) but no data on the vaccination status of these individuals

have been publically released, making it difficult to determine whether these resulted from vaccine failures. Since the introduction of MenAfriVac®, the number of *NmA* cases has dramatically decreased and other serogroups have been more often implicated in IMD and smaller scale epidemics, including *NmW*, *NmX* and *NmC* (78-80). An *NmC* epidemic has even caused a major outbreak in 2015 in Niger with 9367 suspected cases reported (106, 107). A significant increase in number of *Sp* meningitis cases has also been noted since the introduction of the vaccine in 2010 (76).

## Carriage studies

*Nm* is a common inhabitant of the oropharynx and is carried asymptomatically in a proportion of the population, varying with age and geographical location (108). Although most studies have focused on the characterisation of invasive isolates, the importance of the carriage state of the bacterium has now been recognised in order to understand its evolution and transmission. Indeed, invasive isolates only represent a small proportion of the bacterial population and an accidental stage of its life cycle; the large majority of the population remains in the carriage state, which is a pre-requisite for invasiveness.

Different carriage studies have been conducted to understand the bacterial evolution, population dynamics and, most importantly, the impact of vaccination on the carried meningococcal population. One such study was conducted in the UK between 1999 and 2001, to assess the impact of the introduction of the serogroup C conjugate vaccine (MCC) (43). This UKMenCar study found that the MCC vaccine was highly effective at

specifically preventing transmission of serogroup C meningococci, and a significant decrease in the carriage of *NmC* was noted (43). The reduction in *NmC* carriage in the vaccinated population was also associated with a reduction in non-vaccinated people, consistent with the notion of herd immunity whereby vaccination of the group at higher risk of carriage, in this case the teenagers, would decrease bacterial transmission and thereby protect non-vaccinated individuals (109). This phenomenon had previously been observed with the *Hib* conjugate vaccine (110).

Similarly, sporadic carriage studies have been conducted in the AMB over time with the most comprehensive one between 2010 and 2012 by the MenAfriCar consortium in order to assess the impact of the serogroup A *Nm* conjugate vaccine (MenAfriVac®) on carriage. The MenAfriCar consortium was established in 2009, to study meningococcal carriage in seven countries of the AMB prior to and post MenAfriVac® vaccination and evaluate the impact of the vaccine on carriage and immunity (111). The studies took place in selected urban and rural sites of Chad, Ethiopia, Ghana, Mali, Niger, Nigeria and Senegal. Three cross-sectional surveys were undertaken in each site, the first in 2010, the second in 2011 and the third in 2012; except in Nigeria where only one survey was completed. Household contact surveys were also done in households where individuals carrying any *Nm*, index carrier cases, had been identified during the cross-sectional surveys, to allow longitudinal studies of the pattern of infection (111). Each individual participating in the surveys was asked to complete a series of risk factor questionnaires prior to providing a oropharyngeal sample so that risk factors associated with *Nm* carriage could be assessed. Laboratory methods had been standardised and tested in each of the centres of the AMB allowing results to be comparable in downstream

analyses. Overall, 20 cross-sectional carriage surveys were conducted with 48 490 participants and an *Nm* carriage rate of 3.4% (95% CI, 3.2-3.6). Large variation between countries was observed (100). These results were consistent with earlier studies in individual countries of the African continent (112). During the MenAfriCar surveys, the level of *NmA* carriage had been low in the region, and the impact of the MenAfriVac® vaccine could only be assessed in Chad, where a significant decrease in both carriage and invasive cases of *NmA* was observed post vaccination (113). Carriage surveys also took place in Burkina Faso during that same period and similar results were obtained (114). As observed in the UK, herd immunity played a crucial role in the protection of non-vaccinated individuals post vaccination.

### *Transmission*

It is during the carriage state that bacteria are transmitted by close contact with infected respiratory droplets or throat secretion through coughing, kissing or sharing utensils. Transmission has been shown to increase in crowded environments such as military camps, or universities campuses (115). In the recent surveys done by the MenAfriCar consortium, it has been shown that carriage in the AMB was most prevalent in children between 5 and 14 years old, making them the primary source of transmission (100). The study also suggests that transmission occurs mostly within households from older siblings to younger ones but that adults and older children above 5 years of age could also acquire meningococci outside the house and introduce it to the household. The duration of meningococcal carriage appears to be shorter in the AMB compared to industrialised countries; indeed the mean duration of carriage was found to be 3.4

months (95% CI 2.7-4.4) (36) compared to at least 8 months found in the Netherlands (116) and 9 months in the UK (117).

### *Bacterial evolution*

Most of the *Nm* diversity occurs during the carriage state because the bacteria have to adapt to the host induced immunity as well as to the very complex dynamic of the nasopharyngeal environment; having to interact and probably compete with other microorganisms sharing the same niche (118). Different approaches have been used in recent carriage surveys for the molecular characterisation of *Nm*. These include the identification of the bacteria by culture or molecular methods; the determination of the serogroups via sero-agglutination or PCR (119); and the use of sequencing assays such as multi-locus sequence typing (MLST), indexing the allelic variation of seven housekeeping loci (120), and sequencing of the variable regions of the outer membrane proteins porA and fetA (121, 122). This information, when combined, provides a description of a strain type allowing better characterisation of the bacterial diversity. The meningococcus genetic diversity is extensive, with multiple sequence types identified and clustered into clonal complexes (cc); however the population remains structured with strong associations between certain cc and serogroups and a limited number of cc, the hyper-invasive lineages, usually causing disease (123). The carriage studies undertaken in the AMB established that the genetic diversity of the isolates was lower than that usually seen in European countries, indicating a geographically distinct dynamic of carriage that could explain the differences in disease epidemiology (100).

Whole genome sequence analysis is becoming the method of choice for studying *Nm* diversity as it provides better discrimination among closely related strains (124).

### *Neisseria genus*

The meningococcus is a member of the genus *Neisseria*, part of the family of the *Neisseriaceae*, which is a large group of Gram-negative β-Proteobacteria able to colonise multiple different host including, primates (125), mouse (19), human and many others. Ten human restricted *Neisseria* species have been characterised to date: *Neisseria bacilliformis, Neisseria cinerea, Neisseria elongata, Neisseria gonorrhoeae* (*Ng), Neisseria lactamica* (*Nl*)*, Nm*, *Neisseria mucosa, Neisseria oralis, Neisseria polysaccharea* (*Np*)*, Neisseria subflava* (*Ns*) (126).

*Ng* is known to colonise the genitourinary tract, causing the sexually transmitted disease gonorrhoea. The remaining species usually colonise the nasopharynx; unlike *Nm,* the other nasopharyngeal *Neisseria* are considered harmless commensals and have been only rarely associated with disease, mostly in immuno-deficient individuals (127).

Investigations of non-pathogenic *Neisseria* (NPN) remain infrequent, as these organisms do not represent a public health threat. However, *Nl* has been studied due to its particular epidemiology; indeed, the age distribution and diversity of carriage of *Nl* have been studied in different parts of the world (128) including countries of the AMB (129, 130), and it has been shown to be highly diverse and to colonise mostly young children under 5 years old, an age group rarely colonised by *Nm.* These findings suggest that *Nl* could play a protective role against *Nm* carriage and thus prevent disease.

Little epidemiological data are available on the other NPN species, despite evidence that other species, like *Np*, are more closely related to *Nm* at the genetic level (131, 132), which makes it difficult to study any potential protective roles against meningitis. *Neisseria* species have been described as competent bacteria, able to take up DNA from their environment through transformation, and recombination between *Nm* and other NPN species have been documented (133, 134), emphasizing the need for a better understanding of the interactions between these organisms. The results obtained from the recent challenge studies with *Nl* (135) suggest that NPN could play an important role in modulating carriage of *Nm* and stress the importance of a global study of carriage of the human restricted *Neisseria* species.

## B- Chapter 2: Population genomics of pathogenic bacteria exemplified by *Neisseria meningitidis*

### What is population genomics?

Population genomics refers to the genome-wide analysis and comparison of nucleotide sequence data from a representative population sample, in order to understand the phylogenetic relationships of members of the population, and the impact of evolutionary processes and functional variation on them (136). The term found popularity in the study of human genomes but has been adopted in every field studying genome sequences including bacterial genomics (137). Population genomics enables the differentiation among evolutionary processes that influence individual loci i.e. mutation, selection, recombination, leading to bacterial adaptation, and those that act genome-wide, such as genetic drift or population bottlenecks, reflecting the population evolution (138). Such analyses apply the fundamental principles of population genetics to genome datasets with the aim of characterising evolutionary forces (mutation, gene flow, recombination and genetic drift), determining the bacterial population structures, improving isolate characterisation (typing) and studying experimental evolution (139). Because they were initially developed to work with a small number of loci, often individual loci, the applications of most evolutionary models to complete genomes or large quantities of sequence data have to be undertaken with caution, and the assumptions that underlie them have to be kept in mind. Population genomic models remain a developing area of study and it is necessary to adapt the approaches employed to the large-scale data now available as well as to develop new ones applicable in a given setting.

An idealised population genomic study requires an unbiased sample of the population in question, which is usually impractical to obtain due to sampling constraints; however, it is possible to reduce these biases by including an appropriate representation of population diversity. In the case of bacterial pathogens, however, this can be difficult to achieve because study sets typically include mostly invasive isolates.

In the first of such studies, the generation of bacterial genome data was dependent on the ability of the microbiologist to culture the pathogens of interest, however, it is known that culture methods are only effective for a small number of bacterial taxa and often underestimate the diversity of bacterial populations. Additionally, for certain diseases, disease-associated isolates represent only a small portion of the population, albeit the most sampled. Many of these organisms also exist as commensals and are able to transmit asymptomatically. Examples include the three bacteria commonly causing meningitis: *Neisseria meningitidis* (*Nm*); *Streptococcus pneumonia* (*Sp*); and *Haemophilus influenza* type b (*Hib*). The focus on sequencing isolates from cases of invasive disease can introduce bias into studies of the population genomics of such organisms (108). The problem is similar for pathogens that have more than one host or that are found in the environment (e.g. *Campylobacter spp., Salmonella spp*) (140). With improvements in methodologies and reductions in cost it is now possible to sequence all the cells present in a sample, allowing the sequencing of all bacteria present independent of culture. These new metagenomic approaches will enable a more complete analysis of bacterial populations (141).

This chapter will present the evolution of different methods used to study bacterial populations from the phenotypic to the genomic era and the knowledge that has been

gained (Figure 1). The bacterium *Nm*, also known as the meningococcus, will be used as the principal exemplar. This pathogenic organism has been at the forefront of the development of bacterial population genomics. Its particular life style, being most of the time carried asymptomatically as a commensal of the human nasopharynx but also able to cause severe invasive meningococcal disease (IMD), has led to pioneering work in the field of bacterial population genetics and continues to intrigue researchers. The high level of diversity observed in meningococcal populations has also motivated many studies that investigate the phenotype-genotype link.

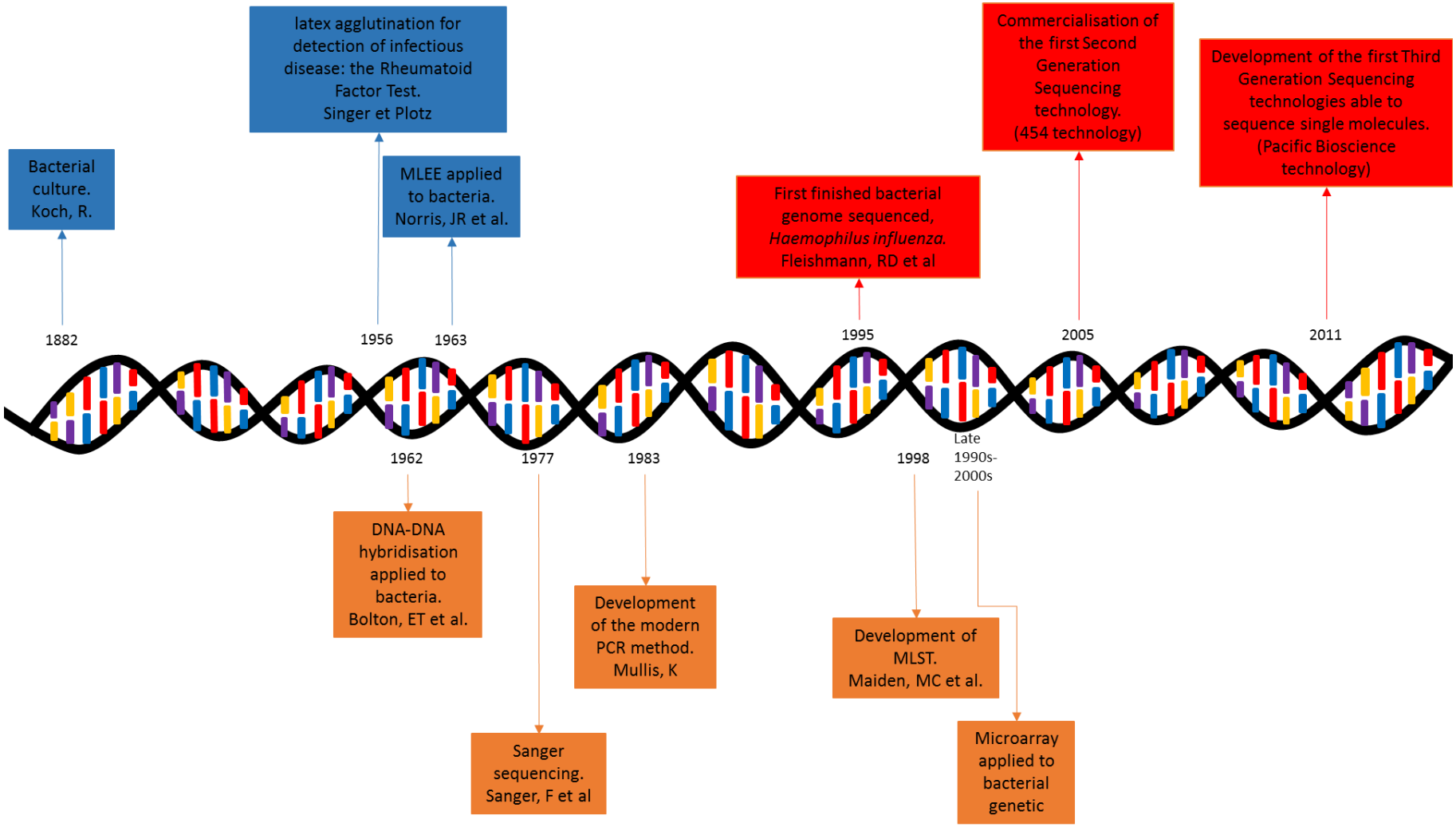



**Figure 1: Time line of the different methodologies used in the study of bacterial populations.**
The phenotype based assays are depicted in blue boxes, the sequence based assays in orange boxes and the genome based assays in red boxes.

## Phenotypic methods for bacterial characterisation and diversity studies

Before the availability and application of sequencing methods, which expanded at the end of the 20th century and the beginning of the 21st, phenotype-based methods were essential for bacterial characterisation and these remain an important part of clinical microbiology. Different tests have been developed to study the diversity of bacteria by exploring the observed phenotypic diversity of the organisms, which ultimately represent the diversity encoded by the genome.

### *Culture*

The ability to culture an organism, pioneered by Robert Koch in the 1980s, remained essential in the study of bacterial diversity until the development of molecular tests; indeed, bacterial growth had to be seen on an appropriate media to allow further characterisation of the pathogens under study. Most known pathogenic bacteria studied in the context of a disease investigation can grow on non-selective agar such as blood agar plates which provide all the nutrients necessary for their growth; however, optimal growth of specific bacteria of interest often requires the use of agar plates with particular properties, e.g. containing specific antibiotics to prevent the growth of other commensal bacteria. For example, *Hib* grows very slowly on blood agar plates and requires chocolate plates which are enriched with lysed red blood cells, introducing their intracellular nutrients into the agar (Haemoglobin, Factor X or Factor V) (142). *Neisseria* species, including *Nm*, grow well on blood agar plates but are often cultivated

on Thayer martin (TM) agar plates containing antibiotics to limit the growth of Gram-positive bacteria such as *Sp*, as well as to reduce the growth of other commensal bacteria that could be present in the sample under study (143). With the increased understanding of the different bacterial growth requirements, specific agar media have been created to facilitate the culture of particular bacterial pathogen.

The agar plates are then incubated in appropriate temperature conditions, in aerobic or anaerobic atmosphere and for particular lengths of time depending on the bacteria under study. Once colonies are obtained, they are further characterized using morphological appearances as well as biochemical properties. Different bacterial morphology can be observed under a microscope: Cocci (round shaped), bacilli (rod shaped), and others (including spiral like shapes). Gram's staining test, which allows the differentiation between Gram-negative and Gram-positive bacteria based on the physical and chemical properties of their cell walls, has also become an essential step in any bacterial characterisation (144). Oxidase, catalase and other biochemical tests can be added to further characterise the bacteria identified. *Nm* grows at an optimal temperature of 37°C in a 5% $CO_2$ enriched atmosphere within 16 to 24 hours and is characterized as oxidase and catalase positive, Gram-negative diplococci known to generate acid from glucose and maltose and to have an active gamma glutamiltransferase (145). Each pathogenic bacterium has a similar series of tests that are required to confirm their identification, which can take multiple days before a final result is obtained.

Decisions on appropriate culture methods require an extensive amount of *a priori* knowledge of the bacterium of interest. Optimal growth conditions have yet to be

identified for the majority of bacterial life, which remain a major challenge for studying its diversity using culture-based methods; however, most human pathogenic bacteria have been well characterised in this respect. Many diagnostic kits have been developed to facilitate bacterial identification and characterisation, which rely on the availability of a pure culture, keeping the culture method at a central place in the study of bacterial population diversity.

### *Serological assays*

Serological methods have been extensively used in the characterisation of certain bacteria including those involved in meningitis cases. These assays depend on the agglutination of cultured bacteria that express a specific antigen with a prepared serum in a direct fashion or indirectly when the antibody of interest is attached to latex beads. Latex agglutination tests have been widely used for the typing of clinically relevant pathogens and many kits have been developed to facilitate the performance of these tests. For *Nm,* the main antigen corresponds to the polysaccharide capsule and has led to the identification of meningococci harbouring diverse capsules classified as serogroups (146); there are currently 12 known *Nm* serogroups (*NmA*, *NmB*, *NmC*, *NmE*, *NmH*, *NmI*, *NmK*, *NmL*, *NmW*, *NmX*, *NmY*, *NmZ*) (38). Although some rapid sero-agglutination assay kits have been developed and commercialised to determine *Nm* serogroups, the majority focus on the six most commonly associated with disease, namely *NmA*, *NmB*, *NmC*, *NmW*, *NmX* and *NmY*. Serotyping assays based on the diversity of outer membranes proteins (OMP) of *Nm* have also given rise to further characterisation named serotype (based on

the diversity of the OMP *porB*; not to be confused with the capsular serotype described for other bacteria) and subtype (based on the diversity of the OMP *porA*)(147, 148).

The classification of bacterial diversity via serological methods has been an essential tool for the epidemiological study of important pathogenic bacteria. The local and global efforts for IMD surveillance initially relied on the proper reporting of the serogroups, serotypes and subtype of the bacterium isolated in each IMD cases (149-154). Certain serotypes were more associated with IMD than others that were more frequently isolated from healthy carriers (155). The method did not allow the characterisation of all the meningococci and left some as non-groupable which could either be the less invasive serogroups, rarely tested for, or *Nm* not expressing the capsules for reasons understood only much later with the availability of sequences (see Antigen typing and MLST section).

Although sero-agglutination assays are known to be labour intensive, difficult to interpret and sometime unreliable due to multiple or self-agglutinations, these tests remain useful tools in the diagnosis of certain bacterial diseases especially in developing countries where new molecular or genomic methods are not yet fully accessible.

### *Multi locus enzyme electrophoresis (MLEE)*

One of the first applications of bacterial population genetic approaches to bacterial diversity was MLEE. This method, first used in the study of *Drosophila* (156) and human (157) diversity was extended to bacteria (158), allowing the assessment of genetic discrimination within bacterial population samples by assigning electrophoretic types (ETs), based on the differences in the electrophoretic mobility of housekeeping enzymes

in starch gel electrophoresis (159). MLEE shed further light onto the population structure of *Nm* by indirectly indexing the sequence diversity of nine enzymes. One of the first studies applied MLEE to 152 *Nm* isolates of diverse serogroups, but with a majority of *NmB*, and identified 55 distinct ETs. No substantive genetic differences were observed between carried and invasive isolates with this method. However, the authors found that ET-5 was associated with invasiveness, representing 58% of invasive isolates but only 18% of the carried ones. The study demonstrated that distinct *Nm* strains could be differentially distributed among isolates from disease and carriage, with some meningococci exhibiting a 'hyper-invasive' phenotype. The analysis of the allele distributions among the different genotypes was also the first indication of extensive horizontal gene transfer (HGT), mediated by homologous recombination in *Nm* populations (159). MLEE was used to study the diversity of invasive and carried *Nm* (160-162). A similar approach, with the additional analysis of the diversity of OMPs, was also used to study the diversity of *NmA* epidemic isolates and identified a clonal population structure (163). MLEE was used in the study of many other organisms including, *Listeria monocytogenes* (164), *Staphylococcus aureus* (165) and *Sp* (166). This method established bacterial population genetics as a discipline, as it assessed variation at a large number of enzymes and could directly be correlated to allelic changes in the enzyme-encoding DNA sequences. It could therefore be used for phylogenetic analysis; however, the method was difficult to reproduce among different laboratories.

## Sequence-based methods for bacterial characterisation

Even though it was possible to sequence the whole genome of a bacterium by the end of the 1990s, it remained very expensive, technically difficult, and mostly undertaken by specialist genome centres. Bacterial genetic studies therefore relied on a series of sequence based molecular methods, focusing on a particular gene or set of genes. These methods were at the interface between population genetics and population genomics as it has subsequently developed.

### *DNA-DNA hybridisation*

DNA-DNA hybridisation (DDH) methods have been used to study the genetic similarities among species, by comparing the ability of their DNA sequences to hybridise with each other to form double-stranded DNA and measuring the level of energy required to separate them in a DNA melting experiment. DDH was, for some time, the "gold standard" method for bacterial species definition and identification by assuming a similarity threshold of at least 70% to consider two bacteria as part of the same species (167). The method was first used in the context of *Neisseria* to study the genetic relationship of the two pathogenic species *Nm* and *Neisseria gonorrhoeae* (*Ng*) and found that they were very closely related (93%) and could even be classified as different subspecies of one species (168); however, because of their different clinical manifestations they remained classified as distinct species. DDH studies also allowed the differentiation between the "true *Neisseria*" (e.g. *Nm* or *Ng*) from the "false *Neisseria*" (e.g. *Neisseria caviae* or *Neisseria ovis*) within the *Neisseriaceae* family (169, 170). The concept remains central to the field of bacterial taxonomy at the time of writing,

however, it is being replaced by analogous values generated from the computational comparison of DNA sequences such as Average Nucleotide identity (ANI)(171) or Genome Blast Distance Phylogeny (GBDP) (172).

### *Antigen typing and MLST*

First generation bacterial population genomics relied on the sequencing of a small number of loci across a large number of isolates using dideoxy Sanger sequencing, named after Fred Sanger who developed the methods in 1977 (173). The method involved the incorporation of chain terminating dideoxynucleotide triphosphates (ddNTPs) by the DNA polymerase during the amplification process. Initially these reactions were run separately for each individual ddNTPs (A, T, C or G), the products were then loaded on individual lanes of sequencing gels and visualised with radioactivity to determine the sequences, which was relatively laborious. The system has been automated with the use of differentially labelled fluorescent ddNTPs, whose light emission can be captured by an optical system enabling automated high-throughput DNA sequencers. The Sanger method provides longer reads, typically determining DNA fragments of up to about 1000 base pairs (bp) within a single run, with relatively high accuracy. The first generation of sequencers allowed high throughput sequencing of individual loci making them suitable for multi locus studies and the sequencing of single complete genomes. The Sanger method continues to have application in sequencing those missing parts of genomes left incomplete after sequencing with next-generation platforms.

One of the most common applications of Sanger sequencing in bacterial population genomics has been multi locus sequence typing (MLST), which at the time of writing remained an important paradigm for bacterial typing (120). MLST schemes have been developed for many different bacteria and 95 bacterial MLST schemes are hosted on the PubMLST database (174). MLST adapted the principles exploited by MLEE, but assessed the variation in the sequences of small number of housekeeping genes, 7 in the case of *Nm* (120). MLST indexes the allelic variation of genes or gene fragments under stabilising selection for conservation of metabolic function and uses the combinations of alleles at these loci to assign sequence types (STs). The method led to the description of clonal complexes (cc), groups of isolates with related STs which persist in bacterial populations through time and geographical spread. As with MLEE, it allowed the identification of the hyper-invasive lineages (123) associated with disease. In 2009 the following hyper-invasive cc were identified: cc1, cc5, cc8, cc11, cc18, cc23, cc32, cc41/44, cc103, cc162, cc269, cc334. Other cc were found principally in *Nm* from asymptomatic carriage (108). The advantage of the sequence-based MLST over MLEE was that it was easier to reproduce and allowed a simpler sharing of data between laboratories using web-based databases such as www.pubMLST.org. However, MLST remained relatively labour intensive, required expensive equipment and some level of computer literacy, making the approach challenging to implement in many routine settings. MLST schemes still remain very relevant to epidemiological studies of many bacteria, but in the era of next generation sequencing (NGS) technologies, it is increasingly more cost effective to determine MLST loci from whole genome sequence (WGS) data.

Single-locus Sanger sequencing assays have also been developed for bacterial species identification, for example, the sequencing of the 16S ribosomal RNA genes (175), the consensus being that bacteria sharing more than 95% sequence identity at this locus are indistinguishable at the species level (176). Although this approach is useful to differentiate members of different genera it is not very accurate at the species level for genera such as the *Neisseria* (177). The sequencing of a fragment of another ribosomal gene, *rplF,* was found to be more effective in discriminating among the different *Neisseria* species and is an alternate target for species identification (132, 178).

Sanger sequencing-based approaches have also been used for pathogenic bacterial typing by assessing the diversity of outer membrane proteins (OMP) to discriminate among different strains of bacteria. This has been the case for *Nm,* with the sequencing of the two genes (*porA* and *porB*) encoding the PorA and PorB porins previously used in sero-subtyping assays (179, 180). Other antigens such as FetA*,* an iron-regulated, tonB-dependent OMP encoded by the *fetA* gene, have subsequently been added to the typing system of *Nm,* and have been readily sequenced to study the global diversity of the meningococcus (121). Finally, sequencing of the capsule synthesis (*cps*) regions allowed the study of the diversity of the genes involved in capsule synthesis (38). This includes characterisation of *Nm* lacking cps genes, leading to the discovery of the capsule null meningococci, *cnl*, which are different from isolates not expressing the *cps* genes but are indistinguishable by serological methods (181).

Phylogenetic inference made by sequence analysis confirmed the importance of HGT, mediated by homologous recombination in the evolution of *Nm,* as suggested by MLEE, and more generally of members of the *Neisseria* genus (133, 182). Sequencing of the

penicillin resistance associated gene *penA* from pathogenic *Neisseria* (*Nm* and *Ng*) revealed the role of HGT in antimicrobial resistance by identifying the formation of mosaic genes in *Nm* and *Ng*, with short sequences acquired from commensal *Neisseria* species (183). Despite the recognition of the occurrence of HGT, the clonal paradigm of bacterial populations was considered predominant and studies of invasive *NmA* isolates suggested a clonal model of evolution of the bacteria (163, 184, 185). However, the inclusion of more carriage isolates in the sequence analysis have shown that *Nm* is actually a highly recombinogenic bacterium with high levels of HGT, as suggested by the distinct phylogenetic relationships inferred from the trees reconstructed using sequences of different genes (186-188). Recombination rates have been described to be up to 10 times those of mutation in *Nm* (189). Different bacterial recombination mechanisms have been defined: transduction, the introduction of genetic variation through incorporation of DNA from a viral phage; conjugation, the transfer of DNA sequences via a direct cell to cell contact between two bacterial cells and transformation, which is the most common mechanism used by *Neisseria* species and the meningococcus involving DNA uptake from the environment (190).

### *Polymerase Chain Reaction (PCR)*

The PCR, developed as a practical tool in 1983 by Karry Mullis, allows the amplification of specific DNA sequences, from as low as a single copy, in a series of iterative temperature changes, by a DNA polymerase enzyme using sequence-specific primers. As this process is repeated, the number of DNA copies increases in an exponential manner and can then be visualised on an electrophoresis gel for traditional PCR methods (191).

Many techniques, such as real time PCR (rt-PCR) which includes a fluorescently labelled probe sequence in addition to the two primers (forward and reverse), allow the visualisation of the amplification in real time as the dye is captured by a camera, with increase of fluorescence associated with an increase in amplified sequences. This technology has been useful in the improvement of first generation sequencing where large amounts of template sequences were required. Since the design of efficient PCR assays depends on the knowledge of the DNA sequence of the targets, the improvement of sequencing methods and access to a more diverse set of gene sequences has allowed the design of more accurate assays. At the time of writing, it was possible to investigate multiple targets simultaneously in multiplex assays, which has been extensively exploited for diagnostic purposes for rapid differentiation among possible pathogens causing diseases like meningitis: many PCR assays have been developed for rapid identification of *Nm,* amplifying species-specific genes including *ctrA, porA, sodC* (119, 192-194). PCR assays targeting genes involved in the synthesis of the polysaccharide capsules have also been designed to rapidly identify the different serogroups, which are called genogroup when characterised by molecular methods (119, 195, 196).

These assays have improved laboratory diagnostic capacity to detect many bacteria, including *Nm* and other bacteria that are otherwise difficult to culture such as *Mycobacterium tuberculosis* (197) and thus allow more accurate and rapid disease surveillance.

### *Microarrays*

Microarray technology, developed in the 2000s, has also been used to study population genomics, but the arrays are typically manufactured on the bases of available sequences from reference genomes. Although this approach is effective in the study of the presence or absence of particular genes found in a reference gene set, and genetic variation within a particular species, it is less suitable for the identification of genomic variation among more divergent isolates. It is also not able to provide any information on genes that are absent from the reference set (139).

## The genome era: the population genomic approach

Improvement in the methods and decrease in cost of WGS technologies, made sequencing of large numbers of genomes feasible, replacing and complementing single gene sequencing. The first bacterium to be fully genome sequenced was *Hib* in 1995. This was achieved with Sanger sequencing methods with individual reads computationally assembled into a single contiguous sequence, or 'contig', of 1 830 137 bp. This took about a year to complete and was a proof of concept that such a method could work with other bacterial genomes (198). The first *Nm* genomes to be sequenced were the *NmA* isolate Z2491 (199) and *NmB* isolate MC58 (200) both published in 2000. It was not until 2010 that the genome sequence of a non-pathogenic *Neisseria*, *Neisseria lactamica* (*Nl*) became available (201); indeed, despite the possibility of WGS, most projects continued to rely on Sanger sequencing methods to study the population genomics of particular medically relevant organisms until a significant drop in the cost of the different technologies to more affordable ranges. Not only has the cost decreased,

but the length of time to generate a genome sequence has also considerably reduced to a few days and user-friendly analysis tools have been developed making the genome assembly and analysis more accessible to microbiologists, without the necessity of extensive training in bioinformatics. Robust population genomic studies of bacterial pathogens have been made possible through those technical improvements and the rest of this chapter will introduce the different sequencing technologies, their impact in the field of *Nm* population genomics and the most common sequence analysis methods developed for such studies.

## *Next generation genome sequencing technologies*

Once the population of interest has been identified and appropriately sampled, different approaches can be used to sequence the isolates, depending on the question(s) to be addressed. DNA extraction must be correctly prepared as it represents the starting point of any WGS analysis. Many kits are commercially available for DNA extraction and purification from various sample types.

### Second generation sequencing

Following the success of first generation Sanger sequencing, new methods commonly called next generation sequencing (NGS) were developed and became available from 2005. The first of such NGS platforms consisted of higher throughput sequencing systems, referred to in this chapter as second generation sequencing (SGS); these have increased throughput by sequencing large number of DNA molecules in parallel. Several companies developed SGS methods and approaches. The first to be commercialized was the GS20, by 454 Life Sciences, which used an array-based pyrosequencing method

(202), relying on the detection of pyrophosphate molecules released upon incorporation of individual nucleotides in the sequence. This method was founded on the principle of "sequencing by synthesis" and the read length, corresponding to the average length of short sequences generated, varied between 700 and 1000 bp. The amount of data generated was relatively low by modern standards at around 700 megabases (Mb) for the GS20, and was ultimately improved with the GSFLX platform offering higher data throughput per run with better data quality (203). However, the GS20 and support for this equipment was discontinued in 2015. Indeed, this platform experienced high error rates when sequencing regions rich in repeated nucleotides as, rather than measuring each nucleotide individually, the number of bases in such tracts was determined by the relative amplitude of the signal, which is an inherently less reliable means of achieving this (204).

The Solexa/Illumina technology has been one of the most widely used SGS platforms in the microbiological world, with equipments created for different throughput capacities (MiniSeq, MiSeq, NextSeq, HiSeq and NovaSeq). These instruments provide shorter read lengths, between 150 and 300 bp, but compensated for that by the ability to sequence large amounts of genetic data, up to 600 000 Mb, increasing the sequence coverage (205, 206). Life Technologies developed the Ion Torrent SGS platforms (Ion PGM, Ion Proton and Ion S5), which have a read length of about 200 bp and a run throughput of a 1000 Mb. Contrary to other technologies, Ion torrent does not use fluorescence or luminescence, instead the nucleotide incorporations are measured by a change in pH occurring during the polymerisation step (207).

All SGS methods rely on a PCR amplification of randomly fragmented DNA attached to an array (illumina), a chip (Ion Torrent, Life technologies) or beads in suspensions (454 Life Sciences). This is followed by the sequencing step involving a series of washing and scanning during which the signals, specific to each nucleotide, are captured by an imaging system. One of the main limitation of SGS is the need for a PCR step, which can introduce errors through a mechanism called dephasing as well as amplification biases. The error rates tend to increase with the read length, but smaller read lengths also make the genome assembly more difficult, leading to incomplete genomes with larger gaps between the contigs. In 2015 the cost ranged from relatively inexpensive (Illumina NextSeq, about $12.5 per genome with a maximum read length of 150 bp) to expensive (Life Technologies Ion PGM, about $107 per genome for a maximum read length of 400 bp) (141).

These SGS platforms allowed sequencing of hundreds of bacterial genomes including *Neisseria* species and *Nm.* At the time of writing, the *Neisseria* pubMLST database stored genetic and epidemiological data for more than 43 172 isolates including and 13 384 whole genome sequences from various geographical regions. Most of the recent knowledge obtained in the field of *Neisseria* research have resulted from the analysis of sequences generated by these platforms; some of these advances will be discussed further below.

- ***Bacterial evolution and population structure***

Genomic analyses of large numbers of *Nm* isolates have elucidated many aspects of the evolution and population structures of the bacterium, allowing an improved

understanding of the mechanisms of HGT in this organism. For example, it has been shown that HGT was favoured by the presence of multiple copies of DNA uptake sequences (DUS) throughout the genome, especially around genes with essential functions. This led to the suggestion that HGT may play more of a conservative role than a diversifying one as it was previously thought (208, 209). Analysis of the first *Nm* genome sequences identified almost 1900 DUS copies (199, 200). These DUS have also been identified in other non-pathogenic *Neisseria* species (134), which are known to exchange DNA with *Nm* (133) and an increased rate of HGT has been observed between meningococci sharing similar DUS (210). Other repetitive elements present in both pathogenic and non-pathogenic *Neisseria* include Correia elements which are mobile sequences (211) flanked by 26 bp inverted Correia repeats (212), and dRS3 elements which are a family of 20 bp repeat sequences abundant in *Nm* genomes and involved in recombination (199), both have been shown to be involved in gene regulation and sequence variation in pathogenic *Neisseria* (213). The repetitive elements also facilitate another important phenomenon, phase and antigenic variation, allowing *Nm* to turn on or off the expression of some of their OMPs allowing immune evasion when they are off; the changes in the length of these repeated sequences in these protein encoding genes are the result of recombination events altering the coding sequences (214, 215). Phase variation mechanisms are found in genes that are important for bacterial adaptation to different environments and for bacterial virulence (216). Although these phase variable genes are present in non-pathogenic *Neisseria* they tend to not have the repeating elements and are probably subject to less phase switching (134) than their homologs in pathogenic species.

Most HGT events in meningococci occur between organisms that are very closely related, by homologous recombination. This makes the process difficult to distinguish from genetic variation arising by mutation as the bacteria exchange sequences that are often similar with few nucleotide changes. The limited number of genomes from carried isolates, only 751 carried *Nm* were recorded in PubMLST at the time of writing, has been a limiting step in our understanding of the evolution of the meningococci.

The study of *Nm* population structures has benefited from the higher resolution characterisation of the isolates. A core genome was established by Bratcher and colleagues, comprising 1605 loci present in 95% of 108 representative meningococcal isolates and distinguishing 10 lineages in agreement with the major invasive clonal complexes characterised by seven locus MLST (217). This core genome has been subsequently used in the analysis of different isolate collections, such as the Meningitis Research Foundation Meningococcus Genome Library (MRF-MGL) a database of all the confirmed cases of *Nm* infection in England and Wales since 2010; the analysis of 899 isolates collected in the epidemiological years 2010-11 and 2011-12 identified more than 20 distinct lineages and a high level of recombination (218). Lineages or genogroup specific population structure studies are now being carried out at genomic resolution as seen with the analysis of the global cc11 isolates identifying a South American/UK *NmW* strain distinct from those identified in other regions of the world (219) or the study of the invasive *NmY* in Sweden (220). The analysis of 92 cc11 *NmW* isolates collected between 1994 and 2012 from the African meningitis belt (AMB) revealed a phylo-geographic clustering of the isolates, as their phylogeny reflected their geographical origin (221); the analysis of 81 *NmC* strains collected during the 2015 epidemic in Niger

showed that they were distinct from *NmC* circulating globally (107). WGS studies have also focused on the identification of genomic determinants of virulence as it was done previously at the MLST or antigen level (222, 223). For example, studies have compared the genomes of disease and carriage isolates to identify genetic differences between both groups of isolates, in *NmY* (224) and *NmA* (225); however, no genomic study has identified a single virulence factor that differentiates both phenotypes although the meningococcal disease associated (MDA) island (226) was shown to be involved in the ability of the bacteria to cause disease especially in young adults (227). Nonetheless, it was found that the bacterial population circulating during the Chadian *NmA* epidemic in 2011 was not homogeneous as was suggested by genogrouping or MLST analysis but was clearly separated into distinct clusters associated with the age of the individuals sampled, indicating that external factors, host related or environmental could play a role in the microevolution of those bacteria (225).

- ***Antimicrobial resistance***

Antibiotic resistance has become a major problem in the fight against infectious disease. Although the level of antimicrobial resistance of meningococci to the most commonly used antibiotics remains low compare to other pathogenic bacteria, isolates with decreased susceptibility to penicillin have been reported globally (228-232), as have those with decreased susceptibility to ciprofloxacin (233-235) and rifampicin, which is commonly used for chemoprophylaxis (236). The genes involved in antibiotic resistance include *penA* for penicillin (232, 237, 238); *rpoB* for rifampicin (236, 239) and *gyrA* for ciprofloxacin (240). Sequence analysis of these genes have assisted in determining the correlation between sequence variants and phenotypically observed level of antibiotic

resistance. Large-scale validations of these genotype-phenotype profiles remain necessary for the future use of genomics in predicting antibiotic resistance in the absence of cultured isolates.

- ***Taxonomy***

The higher resolution obtained from WGS analyses provides improved means of classifying bacteria, when compared to the more traditional phenotypic and biochemical tests used for most of the 20$^{th}$ century. For example, using the 53 ribosomal loci (rMLST) showed improved resolution compared to phenotypic approaches and 16S rRNA gene sequencing, and resulted in similar *Neisseria* species clustering than whole genome MLST (wgMLST), in a taxonomic approach to this genus which is applicable to other bacteria (241). Average nucleotide Identity (ANI), calculated genome-wide, remains the statistic most commonly used for the definition of species and is now being applied to WGS data (171). New approaches such as MASH distances, which measures the similarity among two sequences by estimating the mutation rate between them, are also being developed and tested to classify bacterial species using large quantities of WGS data (242). The genomic analysis of the *Neisseria* genus has led to reclassification of some isolates based on observed phylogenies and identified polyphyletic species such as *Neisseria polysaccharea*, raising the question of whether or not these distinct groups represent different species or not (131, 243). The inclusion of sequences of geographically diverse origins is likely to identify phylogenetically distinct strains.

- ***Vaccine target studies***

The increased knowledge of the meningococcal population structure obtained from the studies described above had major implications for the development of novel vaccines.

Indeed, a better understanding of the diversity of bacterial membrane exposed proteins was crucial for the development of new vaccines either by (i) the identification of novel vaccine targets or (ii) in the determination of the best components for protein based "cocktail vaccines". The first of these is best exemplified by the "reverse vaccinology" approach, which was used to search for novel meningococcal vaccine antigens and which led to the design of the 4CMenB vaccine (Bexsero®) which targets *NmB* (63). This vaccine incorporates four immunogenic protein antigens, with the intention that the combination of antigens would cover the majority of circulating invasive meningococci (244); however, because of the diversity of these bacteria, continuous monitoring of the diversity of those proteins will be necessary to ensure that adequate coverage is maintained over time (245).

A genomic approach has been developed to assess the sequence coverage of these antigens in circulating meningococcal populations (246) but, at the time of writing, the impact of those vaccines remained uncertain because protective immunological cross-reactivity between closely related sequences was difficult to predict solely on genetic information. Similar tools will be needed to study the potential coverage of specific protein vaccines in constantly evolving bacterial populations, along with better ways to correlate that with actual coverage. WGS data can also be used to study host pathogen interaction through sequencing of both pathogens and host genomes and studying of the change in gene expression (transcriptome) post bacterial infections. This will increase our understanding of the menchanisms triggered by the infection which would help define the best strategy to fight the it and to identify new targets for vaccine developments (247).

- ***Disease surveillance***

With the decline of the disease-associated meningococci that characterised the latter half of the 20th century, at least partially in response to immunisation campaigns, epidemiological surveillance continues to be necessary to identify the possible rise of other invasive meningococci, perhaps belonging to genotypes or serogroups previously rarely associated with disease.

In high-income countries, WGS increasingly became the preferred choice of meningococcal isolate characterisation from 2010, as the WGS approach became the most cost-effective mean of collecting multi locus data such as MLST and antigen typing data. In addition, WGS provided additional information for the remainder of the genome. The first routine uses of WGS for meningococci, and one of the first for any bacterium, was the establishment of the MRF-MGL hosted on the pubMLST.org/neisseria database (174, 248). The MRF-MGL contains high-quality draft genome sequences for all meningococcal isolates received at the UK national reference laboratories (249). This allows automatic typing of the isolates, rapid sharing of data *via* the internet, and the possibility of additional genomic analysis and comparisons with other genomes, from other countries, present in the database. As more European countries systematically sequence their isolates and deposit them in web-accessible databases, a regional genomic surveillance system has emerged, monitoring the molecular epidemiology of disease-causing isolates; however, a complete picture of the molecular diversity of meningococcal populations requires the simultaneous collection and characterisation of carried isolates.

In low income countries, however, WGS currently remained very far from being accessible even in well-established research centres and certainly not in national reference laboratories. The national surveillance systems still rely mostly on clinical diagnosis and classical laboratory methods, although more national reference laboratories are equipped to perform molecular tests such as PCR confirmation or occasionally MLST. Nevertheless, the regional meningitis surveillance supported by the World Health Organization (WHO) (76) provides a platform to implement genomic surveillance of meningococcal disease or any other bacterial disease of interest using a web-based interface which would facilitate the sharing of results and encourage a community data analysis.

Examples of the potential of this approach include the use of WGS-based surveillance to identify: (i) aggressive *NmW* lineages in the UK and South America that are distinct from the classical "Hajj strain"(219), indicating the evolution of the global cc11 *NmW* (250) and (ii) *NmC* strains circulating in the AMB that have recently caused large epidemics ((107). Other WGS studies defined the meningococci responsible for distinct waves of *NmA:*cc5 meningococci (ST7 and ST2859) in the AMB: one study suggested this might be due to herd immunity evasion via homologous recombination affecting non capsular exposed antigens (251), but an alternate study suggested that this might be due instead to changes in genes involved in metabolic functions (252). Such analyses improved understanding of the evolution of the disease isolates and would not have been possible at lower resolution.

WGS analyses have been crucial in meningitis outbreak investigation in different regions of the world, allowing the identification of new variants that were indistinguishable at

the MLST level (225, 253, 254). It has also been used for identification of outbreak strains and their discrimination from unrelated cases (255). If coupled with epidemiological data, it would be possible to study the bacteria transmission dynamics, as previously doe for other bacterial pathogens, such as in methicillin-resistant *Staphylococcus aureus* (MRSA) outbreaks (256).

**Third generation sequencing**

Novel NGS methods, referred to here as third generation sequencing (TGS) focus on the real-time sequencing of single DNA molecules, avoiding the necessity of an amplification step using PCR and the related biases or dephasing issues. The advantages of TGS include: rapid turnaround times, sometimes down to hours or few minutes; the requirement for very small amounts of starting material and longer read lengths. However, because a single molecule is being observed in each read, the error rates are inherently higher, and this has to be compensated with high sequence coverage to increase the accuracy of the final consensus sequence. In principle these approaches have the potential for very low cost, particularly due to their simpler sample preparation steps.

Pacific Bioscience developed a technology at the boundary of SGS and TGS: although their platform PB RSII, launched in 2013, uses a polymerase PCR-based approach, it also allows the sequencing of a single molecule in real time, with extremely long read length up to 10 000 bp or longer. This has become the method of choice to generate complete bacterial genomes for reference purposes, but remains costly for routine sequencing of organisms, with an average price of $400 per genome in 2015 (141). This method, however, has the advantage of identifying methylation patterns and allowing the design

of epigenetic studies as exemplified with the study of the DNA methyltransferase, *mod* genes, in *Nm* (215).

Another promising approach to single molecule sequencing is the use of nanopores, molecule-sized pores in a membrane, which enable the measure of differential ion concentrations across the membrane as DNA strands transverse the pore. This generates an electrical signal specific to the sequence of the DNA strand being translocated. One of the leading companies pursuing that market is Oxford Nanopore Technologies, which currently have three platforms: the MinION, a portable usb like device; the GridION, a module of 5 MinION; and the high throughput PromethION which can hold up to 48 MinION flow cells. Another smaller device the SmidgION has also been designed to be operated from a smartphone, providing the potential of using NGS as a bedside point-of-care portable diagnostic tool deployable in the most rural of locations. These nanopores represent an exciting development for field workers allowing easy transport and preparation for genome sequencing in the field with little technological resources, as exemplified by their use for real time genome sequencing of the ebola viruses during the 2015 epidemic in Guinea (257). However, the quality of the data generated was low and required improvements in the algorithm that translates ion signals into nucleotide sequences and reduction in the inherent nanopore error rates.

As technology improves, new methodologies and platforms are likely to evolve, increasing the number of options available and simultaneously decreasing the cost of sequencing making it more accessible. Which approach is used for which application will depend on a trade-off between accuracy, genome completeness and price. Decisions on

these trade-offs are best made during the project design phase so that the most appropriate technology is used for the particular questions being addressed.

## *Sequence assembly and analysis*

Generating whole genome sequences will eventually become technically trivial; however, their analysis remains challenging. It is important to keep in mind that the complete genome sequence is not always necessary to answer all questions and it is therefore important to decide what part of the genome an analysis will focus on early in the design of a project. A variety of analysis approaches have beend developed; however, most of them necessitate similar steps to transform the raw sequence reads obtained from a sequencer into genome sequences from which meaningful information can be extracted (Figure 2).

### Genome assembly

The first step is genome assembly. This can be done either by aligning the sequence reads to a reference genome of interest or *de novo* by assembling overlapping raw reads to create longer contigs or a combination of these two approaches. The alignment of sequence reads is quicker and less computationally demanding; however, it is less suitable for diverse groups of organisms, as the sequences will be limited to what is present in the reference genomes. The *de novo* approach, which is most common, is computationally more intense but many assemblers have been developed and typically employs either graph-based methods such as de Bruijn graphs (258) used in Velvet

(259) and the more recent SPAdes (260), two assemblers most commonly used in bacterial genome assembly or Seed Extension methods like SSAKE (261).

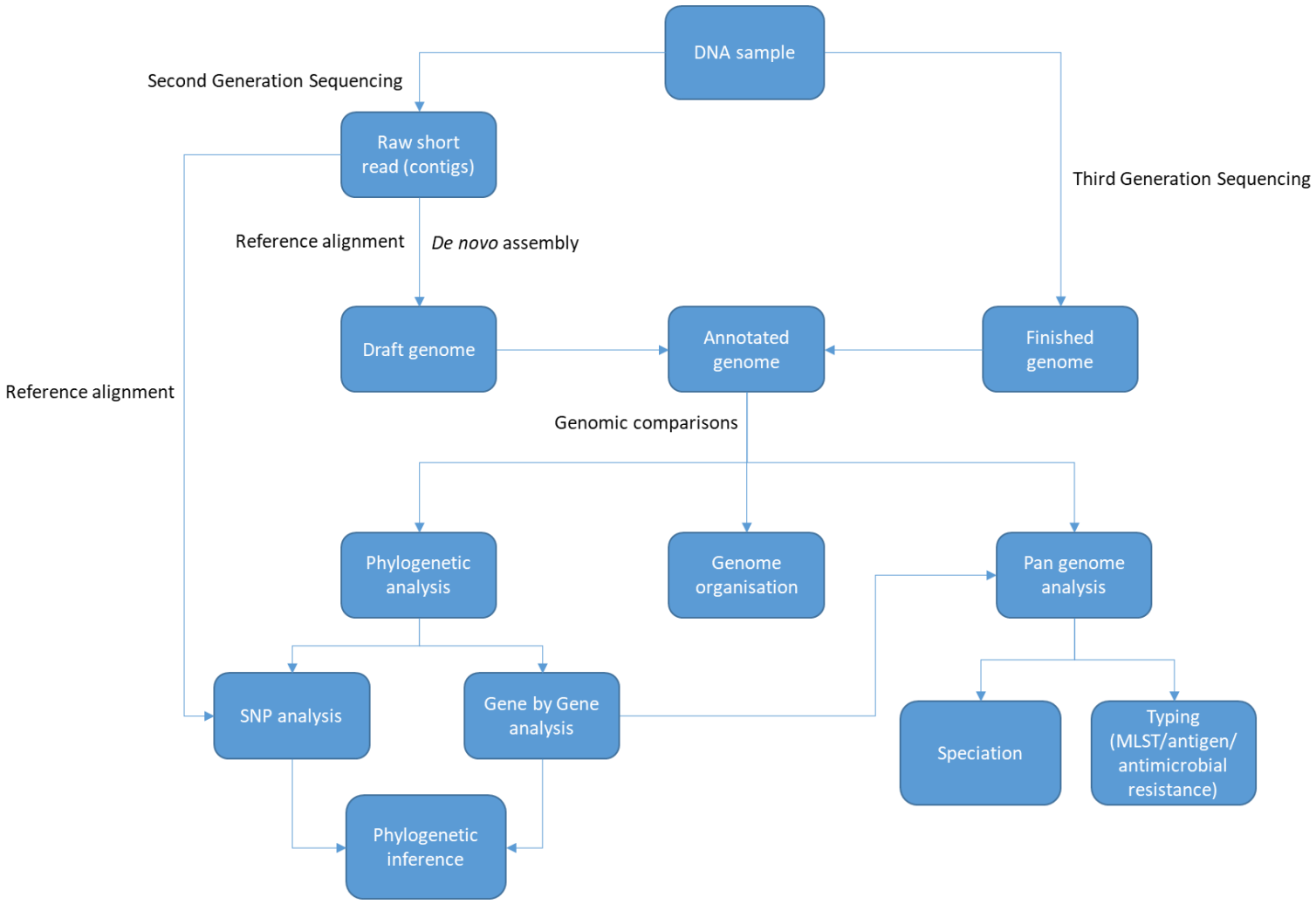



**Figure 2: Schematic of a genomic analysis pipeline**

**Genome annotation**

The second step is the genome annotation, which corresponds to the functional assignment of open reading frames (ORFs) and other features to regions of the sequences present in the assemblies. This is usually an automated or semi-automated process, involving the uploading of the assemblies into databases and the use of search algorithms to identify identical or similar gene sequences. These databases can be pathogen specific, such as the PubMLST (174, 248) databases or more general ones, such as GenBank. Several annotation tools have been developed; online tools include: RAST (262); the PubMLST "autotagger" (248); and the NCBI Prokaryotic Genome Annotation Pipeline (263). Other tools use a computer command-line, such as DIYA (264) or the most commonly used application Prokka (265). The quality of the annotations relies on appropriate curation and data quality checking of the database being queried, which requires some level of downstream manual verification.

**Genome comparison**

The third step corresponds to the comparative analysis which is question driven (266, 267).

- ***Genome organisation***

Once genomes have been assembled, it is possible to compare their organisation. This is more straightforward in the case of finished genomes; however, it can also be done with draft genomes through alignment to a complet reference genome as long as there are not too many contigs in each sequence. These analyses compare genome summary statistics such as the size of the genomes or the percentage of guanine and cytosine base pair (GC

content) and evaluate the order and orientation of genes (synteny), searching for rearrangements, deletions, insertions or duplications among the compared genomes. Many programs can be used to evaluate these parameters. Programs such as Artemis (268) or MEGA (269) can be used to visualise the sequences, calculate the GC content and examine specific sequences of interest, whether coding or not. The Artemis Comparison tool (ACT) (270) and Mauve (271) allow the alignment of two or more genomes and a visual evaluation of the gene arrangements, with tools indicating orthologous gene presence and orientation, and providing an effective method to identify large inversions, deletions, or duplications.

- ***Pan-genome analysis***

To date, most analyses have compared the gene content of isolates, especially the number of coding DNA sequences (CDS) that are variable from one species to the other, but which are expected to be in a similar range between closely related bacteria. These analyses allow the separation of the genes that are present in all the genomes analysed, known as the "core genome", from those that are variably present in the "accessory genome". The entirety of the core and accessory genomes forms the "pan genome": the total of all genes present in a subset of isolates. It is important to note that such analyses are dependent on the number of isolates included in a particular study and that the core genome tends to decrease with increased number and diversity of genomes included, whereas the pan genome will increase. Although this approach is relatively straightforward with complete genomes, the analysis of incomplete (unfinished, or 'high quality draft') genomes (272), generated from SGS necessitate the relaxation of some of the criteria because some genes may be absent due to the draft nature of these genomes.

For this reason non-strict core genomes are often generated considering genes present in a percentage (varying between 90-98%) of the isolate collections to account for the uncertainty. Many programs have also been developed to study gene content, such as: Genome Comparator (248); Protein Ortho (273); or Roary (274). Each of these provides a different level of complexity. Once the pan genome has been determined a focus on specific functional gene group can be made to address more specific questions. This requires functional analysis of the coding sequences using databases like COG (275) or KEGG (276) to determine which functional gene groups are present in the genomes of interest.

- ***Phylogenetic analysis***

The use of phylogenetic analysis to reconstruct the ancestral relationships of organisms has become increasingly important in the investigation of clinical isolates of pathogenic bacteria. These reconstructions can be used to address a range of questions, including the spread of pathogens at various scales, the evolution of bacterial strains and the emergence of pathogenicity and virulence.

Essentially two different approaches have been applied in bacterial population genomics. The first, whole genome single nucleotide polymorphism (wgSNP) analysis, was initially developed for the comparison of human genomes that exhibit much less genetic diversity than most bacterial populations, and was adapted to bacterial genomes. Although this approach is appropriate in the analysis of monomorphic species such as *Mycobacterium tuberculosis* or *Salmonella enterica* serovar Typhi, it is not appropriate for more diverse bacteria with the discovery that they exhibit higher rates of HGT (217). The use of SNP-based approaches in bacteria needs to take into account the bias

introduced at the nucleotide level by HGT. Consequently, the more sophisticated SNP-based approaches introduced a step that discards SNPs that appear to be the results of HGT, but the methodologies are variable, based on specific in-house algorithms making it difficult to reproduce. Programs such as Gubbins (Genealogies Unbiased By recomBinations In Nucleotide Sequences) (277) and ClonalFrameML (278) have been developed for the purposes of identifying the recombination prone area in large genome datasets and generate phylogenies based on sequence variations outside of those HGT "hot spots".

The development and widespread availability of analysis pipelines provides improved standardisation among the different studies interested in wgSNP (277, 278, 279). Another challenge with wgSNP was the necessity for a good quality complete genome from a closely related strain in order to accurately identify SNPs, but as sequencing technology improves and the cost decreases, this will become less of an issue. Also, kmer-based approaches to wgSNP analysis that compare short nucleotide sequences may provide an alternative to the need for a reference genome, although more validation is required.

An alternative approach to wgSNP is provided by the gene-by-gene analysis which focuses on allelic diversity of individual genes (280). This approach builds on MLEE and MLST analyses, by indexing allelic variability at individual loci. Depending on the analysis required, different loci can be used and these can be built into 'schemes', groups of loci that form a coherent set for analysis purposes. One such scheme is ribosomal MLST (rMLST), which indexes the allelic variation at the 53 ribosomal genes, providing a powerful tool for discrimination between emerging species (241) and within species.

Core genome MLST (cgMLST) schemes include those loci common to a particular group of organisms, providing very high resolution mean of studying the variation among the essential genes always present in the members of that group (217). Whole genome MLST (wgMSLT) indexes the diversity in the total number of genes identified, often using finished and annotated genomes as references allowing the ultimate genetic characterization to the level of very closely related bacterial clones (280). More specific schemes can also be generated based on any functional gene groups of interest, such as metabolic genes, iron metabolism genes, and so on.

At the time of writing (mid-2017) the cgMLST approach had been primarily used to index variation in coding sequences; however, it can in principle be extended to index intragenic regions, gene promoters and regulatory sequences, or any other non-coding sequences. Similarly, to the seven locus MLST, an allele number is assigned to the variant of each locus building a database of their diversity: each combination of numbers can then be further grouped into lineages. The advantage of focusing on allelic diversity is that it avoids the bias introduced by HGT at the sequence level in very recombinogenic organisms, such as the meningococcus (217). These hierarchical gene-by-gene analyses are accessible on open access web-based bioinformatic tools such as the bacterial isolate genome sequence database (BIGSDB) software running in pubMLST databases, providing a relatively user-friendly interface and many genomic analysis tools such as Genome Comparator, used to compare genes sequences in multiple genomes (248).

Both wgSNP or wgMLST approaches provide distance matrices from the pairwise comparisons of each genomes allowing the phylogenetic relationship to be visualised with different trees: Neighbor-joining trees (NJT) (281) generate agglomerate clusters,

using minimum evolution criteria (282). This has the advantage of being very rapid, compared to other methods not based on distance matrices, which can be very important for the analysis of large datasets. Neighbour-net trees use a similar algorithm to NJT, but are represented using split networks and cannot be used to make any evolutionary conclusions, they are simple representations of the diversity and are often preferred for species with high levels of HGT (283, 284). Other reconstruction methods employ character-based methods, rather than distance-based ones, and use more sophisticated algorithms such as maximum likelihood (285) or maximum parsimony (286), which are based on statistical simulations models, and heuristic parsimony search methods, respectively. They can provide more sophisticated phylogenetic reconstructions, but are more computationally demanding, limiting their use for large-scale analyses.

Additionally, genome wide association studies (GWAS), which were also first exploited in human genome studies, have been adapted to the investigation of bacterial populations. In GWAS studies, the genetic variation of two phenotypically distinct groups of isolates is compared to identify genomic elements associated with the phenotype difference. Such studies, however, remain challenging due to the strong and variable population structures observed in most bacterial populations, driven by the variable impact of HGT events, necessitating the development of more appropriate tools for the analysis of bacterial genomes (287).

## Challenges and future perspectives

The advent of WGS has provided a powerful tool for the analysis of pathogenic bacterial populations. Population genomics has been exploited to investigate a wide range of questions, ranging from bacterial evolution and population structure to host-pathogen interactions and virulence. There are also major opportunities for the investigation of antibiotic resistance, the establishment of global bacterial disease surveillance databases, and the development of new vaccines. However, the accessibility to such technologies are still skewed to high-income countries, despite the highest burden of infectious disease being localised in developing countries, especially sub-Saharan Africa. The under-sampling of particular regions of the world and oversampling of others increase the risk of biases and often depict an inaccurate picture of the diversity of a bacterial population. It is therefore important that sustainable systems be put in place for improved access to those technologies, combined with adequate training of infectious disease scientists and improved surveillance systems in developing countries. Similarly, the emphasis on disease isolates is likely to create another sampling bias and development of effective metagenomic analysis and increase environmental sampling and asymptomatic infection studies will have important implications.

When it comes to applications in public health, is it important that the different analysis methods and bioinformatics pipelines are standardised with clear and reproducible procedures that can be validated with clinical trials. Regulatory bodies will need to generate guidelines for the certification of genomic methods and agree on protocols and algorithms to be implemented. Further studies are also required to establish the

practical impact of implementing these approaches in hospital settings, for patient care management and disease outcomes. Such studies are also needed to determine the level at which genomic analysis should be performed (hospital, regional, national or international), and when real time genomic data is clinically relevant. The increase in data availability create challenges in data storage and handling, and generates a requirement for increased computational power and bioinformatics expertise. Population genomics has not answered all the questions raised by the intriguing life cycles of bacteria such as *Nm*. For example, it remains unclear why hyper-invasive variants of this accidental pathogen persist; however, the integration of genomics with the other "omics" approaches, trancriptomics, proteomics, epigenomics is likely to generate new insights into such questions.

In conclusion, population genomics has revolutionised the study of pathogenic bacteria, providing tools to address a wide range of questions but also providing useful information for public health purposes. As technologies and analysis approaches continue to develop, their utility and dissemination will increase in all settings but, perhaps most importantly, they provide the prospect of a 'technology jump' in low income settings, where it is possible to envisage a move directly from first generation technology, involving culture and serotyping, to near-patient sequence analysis, with a consequent revolution in clinical microbiology and public health.

## C- Justification for the Research

The African meningitis belt (AMB) is known for its distinct epidemiology of invasive meningococcal disease (IMD), with large epidemics occurring in unpredictable ways. A change in the epidemiology has been noted since the introduction in the region of the serogroup A *Neisseria meningitidis* (*NmA*) conjugate vaccine, MenAfriVac®, and no large-scale epidemic has been recorded since, although smaller localised outbreaks have been caused by other serogroups like serogroup C *Neisseria meningitidis* (*NmC*). Despite carriage being a pre-requisite for IMD, the transition of *Nm* from an asymptomatically carried organism to a virulent invasive pathogen is not well understood. No strict determinant of virulence had been identified at the time of writing, and meningococcal pathogenicity appears to be multifactorial, making epidemic predictions very difficult from available carriage data. Multiple different factors may play an important role in this change of phenotype and most can be classified into three groups: (i) meningococcal genetics, (ii) changes in the interactions of the bacteria with the mucosal environment, including with other species sharing the same ecological niche, and (iii) changes related to the infected host.

The overall aim of this work was to apply bacterial population genomic approaches to study the first two factors, in order to understand the role of meningococcal genetics in modulating *Nm* phenotypic transition and improve our knowledge of the diversity and population structure of the nasopharyngeal *Neisseria* species and their potential role in influencing *Nm* carriage in the AMB. This was done using *Neisseria* isolates collected in the AMB during carriage surveys or as part of a national meningitis surveillance system.

Combinations of sequencing methods were used throughout, from Sanger sequencing technology to Illumina® whole genome sequencing.

The role of the environment is investigated in Chapters 3 and 5, where the ecological diversity of the *Neisseria* species is characterised and the dynamics and risk factors for nasopharyngeal carriage of non-pathogenic *Neisseria* are compared to those of *Nm*. The objective was to evaluate the diversity of carried isolates, and to investigate whether non-pathogenic bacteria could influence carriage of *Nm* and, therefore, its ability to cause IMD.

The role of meningococcal genetic content is addressed in Chapter 4 where whole genome sequencing methods were used in the comparison of carried and invasive *NmA* isolates collected in Chad during the 2011 meningitis epidemic, in order to dissect the genetic differences between the two groups.

# II- Results

## A- Chapter 3: Pharyngeal carriage of *Neisseria* species in the African meningitis belt


### Abstract

**Objectives.** *Neisseria meningitidis,* together with the non-pathogenic *Neisseria* species (NPNs), are members of the complex microbiota of the human pharynx. This paper investigates the influence of NPNs on the epidemiology of meningococcal infection.

**Methods.** *Neisseria* isolates were collected during 18 surveys conducted in six countries in the African meningitis belt between 2010 and 2012 and characterized at the *rplF* locus to determine species and at the variable region of the *fetA* antigen gene. Prevalence and risk factors for carriage were analysed.

**Results.** A total of 4694 isolates of *Neisseria* were obtained from 46 034 pharyngeal swabs, a carriage prevalence of 10.2% (95% CI, 9.8-10.5). Five *Neisseria* species were identified, the most prevalent NPN being *Neisseria lactamica.* Six hundred and thirty-six combinations of *rplF*/*fetA_VR* alleles were identified, each defined as a *Neisseria* strain type. There was an inverse relationship between carriage of *N. meningitidis* and of NPNs by age group, gender and season, whereas carriage of both *N. meningitidis* and NPNs was negatively associated with a recent history of meningococcal vaccination.

**Conclusion.** Variations in the prevalence of NPNs by time, place and genetic type may contribute to the particular epidemiology of meningococcal disease in the African meningitis belt.

## Introduction

The human pharynx hosts a complex microbiota, including bacteria belonging to the genus *Neisseria*. Most members of this genus are non-pathogenic commensals (non-pathogenic *Neisseria*, NPNs), which very rarely cause invasive disease, but *Neisseria meningitidis* (*Nm*), the meningococcus, is an exception (288). Despite advances in vaccine development, invasive meningococcal disease remains a public health challenge globally and especially in the African meningitis belt, where very large epidemics continue to occur (289, 290), despite the recent widespread deployment of a serogroup A meningococcal conjugate vaccine (PsA-TT, MenAfriVac®)(54, 55, 113, 291, 292).

Most pharyngeal carriage studies in the African meningitis belt have focused on the meningococcus (100, 111, 112, 293), with little attention paid to other *Neisseria* species apart from *Neisseria lactamica* (*Nl*). In northern Nigeria, pharyngeal carriage of *Nl* was common, especially in young children (129) and genetic exchange among *Nm*, *Nl* and unspecified *Neisseria* species has been demonstrated in The Gambia (294). Molecular epidemiological studies of *Nm* and *Nl* conducted in Burkina Faso from 2009 to 2012 reported a high overall prevalence of *Nl* carriage (18.2%), a higher prevalence of *Nl* in males than in females, except in those aged 18-29 years, no change between dry and rainy season and no significant changes following vaccination with PsA-TT (114, 130, 293, 295). It has long been considered likely that carriage of NPNs influences host susceptibility to infection and invasion by *Nm,* a view supported by the fact that healthy subjects inoculated with *Nl* exhibit some protection against colonization with *Nm* (135). Until recently, *Nl* was considered to be the NPN genetically most similar to *Nm*. However,

recent whole genome sequence (WGS) studies have shown that *Neisseria polysaccharea* (*Np*) and *Neisseria bergeri* (*Nb*) are more closely related to *Nm* than *Nl* (131). Consequently, these bacteria may also influence the epidemiology of *Nm* colonization and invasion. For this reason, we have studied the prevalence of carriage with various *Neisseria* species in six countries of the African meningitis belt and investigated risk factors for their carriage.

## Materials and Methods

The methods employed in the MenAfriCar surveys, during which the isolates described in this paper were collected, have been described in detail previously (111) and are summarized briefly here. Ethical approval for the surveys was obtained from the ethics committee of the London School of Hygiene & Tropical Medicine and from ethical committees in each partner country. The study was registered with ClinicalTrials.gov (NCT01119482).

### *Carriage surveys*

Bacteria were isolated during 18 cross-sectional surveys conducted in Chad, Ethiopia, Ghana, Mali, Niger and Senegal during 2010-2012 (Figure 1). Pre-vaccination surveys in Mali, Niger and Chad had a target of 5,000 participants and post-vaccination surveys a target of 2,000 participants in Mali and Niger and 6,000 in Chad. The remaining surveys aimed to recruit 2,000 participants. A representative sample of households was obtained either from an updated demographic surveillance system (DSS) or from a census conducted for the study. Within selected households, individuals in four different age

groups (0-4 years, 5-14 years, 15-29 years and 30 years or more) were chosen randomly until the required sample size was reached, with a maximum of 5 individuals recruited per household. Once written consent had been obtained, standardized household and individual questionnaires enquiring about risk factors for meningococcal infection were administered. Pharyngeal swabs were obtained using a standardized technique that involved swabbing both the posterior-pharyngeal wall and the tonsils (296).

### *Bacteriology*

NPNs were isolated using the same conventional microbiology techniques that were employed for the detection of *Nm* described previously (111). Briefly, pharyngeal swabs were plated onto modified Thayer Martin agar plates and incubated 24-48h at 37°C in 5% $CO_2$; oxidase and gram stain testing identified oxidase positive, Gram-negative diplococci. Further biochemical tests (ortho-nitrophenyl-β-galactoside, γ-glutamyl transpeptidase and tributyrin) were used in each site to differentiate between putative *Nl* and *Nm* isolates and members of the genus *Moraxella*.

### *Molecular methods*

A boiled cells suspension of each oxidase positive, Gram negative diplococci (OPGND) isolate was sent to the Department of Zoology at the University of Oxford for molecular typing, where Sanger sequencing was used to characterize gene targets as described in the supplement. Sequences were assembled using SeqSphere (http://www.ridom.de/seqsphere/) and imported into the isolate's record previously created in a BIGSdb database (248).

### *Neisseria speciation*

Amplification and sequencing of a 413 bp fragment of the *rplF* gene was used to differentiate among *Neisseria* species as described previously (132). A phylogeny based on the *f_rplF* alleles from Bennett et al. (2014) and the unique alleles found in this study was reconstructed using the Neighbor-Joining algorithm (281) and the Kimura 2-parameter substitution model (297) in MEGA version 6.0 (269). For isolates that did not yield results for the *rplF* assay, sequencing of the *rrna* gene, encoding 16S rRNA (177), was used to confirm the presence or absence of a bacterium and to determine its genus. Only *rplF* confirmed NPNs were included in this study with the exception of four *Nm* speciated on the basis of the 16S rRNA and the *porA* sequences. New alleles were investigated by a BLAST of obtained sequences against the 16S rRNA sequence data of the EzTaxon server (http://www.ezbiocloud.net/eztaxon; (298)).

### *Genetic diversity*

Sequencing of the variable region of the *fetA* gene (*feta_VR)* was used to assess the genetic diversity of the *Neisseria* identified as described in the supplementary methods (121). The sequences were assembled as for the other targets using SeqSphere (http://www.ridom.de/seqsphere/). The trace files of each new allele were manually curated in MEGA version 6.0 (269), the quality of the sequences were assessed and the modified bases checked in both the forward and reverse trace files. The corresponding protein sequences were also aligned and compared with known sequences stored in the *Neisseria* sequence definition database of pubMLST (174) before being entered into the allele database and the appropriate isolate record.

For isolates for which *fetA_VR* could not be amplified, an assay identifying the absence of the *fetA* gene (*fetA* null, *fnl*) was employed, using primers placed on genes on each side of the *fetA* gene: *thdF* and *fetB* as described in the supplementary methods (299).

### *Statistical methods*

Analyses were performed using Stata v12.0 (StataCorp, Texas). Survey design and potential household clustering were taken into account using the survey commands in Stata. Carriage prevalence of each of the different *Neisseria* species, together with 95% confidence intervals, was calculated for each country and each survey. Risk factors for carriage of *Nm* and NPNs were assessed simultaneously using multinomial logistic regression. Each risk factor was considered in turn using univariable, multinomial logistic regression. A multivariable model was then constructed including country, age group and sex *a priori* and any variable with a p-value <0.1 in the univariable analyses; only the variables with a p-value <0.05 in the multivariable analysis were kept in the final model. As a final check, dropped variables were re-entered into the model one at a time and the p-values re-examined; the variable was retained as significant if the p value was <0.05.

## Results

### *Prevalence of carriage with Neisseria species*

A total of 4694 of the 46,034 pharyngeal swabs collected yielded a *Neisseria* species, giving a carriage prevalence of 10.2% [95% CI, 9.8-10.5%]: 696 *Neisseria* were identified out of the 946 OPGND samples received from Chad; 838 out of the 994 received from Ethiopia; 446 out of the 544 received from Ghana; 298 out of the 504 from Mali; 1644 out of 2321 from Niger and 773 out of the 971 received from Senegal. The most frequently isolated species was *Nl* with a 5.6% point prevalence [95% CI, 5.3-5.8%], followed by *Nm* at 3.6% [95%CI, 3.4-3.8%]), *Np* at 0.6% [95% CI, 0.5-0.7%], *Nb* at 0.2% [95% CI, 0.2-0.3%] and *N. subflava* (*Ns*) at 0.05% [95% CI, 0.03-0.1%] (Supplementary Table 1). Twenty isolates from Chad were identified as belonging to the *Neisseria* genus but did not cluster with any known species on the Neighbor-Joining Tree (NJT; data not shown); they were designated *Neisseria sp.* and will be investigated further by whole genome sequencing methods.

### *Factors influencing the prevalence of carried Neisseria species.*

Country, season, age, gender, and a history of recent vaccination against *Nm* were associated with carriage of NPNs. Additionally, area of residence, household crowding and kitchen location were significant risk factors for carriage of *Nm* (Table 1).

*Country:* The prevalence of carriage of *Neisseria* species overall varied significantly among countries with Niger having the highest point prevalence (19.9% [95%CI, 18.9-20.9]), followed by Senegal (17.5% [95%CI, 16.1-18.8]), Ethiopia (13.8% [95%CI, 12.8-14.8]), Ghana (8.5%[95%CI, 7.6-9.4]), Chad (5.3%[95%CI, 4.9-5.7]) and Mali (3.4%

[95%CI, 2.9-3.8]) (Supplementary Table 1). The distribution of the different species of *Neisseria* by country is shown in Figure 1. The prevalence of *Nm* carriage varied significantly among countries, being highest in Senegal (8.0% [95%CI, 7.1-9.0]) and lowest in Mali (0.9% [95%CI, 0.7-1.1]). There were also major differences in the prevalence of carriage of NPNs by country and some NPNs were not identified in some countries, for example no *Nb* were isolated in Ethiopia and Senegal and no *Ns* in Ghana. Ethiopia was the only country where the prevalence of *Nm* carriage was higher than that of *Nl.*

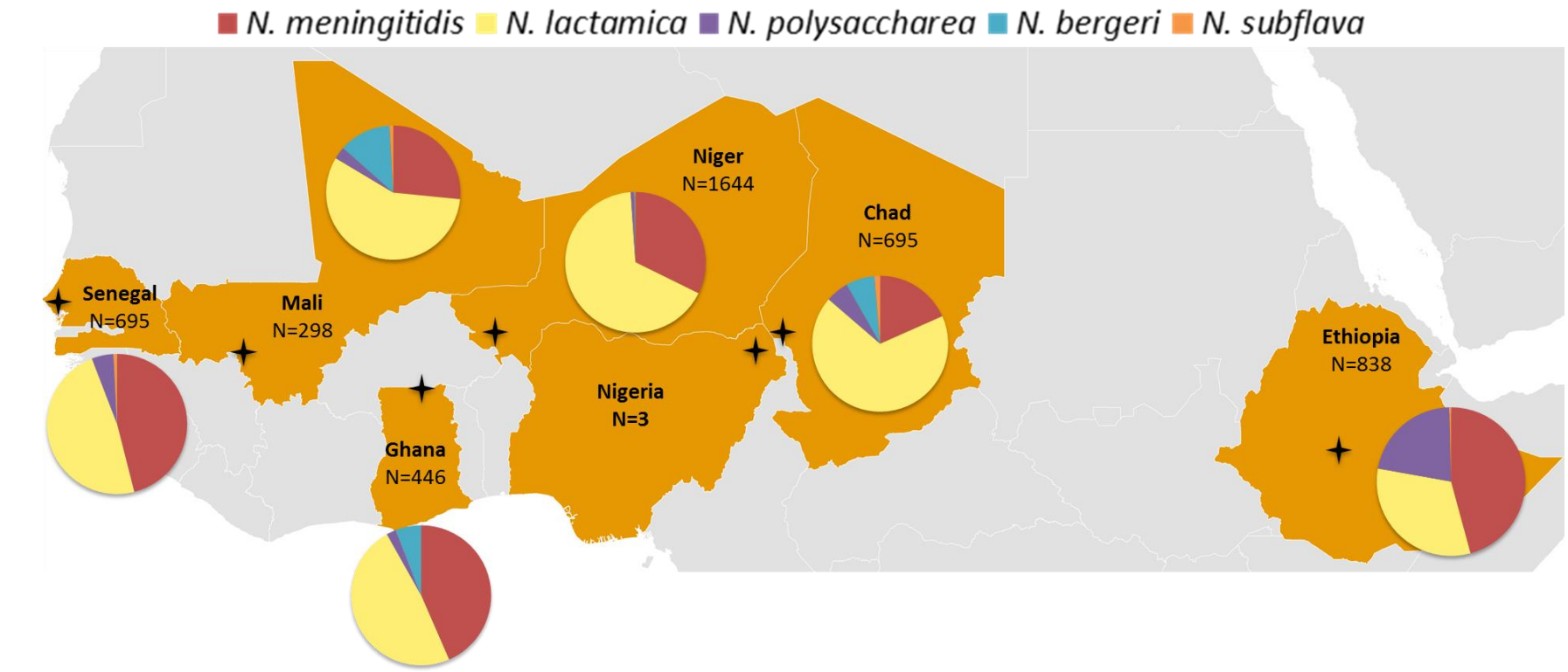
**Table 1: Factors associated with carriage of *Neisseria meningitidis* and non-pathogenic *Neisseria*; results from a multinomial multivariable logistic regression.**

| Factor | | Number (carriers) | Adjusted RRR *Neisseria meningitidis* (95% CI) | Adjusted RRR Non-pathogenic *Neisseria* (95% CI) |
|---|---|---|---|---|
| Age | <1 year | 2074 (207) | 0.40 (0.29, 0.55) | 3.11 (2.60, 3.73) |
| | 1-4 years | 8291 (1355) | 0.70 (0.59, 0.82) | 5.90 (5.23, 6.65) |
| | 5-14 years | 12563 (895) | 1.49 (1.31, 1.69) | 2.59 (2.29, 2.94) |
| | 15-29 years | 11863 (4372) | 1.0 | 1.0 |
| | 30+ years | 11243 (206) | 0.59 (0.50, 0.68) | 0.51 (0.43, 0.61) |
| Sex[+] | Female | 26619 (1701) | 1.0 | 1.0 |
| | Male | 19296 (1313) | 1.34 (1.21, 1.48) | 0.87 (0.80, 0.94) |
| Season | Rainy (XS1 and XS2) | 30522 (220) | 1.0 | 1.0 |
| | Dry (XS3) | 15512 (815) | 1.53 (1.35, 1.74) | 0.78 (0.70, 0.86) |
| Country | Chad | 13396 (584) | 1.0 | 1.0 |
| | Ethiopia | 5970 (450) | 7.11 (5.43, 9.29) | 1.70 (1.44, 2.01) |
| | Ghana | 5209 (253) | 4.81 (3.64, 6.35) | 1.25 (1.03, 1.51) |
| | Mali | 8837 (219) | 1.45 (1.05, 1.99) | 0.48 (0.40, 0.58) |
| | Niger | 8213 (1112) | 11.39 (9.00, 14.43) | 3.58 (3.13, 4.01) |

| | | | | |
|---|---|---|---|---|
| | Senegal | 4409 (427) | 10.85 (8.28, 14.23) | 2.39 (1.97, 2.89) |
| Area | Urban | 19462 (1398) | 1.0 | 1.0 |
| | Rural | 26572 (1637) | 1.44 (1.09, 1.60) | 0.97 (0.88, 1.06) |
| Crowding[#] | <2 people per room | 16299 (889) | 1.0 | 1.0 |
| | ≥ 2 people per room | 29679 (2127) | 1.27 (1.12, 1.45) | 1.08 (0.98, 1.19) |
| Kitchen location | Open air | 17805 (1274) | 1.0 | 1.0 |
| | Inside house | 12741 (1027) | 1.32 (1.09, 1.60) | 0.90 (0.79, 1.02) |
| | Separate hut | 14927 (677) | 0.94 (0.76, 1.17) | 0.96 (0.84, 1.09) |
| | Missing information | 504 (38) | 1.06 (0.57, 1.98) | 0.77 (0.51, 1.17) |
| Vaccinated recently with meningitis vaccine | No | 31338 (2060) | 1.0 | 1.0 |
| | Yes, <1 year ago | 9048 (545) | 0.71 (0.59, 0.84) | 0.82 (0.73, 0.92) |
| | Yes, 1-3 years ago | 4543 (356) | 0.51 (0.42, 0.63) | 0.94 (0.81, 1.10) |
| | Don't know/ missing | 1020 (55) | 0.68 (0.47, 1.00) | 0.62 (0.46, 0.84) |

+ Sex not reported for 119 individuals
[#] Data not reported for 57 individuals
The final multivariable logistic regression model included age group, sex, country, season area, crowding, kitchen location and recent vaccination
Other risk factors used in the univariable model but not significant in the adjusted model: smoking, living in a house with smokers, cooking fuel, respiratory symptoms and attendance of social gatherings.

**Figure 1: Frequency distribution of *Neisseria* species in each country of the study.**




A map of the African meningitis belt with pie charts depicting the prevalence of *Neisseria* species identified in each country.
N correspond to the total number of *Neisseria* isolates identified and is the denominator.

✦ Correspond to the sampling area

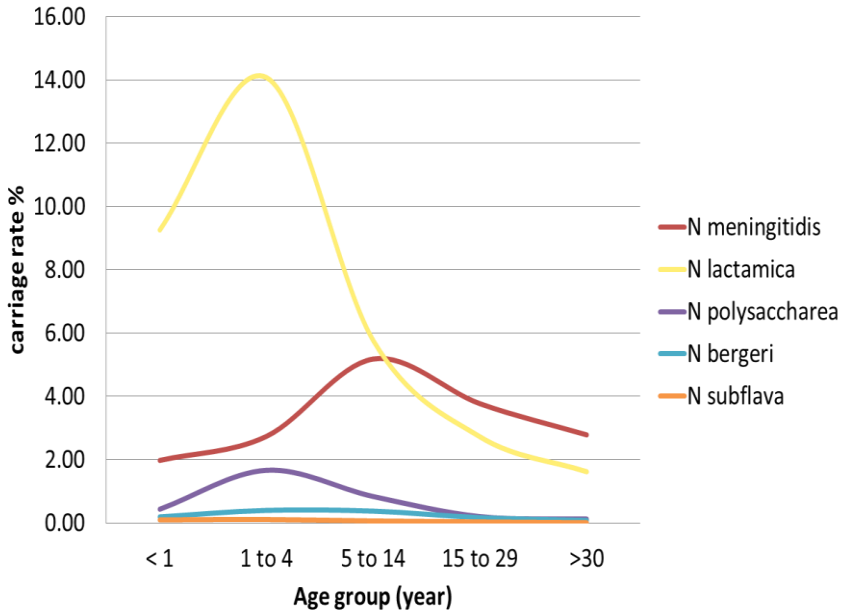
*Year and season:* The prevalence of carriage of *Neisseria* species overall varied little over the three years of the study: 10.0% [95% CI, 9.4-10.5%] in the first survey, 11.1% [95% CI, 10.6-11.7%] in the second survey and 9.4 % [95% CI, 8.9-9.9%] in the third survey (Table 2). The prevalence of carriage with both *Nm* and NPNs was also similar over time, with *Nl* being the most carried species, regardless of survey or season. There was, however, variation in the prevalence of carriage of NPNs over time at the country level: for example, there was an increase in the prevalence of *Nl* between surveys 1 and 2 in both Chad (from 1.1% to 5.9%) and Ghana (from 0.8% to 6.3%) and an increase in *Nm* prevalence between survey 2 and 3 in Senegal (from 3.1% to 19.8% [4]) (Supplementary Figure 1). The relative risk of carriage of NPNs was significantly lower during the dry compared to the rainy season with an adjusted Relative Risk Ratio (aRRR) of 0.78, [95% CI, 0.70-0.86], whereas the opposite was true for *Nm* with an aRRR of 1.53, [95% CI, 1.35-1.74] in the dry season.

**Table 2: Number of isolates identified as a *Neisseria* species per survey**

| | *N meningitidis* | Prevalence [CI] | *N lactamica* | Prevalence [CI] | *N polysaccharea* | Prevalence [CI] | *N bergeri* | Prevalence [CI] | *N subflava* | Prevalence [CI] | **Total** | Prevalence [CI] |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Survey 1 | 577 | 3.6 [3.3-3.9] | 896 | 5.7 [5.3-6.1] | 79 | 0.5 [0.4-0.6] | 17 | 0.1 [0.1-0.2] | 4 | 0.03 [0-0.05] | 1573 | 10.0 [9.4-10.5] |
| Survey 2 | 454 | 3.0 [2.7-3.3] | 1010 | 6.7 [6.3-7.2] | 117 | 0.8 [0.62-0.9] | 62 | 0.4 [0.3-0.5] | 17 | 0.1 [0.1-0.2] | 1660 | 11.1 [10.6-11.7] |
| Survey 3 | 648 | 4.2 [3.8-4.5] | 682 | 4.4 [4.0-4.7] | 94 | 0.6 [0.5-0.7] | 34 | 0.2 [0.1-0.3] | 3 | 0.02 [-0.002-0.04] | 1461 | 9.41 [8.9-9.9] |
| **Total** | **1679** | **3.6 [3.4-3.8]** | **2588** | **5.6 [5.3-5.8]** | **290** | **0.63 [0.5-0.7]** | **113** | **0.2 [0.2-0.3]** | **24** | **0.05 [0.03-0.1]** | **4694** | **10.2 [9.8-10.5]** |

*Age and gender*: The relative risk of carrying NPNs overall was higher in children aged less than 15 years compared to the young adult age group (age 15-29 years) with an aRRR of 3.11 [95% CI, 2.60- 3.73] for those <1 year, 5.90 [95% CI, 5.23- 6.65] for the 1-4 year olds and 2.59 (95% CI, 2.29- 2.94) for the 5-14 year olds. The oldest age group >30 years had a lower aRRR of 0.51 (95% CI, 0.43- 0.61). The prevalence of carried *Nl* was highest in the 1-4 year old age group, reaching a peak of 14.1% [95% CI, 13.3-14.8%] in contrast to carriage of *Nm,* which reached a peak of 5.2% [95% CI, 4.8-5.6%] in the 5-14 year age group. Similarly to *Nl, Np* carriage also reached a peak prevalence of 1.7% [95% CI, 1.4-1.9%] in the 1-4 year old age group (Figure 2). Carriage prevalence of *Nb* and *Ns* was too low to identify an overall trend in age group distribution. Males had a lower risk of carrying NPNs than females (aRRR of 0.87 [95% CI, 0.80-0.94]) but a higher risk of carrying *Nm* (aRRR of 1.34 [95% CI, 1.21-1.48]).

**Figure 2: Prevalence of *Neisseria* species carried by age group**



*Vaccination history*: A history of vaccination within the past 12 months with any meningococcal vaccine was associated with a decrease in *Nm* carriage, as reported previously [8], but additionally with a decreased risk of carrying NPNs (aRRR of 0.82 [95% CI, 0.73-0.92]. In the three countries where MenAfriVac® was introduced during the course of the study (Chad, Mali, and Niger) a significant decrease in the prevalence of carriage of *Nl* from 6.4% to 4.9% was observed. An overall decrease in carriage of *Nm* was also observed in the three countries but this reduction was not consistent in all countries with Mali experiencing an increase from 0.6% to 1.2% (Supplementary Figure 2).

*Other risk factors:* Area of residence (rural vs urban), crowding, cooking with cow dung or straw, kitchen location, and attendance at social gatherings in the past week all had a significant impact on the odds of carrying NPNs in the univariable regression model, but their effect was not significant in the multivariable model. Some of these risk factors were retained in the final model as, although they had no effect on NPN carriage, they were significant for *Nm* carriage.

### *Genetic diversity of identified Neisseria species.*

Forty-two different alleles were identified for the *rplf* fragment (*f_rplf*). *Nl* was the most diverse species with 17 *f_rplf* alleles, the most frequent of which was *f_rplf 6* (1453 isolates, 56.1%). Eleven alleles were found for *Nm* the most frequent being *f_rplf 2* (749 isolates, 44.6%) and *f_rplf 1* (707 isolates, 42.1%); four *f_rplf* alleles were identified in *Np,* the most frequent of which was *f_rplf 9* (207 isolates, 71.4%). Four alleles were also found among the *Nb* alleles with *f_rplf 62* (57) and f_rplf 69 (46) representing 91.2% of

these isolates. Finally, seven alleles were observed for *Ns*, with predominance of *f_rplf 43* (15 isolates, 62.5%) (Supplementary Table 2). A Neighbor Joining tree was used to represent the phylogeny of the *rplF* fragment present in the *Neisseria* isolates of this study in relation to the original isolates used to create the *f_rplF* assay (132) (Supplementary Figure 3).

The diversity of *fetA* alleles varied by country (Figure 3A; Supplementary Table 3); Niger had the highest number of *fetA_vr* alleles (111) and Ghana had the least (55). Some allele variability was seen between surveys, for example the proportion of the F1-1 allele increased from 61 (3.63%) in survey 2 to 342 (23.38%) in survey 3 and similar changes were observed for others alleles in survey 3 (Figure 3B; Supplementary Table 4). A total of 234 different alleles were identified across all species: 75 of these were found in only one isolate; 184 in fewer than 20 isolates. A total of 194 alleles were observed for *Nl*, 80 for *Nm*; 35 for *Np*; 21 for *Nb*; and 16 for *Ns*. Most alleles were found predominantly in only one species, for example 99.61% of *fnl* alleles were found in *Nm* (11, 299), all F5-84 variants were only detected in *Nl*, all F5-1 were exclusive to *Nm*, all F11-4 were found only in *Np* and all F1-169 and all F1-193 variants were only observed in *Ns.* Some variants, however, were shared among different species, *e.g.* F1-72, F1-21, F2-24, F6-3 (Figure 3C; Supplementary Table 5). Neither the *fetA_VR* nor the *fnl* fragment was successfully amplified in 643 isolates, which were designated Not Determined (ND). As defined by *f_rplf* and *feta_VR* alleles, there were 636 different *Neisseria* strain types identified, with almost half of these (297, 46.70%) observed only once. There was appreciable variation in the frequency of the strain types observed more than 20 times (Table 3).

**Figure 3. Frequency distribution of *fetA_VR* alleles**

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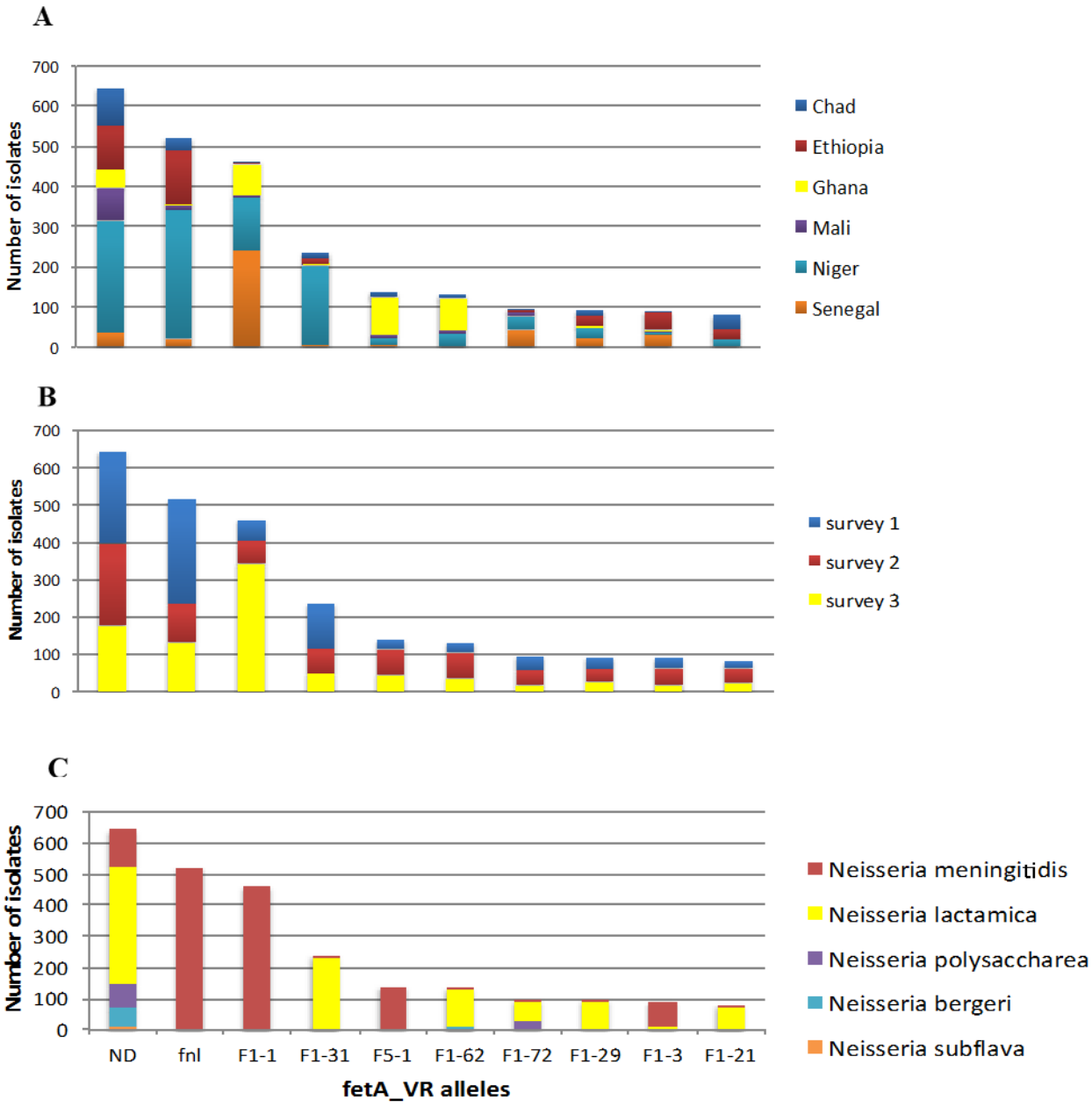



Frequency distribution of different alleles of the variable region of *fetA*. Only the 10 most common alleles are displayed; distribution by country (A), by survey (B) and by species (C).

**Table 3: Number of isolates for the most common commensal strain types per species**

| Commensal strain_type *"f_ rplf:fetA"* | *Neisseria bergeri* | *Neisseria lactamica* | *Neisseria meningitidis* | *Neisseria polysaccharea* | Total |
|---|---|---|---|---|---|
| 1:fnl | - | - | 470 | - | 470 |
| 2:F1-1 | - | - | 452 | - | 452 |
| 6:F1-31 | - | 205 | - | - | 205 |
| 2:F5-1 | - | - | 135 | - | 135 |
| 6:ND | - | 122 | - | - | 122 |
| 32:ND | - | 88 | - | - | 88 |
| 52:ND | - | 82 | 0 | - | 82 |
| 2:F1-3 | - | - | 74 | - | 74 |
| 1:ND | - | - | 68 | - | 68 |
| 9:ND | - | - | - | 66 | 66 |
| 6:F1-29 | - | 62 | - | - | 62 |
| 34:F1-62 | - | 56 | - | - | 56 |
| 6:F1-62 | - | 47 | - | - | 47 |
| 52:F3-60 | - | 46 | - | - | 46 |
| 6:F1-100 | - | 46 | - | - | 46 |
| 6:F1-72 | - | 46 | - | - | 46 |
| 1:F3-1 | - | - | 45 | - | 45 |
| 6:F5-133 | - | 45 | - | - | 45 |
| 6:F4-5 | - | 43 | - | - | 43 |
| 6:F4-17 | - | 42 | - | - | 42 |
| 9:F7-3 | - | - | - | 37 | 37 |
| 6:F5-84 | - | 36 | - | - | 36 |
| 33:F2-17 | - | 35 | - | - | 35 |
| 52:F1-21 | - | 35 | - | - | 35 |
| 62:ND | 35 | - | - | - | 35 |
| 33:ND | - | 34 | - | - | 34 |
| 88:fnl | - | - | 32 | - | 32 |
| 9:F2-24 | - | - | - | 32 | 32 |
| 1:F5-5 | - | - | 31 | - | 31 |
| 34:ND | - | 31 | - | - | 31 |
| 69:ND | 31 | - | - | - | 31 |
| 6:F4-6 | - | 29 | - | - | 29 |
| 6:F5-12 | - | 29 | - | - | 29 |
| 2:ND | - | - | 28 | - | 28 |
| 6:F5-18 | - | 26 | - | - | 26 |
| 2:F6-3 | - | - | 25 | - | 25 |
| 52:F1-29 | - | 25 | - | - | 25 |
| 6:F1-21 | - | 25 | - | - | 25 |
| 9:F11-4 | - | - | - | 25 | 25 |

| | | | | | |
|---|---|---|---|---|---|
| 4:F1-7 | - | - | 23 | - | 23 |
| 63:F1-72 | - | - | - | 23 | 23 |
| 6:F6-2 | - | 23 | - | - | 23 |
| 1:F4-23 | - | - | 22 | - | 22 |
| 33:F4-6 | - | 22 | - | - | 22 |
| 33:F5-34 | - | 22 | - | - | 22 |
| 6:F2-23 | - | 22 | - | - | 22 |
| 6:F1-120 | - | 21 | - | - | 21 |
| 6:F1-101 | - | 20 | - | - | 20 |

## Discussion

Although the introduction of PsA-TT into the African meningitis belt has had a major impact on serogroup A epidemics (113, 300), the region will remain at risk of meningococcal disease until comprehensive vaccines targeting all serogroups are available (290). The reasons for the unique epidemiology of the African meningitis belt remain poorly understood (69), making it difficult to predict when and where epidemics caused by non-serogroup A meningococci might occur. Variations in the prevalence of NPN species, which potentially contribute cross immunity through sub-capsular antigens, could play a role in determining susceptibility to a potentially epidemic strain. A number of studies have indicated the movements of genes encoding various protein antigens from NPN to *Nm* (294, 301) and variants of the FetA antigen have been previously shown to be shared amongst *Neisseria* species (133, 294). This antigen is known to generate protective responses in humans (302). Colonization with NPNs also affects *Nm* colonization of humans in experimental studies (135).

The novel sequence based techniques employed in this study enabled *Nm* and NPN to be identified and characterized rapidly and cost effectively from the very large numbers of

samples obtained in the African centres. The *rplF* assay (132) achieved reliable speciation, which would not have been possible with conventional methods such as 16S rRNA gene sequencing. An indication of diversity within species was achieved by sequencing the variable region of the gene encoding FetA (*fetA_VR,*), an outer membrane protein (OMP) found in most *Neisseria*, and which is involved in iron metabolism and been shown to elicit protective immune responses (121). Further characterization of the meningococcal isolates has been previously published (100).

Of the five known *Neisseria* species identified, with a possible novel species present in Chad, the most common were *Nl* and *Nm*. These are the species that have been observed most frequently in previous investigations in the African meningitis belt and they are known to have antagonistic interactions in colonization (135, 303). It is possible that the isolation of some of the other species was affected by the selective media used in this and other studies. Although growth of *Np* (304), *Nl* (128, 130, 305, 306) and *Ns* (307) on colistin containing agar (such as modified Thayer-Martin or New York city medium) has been reported, other species such as *Neisseria perflava*, *Neisseria sicca*, *Neisseria mucosa, Neisseria cinerea* may not have been identified using the culture technique employed in this study (308). The impact of these media on *Nb* is unknown. In future, the identification of NPNs could be enhanced by the use of molecular approaches, although these will have to have species-level resolution, such as the *rplF* assay (132). The *Neisseria* identified were highly diverse at both the strain and the species level and varied markedly over time and place. This is consistent with other carriage studies in the meningitis belt, but is different from the relatively stable carriage observed in countries that do not experience large-scale epidemic disease (43).

The most common NPNs recovered, *Np* and *Nl*, were isolated predominantly from young children as opposed to *Nm*, which was isolated most frequently from older children. *Nl* is known to colonize infants and young children preferentially in many settings (309) and this is consistent with carriage of NPNs having a role in the rapid acquisition of antibody against *Nm* among children in the meningitis belt, although given the age distribution of meningococcal disease these antibodies may not be protective (310).

The risk factors for Nm and NPNs carriage were not the same and in some cases (eg. age, sex and season) were inversely related. Individuals were more likely to carry NPNs during the rainy season if they were a female and under 5 years old whereas they were more likely to carry *Nm* during the dry season, if they were male and between 5 and 29 years old (100). These results suggest that the physical presence of an NPN in the pharynx may prevent the colonization by *Nm* although this may not apply to the hyper-invasive meningococci since the incidence of meningococcal disease in the African meningitis belt is highest in under five year olds. Recent vaccination with a meningitis vaccine (primarily MenAfriVac®, which was used in Mali, Niger and Chad during the course of our study) appeared to be protective both against carriage of Nm and NPNs overall in the regression analysis. This effect could possibly be explained by disturbance of the microbiome following vaccination but could also be due to residual confounding or a reflection of the naturally dynamic patterns of carriage. In Mali, an increase in Nm was observed post-vaccination, due to an expansion of serogroup W (100). This seems unlikely to be an effect of MenAfriVac® but it is not known how the removal of one serogroup from the nasopharyngeal environment could affect the other serogroups. The influence of host factors on carriage of *Nm* and NPNs has not been investigated in this

study but the IgA secretory status of the individuals sampled could also play a role as previously shown (311).

Few published studies have characterized pharyngeal NPNs in the African meningitis belt. One recent study in Burkina Faso, which did not survey adults over the age of 30 years or identify species other than *Nm* and *Nl* (130), reported a number of differences compared to the MenAfriCar surveys described here: there was a higher overall prevalence of *Nl* carriage (18.2%); a higher prevalence in males, although it was significantly higher in women (9.1% vs 3.9%) for the 18-29 year age group and no significant changes between seasons or post vaccination. The reasons for these inconsistencies are unclear, although both studies indicated fluctuations in prevalence among surveys and these differences may reflect the highly dynamic nature of *Neisseria* carriage.

Some of the *fetA_VR* alleles found were shared among the different species, as reported previously (133, 294). Since the variable region of *fetA* plays an important role in its immunogenicity (121), the shared protein variants could create a cross-reactive immunity at the subscapular level. The inclusion of *fetA_VR* in the meningococcal typing system also increased discrimination between strains (supplemental table 6). Although there was correlation between *porA* and *fetA_VR* alleles for some *Nm* strains (e.g. *cnl*:P1.18-11,42-1:*fnl*), in others the *fetA_VR* (e.g. W:P1.5,2:F1-1 and W:P1.5,2:F6-3) or both OMPs (e.g. W:P15-1,2-36:F5-1) sequences varied, suggesting that the serogroup W *Nm* strains are antigenically diverse. This has potential implications for using proteins such as *porA* or *fetA* in vaccine formulations (312). The Neighbor Joining phylogeny

(Supplemental figure 3) shows the clustering of all of the isolates with the appropriate species except for one, which has the *f_rplF* allele 58 defined previously as *Ns* (132) but clusters more closely, in this study, with the *Nb* species which was not discovered at the time of the previous study. This particular isolate may also be a *Ns* with a *f_rplF* allele similar to *Nb*. More sequence data from this isolate will clarify this issue.

This study has demonstrated the dynamic nature and high diversity of the genus *Neisseria* in pharyngeal carriage in countries of the African meningitis belt. The results are consistent with the idea that the carriage of NPNs may influence invasive meningococcal disease epidemiology in the African meningitis belt. Although more research is needed to elucidate such effects, understanding these organisms could potentially contribute to meningococcal disease control. This is of particular importance given the absence of comprehensive vaccines against all meningococcal serogroups and the continuing interest in the development of protein based vaccines.

# B- Chapter 4: Hierarchical genomic analysis of carried and invasive serogroup A *Neisseria meningitidis* during the 2011 epidemic in Chad


## Abstract

***Background:*** Serogroup A *Neisseria meningitidis* (*NmA*) was the cause of the 2011 meningitis epidemics in Chad. This bacterium, often carried asymptomatically, is considered to be an "accidental pathogen"; however, the transition from carriage to disease phenotype remains poorly understood. This study examined the role genetic diversity might play in this transition by comparing genomes from geographically and temporally matched invasive and carried *Nm*A isolates.

***Results:*** All 23 *Nm*A isolates belonged to the ST-5 clonal complex (cc5). Ribosomal MLST comparison with other publically available *Nm*A:cc5 showed that isolates were closely related, although those from Chad formed two distinct branches and did not cluster with other *Nm*A, based on their MLST profile, geographical and temporal location. Whole genome MLST (wgMLST) comparison identified 242 variable genes among all Chadian isolates and clustered them into three distinct phylogenetic groups (Clusters 1, 2, and 3): no systematic clustering by disease or carriage source was observed. There was a significant difference (*p=0.0070*) between the mean age of the individuals from which isolates from Cluster 1 and Cluster 2 were obtained, irrespective of whether the person was a case or a carrier.

***Conclusions:*** Whole genome sequencing provided high-resolution characterization of the genetic diversity of these closely related *Nm*A isolates. The invasive meningococcal isolates obtained during the epidemic were not homogeneous; rather, a variety of closely

related but distinct clones were circulating in the human population with some clones preferentially colonizing specific age groups, reflecting a potential age-related niche adaptation. Systematic genetic differences were not identified between carriage and disease isolates consistent with invasive meningococcal disease being a multi-factorial event resulting from changes in host-pathogen interactions along with the bacterium.

## Background

*Neisseria meningitidis* (*Nm*) is a Gram-negative bacterium, which is frequently carried asymptomatically in the human nasopharynx. It is considered to be an "accidental pathogen": a normally commensal organism that occasionally invades the bloodstream causing septicaemia and/or meningitis. The factors that determine whether a person infected with *Nm* becomes a carrier or a case remain poorly understood. Meningococcal genetic and antigenic diversity are likely to be important and whole genome comparative analysis of carriage and disease isolates provides one means of investigating this. Different approaches have been used to compare carried and invasive isolates. Early studies compared the proportions of clonal complexes (cc), defined by Multi Locus Sequence Typing (MLST), among serogroups and identified hyper-virulent lineages that were overrepresented in invasive isolates and less common in carriage samples (120). More recent studies have used whole genome technology to compare a broad range of disease and carriage isolates. These studies have, for example, identified a prophage present in some disease-associated isolates but not limited to them (226, 227, 313). Another recent study compared carried and invasive serogroup Y *Nm* (*Nm*Y) from the UK and identified a disease-associated clone (224); however, there is still much

uncertainty over what determines the carried or invasive state, especially during epidemics.

For over 100 years, the Sahelian and sub-Sahelian regions of Africa, the African meningitis belt, have experienced large epidemics of meningococcal disease (85, 88, 91, 289, 314-317). Serogroup A *N. meningitidis* (*Nm*A) was the most common cause in this region before the introduction of the TT-PsA conjugate vaccine (MenAfriVac®), which started in 2010 and will have been deployed in all 26 countries of the meningitis belt by the end of 2016, with 235 million doses administered at the time of writing. Since vaccine implementation, other previously less common groups including W (*Nm*W), C (*Nm*C), X (*Nm*X), and Y (*Nm*Y*)* have been more frequently associated with meningococcal disease in this region (77).

The southern part of the Republic of Chad lies in the African meningitis belt and has been subject to recurrent meningitis outbreaks since the early 1900s (113). Since 2005, *Nm*W and *Nm*A have alternated as the major epidemic strains in small-scale outbreaks (318). A large epidemic was recorded in Chad in 2011: seventeen districts reached the epidemic threshold of 10 per 100,000 per week and a total of 5960 suspect cases and 270 deaths were reported. Cerebrospinal fluid samples (CSFs) were obtained from only 3.8% of the cases for laboratory confirmation, but *Nm*A was the pathogen identified most commonly by culture and sero-agglutination methods (77). Vaccination with MenAfriVac® of all subjects aged 1-29 years old was undertaken in the capital N'Djamena and in the surrounding area in 2012 with a dramatic impact on the epidemic, which continued in the rest of the country (113). Vaccination of all previously unvaccinated areas the following year ended the epidemic and few cases of meningitis have been recorded since

(300). The MenAfriCar consortium, established in 2009 to study the carriage of *Nm* before and after the introduction of MenAfriVac® in the African meningitis belt, undertook three carriage surveys in the Mandelia district of Chad, two before and one after the vaccination campaign (111, 113). Carriage of *Nm*A was low (<1%) prior to vaccination but fell to almost zero following vaccine implementation (113).

Isolates from serogroup A carriers and from patients with serogroup A invasive disease were retained, providing an opportunity to compare the genomic characteristics of carried and invasive isolates obtained during the same *Nm*A African epidemic. Here we describe the high-resolution provided by whole genome sequence (WGS) analysis and demonstrate how this can identify differences among closely related isolates. No systematic clustering by carried or invasive phenotype was observed, but three distinct clusters were identified circulating during the 2011 Chadian epidemic, two of them preferentially isolated from different age groups.

## Methods

### *Isolate collection*

A total of 33 *Nm*A carried isolates were collected during the second MenAfriCar carriage survey in Chad in 2011 and stored in BHI and 20% glycerol in a -80˚C freezer. These isolates were revived by inoculation on blood agar plates (BAP) and incubated at 37˚C with 5% $CO_2$ for between 16 and 48 hours. Ten viable isolates were recovered and were included in this dataset.

CSF samples were collected from patients with meningitis for laboratory confirmation as part of the national meningitis surveillance program. The majority of meningococci recovered from these specimens by culture methods were stored at the meningitis reference laboratory in N'Djamena, Chad and a small number of isolates were also stored at the WHO collaborating center for reference and research on meningococci, based at the Norwegian Institute of Public Health. A total of 13 invasive *NmA* were recovered and included in this analysis out of the 98 reported in the 2011 surveillance records (77).

Ethical approval for the MenAfriCar studies was obtained from the ethics committee of the London School of Hygiene & Tropical Medicine and ethical committees of each of the African partner institutions, with the exception of Chad, which did not have a formal ethical committee at the time of this study. Here, approval was granted by a committee that was established to oversee the MenAfriCar studies by the Chad Ministry of Health. Written informed consent or assent was obtained from subjects who participated in the pharyngeal carriage study. Invasive isolates from Chad were obtained from CSF samples collected from patients during the course of routine clinical care following a national protocol. The MenAfriCar studies were registered with ClinicalTrials.gov (NCT01119482).

### *DNA extraction and sequencing*

DNA was extracted in two different laboratories: the first batch included 19 isolates and DNA was extracted using the DNeasy® Blood and Tissue kit (Qiagen) as previously described (249). Briefly, a sterile 1 µl loop was used to transfer bacterial growth into a tube containing 180µl of buffer ATL and 20µl of Proteinase K. The tube was then

incubated at 56˚C for at least 2 hours with intermittent mixing to lyse the cells. Following treatment with RNase A and subsequent addition of buffer AL/ethanol, the lysate was loaded on to the spinning column provided and the DNA was extracted and purified through a series of spinning and washing steps in accordance with the manufacturer's instructions employing two elution steps each using 75 µL of buffer AE. The second batch included the remaining 4 isolates and DNA was extracted using an Eppendorf robot and the NucleoSpin 96 tissue kit (Macherey-Nagel) according to manufacturer's instructions.

DNA samples were sequenced at the Oxford Genomics Centre. The library preparation was done using the Ultra DNA Sample Prep Kit (NEBNext) according to the manufacturer instructions and automated using a Biomek FX (Beckman Coulter). The genomic DNA (gDNA) was fragmented using the Episonic 2000 sonication system (Epigentek), then end-repaired, A-tailed and adapter-ligated using adapter designed "in house" (319), before the size selection, amplification and paired end sequencing performed on the Illumina HiSeq 2000 using a 100 base pair paired-end protocol as previously described (217).

### *Genome annotation*

Short-read sequences were assembled using the Velvet genome assembly program (v1.2.08) (259), after a performance comparison with the program Spades (v3.9.1) (Supplemental Table 3). All odd-numbered kmer lengths between 21 and 99 were sampled using the VelvetOptimiser software (v2.2.4) (320) to automatically calculate the optimal assembly parameters for Velvet (default optimization functions used).

Assembled contigs were deposited into the *Neisseria* PubMLST database (174) which uses the Bacterial Isolate Genome Sequence Database (BIGSdb) software (248). Draft genomes were first automatically curated at all loci defined in the database using the BLAST algorithm (321) and a sequence similarity threshold of >98%, allowing rapid annotation of known alleles and sequences which were very similar to defined loci (217). Manual verification was then performed for variable loci, such as those containing internal stop codons, frame shifts or those with sequence similarities lower than 98%. Incomplete gene sequences at the beginning or end of a contig were identified as such and were excluded from further analyses.

### *Hierarchical genomic analysis*

Hierarchical gene-by-gene analysis was performed: conventional seven locus MLST (120), rMLST (241) and wgMLST (217) using the BIGSdb Genome Comparator tool (248) as previously described; briefly , the loci of interest: (i) 7 housekeeping genes of MLST (120); (ii) 53 ribosomal genes of rMLST (241); and (iii) 2070 genes annotated in the WUE2594 reference genome for wgMLST (322) were extracted from the 24 assembled genomes and a pairwise allelic comparison was performed using Genome Comparator with the following parameters: Min % identity of 70, Min % alignment of 50 and BLASTN word size of 15. A total of 141 publically available *Nm*A from the ST-5 clonal complex (*Nm*A:cc5), were obtained from PubMLST.org/neisseria (174) and included in the rMLST analysis to provide a global perspective to the epidemic using Neighbor-Joining trees with 50 bootstrap replications and the kimura 2-parameter model, generated with MEGA6 (269). Only the unique strains were represented and they were defined as

groups of isolates sharing the same alleles at all 53 ribosomal loci. The finished genome WUE2594 (GenBank accession number FR774048), an *Nm*A*:*cc5 invasive isolate (322), was used as a reference genome for the wgMLST analysis. Neighbor-Net trees were computed with SplitsTree (version 4.13.1) (284) using distance matrices generated by Genome Comparator after pairwise allelic comparisons of all 23 genomes at the loci of interest described above. Isolates with allelic variations specific to each of the clusters were identified from the variable gene lists generated by Genome Comparator. The nucleotide sequences of these genes were then extracted from the database for each genome and aligned in MEGA6 (269). All nucleotide sequences and amino acid changes specific to a cluster were noted. The Artemis Comparison Tool (270) and MAUVE (271) were used to visualize, align and compare the organization of the loci on the contiguous sequence assemblies (contigs) obtained using default settings.

WgSNP analysis was performed using the program kSNP3 (279) using first the velvet assembled fasta files, then the raw fastq files of all 23 isolates alongside the finished reference genome WUE 2594. In order to use the fastq files, first these were downloaded from the European Nucleotide Archive (ENA) (323) using the ENA accession numbers available in the PubMLST isolate records and then processed with the tools from the FASTX-toolkit (324), using the command-line : the low quality reads were trimmed for each isolate data using "fastq_quality_trimmer" with a quality threshold of 28, then "fastq_to_fasta" was used on the trimmed data to obtain fasta files for each isolates (the –n option was used to keep all the sequences' information available in the trimmed files). Once the fasta files were obtained, the built in option "MakeKSNP3infile" of kSNP3 was used to make the required input file, "MakeFasta" was

used to transform that "infile" into a fasta format that was used to run "Kchooser" in order to determine the optimal kmer size (k) or the length of the sequence that kSNP3 will find in each isolate sequence data; the optimal k was 19 for the velvet assembled fasta files and 21 for the original fastq files. The values of k obtained were then used to run kSNP3 with the annotations from the reference genome WUE2594 manually downloaded from genbank and including the gi numbers (-genbank argument). Finally the output files were filtered out to remove all the SNPs found in a coding region. The Neighbor Net trees were computed using SplitsTree (version 4.13.1)(284). Further SNPs characterization was done when necessary by visualizing the genome sequences in Artemis and aligning the sequences of interest in MEGA6 (269), using MUSCLE (325).

### *Statistical analysis*

The age, sex and geographical location of the meningococcal cases and carriers were recovered. A t-test was used to measure the statistical significance of the changes in age distribution observed between Cluster 1 and 2 identified, by comparing the mean age of the individuals from which the isolates from each cluster were collected. A t-test was also used to measure significant differences in the proportions of gender and provenances between the clusters by comparing the proportion of the gender group and the proportions of different provenance of the individuals from which the isolates came from between both clusters. T-tests were performed in Excel (version 2013).

## Results

### *Genome assembly statistics*

High-quality draft genomes (217) were obtained for each isolate (Supplemental Table 1). In summary: the average number of contigs was 154 (range 113 to 243), the average N50 was 43378 (range 28533 to 52853); and the average length of the assembled genome was 2164341 (range 2155465 to 2174025). The average number of genes with allele designations, based on the 1605 *Neisseria* core genes list (217), was 1568 (97.7%) ranging from 1539 (95.9%) to 1577 (98.3%) loci.

### *MLST analysis*

The 23 isolates all had *Nm*A-associated capsule synthesis genes in region A of the capsule polysaccharide region of the genome (38), as expected, and belonged to cc5. Three different sequence types (ST) were found (Table 1), with their Multi-Locus Sequence Typing (MLST) profiles varying at up to two loci from the central Sequence Type, ST-5. The majority of isolates (21/23, 91%) were ST-7 and one isolate was ST-9021. Both STs had a single allelic difference at the *pgm* locus from ST-5. One invasive isolate lacked the *gdh* gene and therefore could not be assigned an ST. Comparison of the contig lacking *gdh* from this isolate with another isolate where *gdh* was present identified the deletion of six contiguous genes all involved in glucose metabolism, *NEIS1325, NEIS1326, NEIS1328* to *NEIS1331* (Supplemental Figure 1).

**Table 1. Summary of MLST profiles**

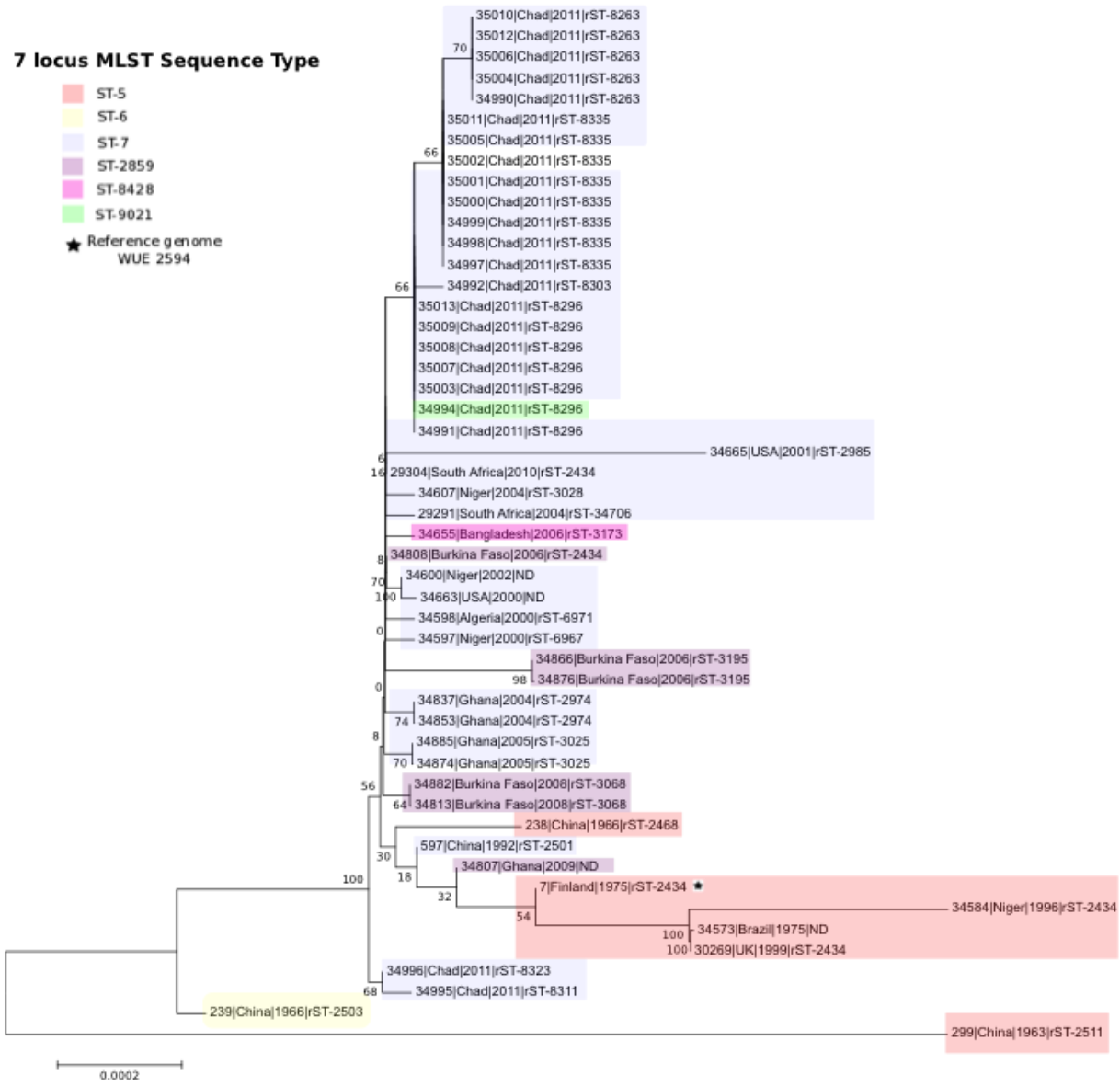
| Number of isolates | *abcZ* | *adk* | *aroE* | *fumC* | *gdh* | *pdhC* | *pgm* | ST (MLST) | Clonal complex (MLST) |
|---|---|---|---|---|---|---|---|---|---|
| 21 | 1 | 1 | 2 | 1 | 3 | 2 | 19 | 7 | ST-5 complex/subgroup III |
| 1 | 1 | 1 | 2 | 1 | 3 | 2 | 599 | 9021 | ST-5 complex/subgroup III |
| 1 | 1 | 1 | 2 | 1 | - | 2 | 19 | ND | ST-5 complex/subgroup III |

ND: Not Determined

## *rMLST analysis*

Higher resolution relationships were obtained through the comparisons of the 53 ribosomal MLST (rMLST) loci, which identified six new rSTs: rST-8263; rST-8296; rST-8303; rST-8311; rST-8323; and rST-8335. The *Nm*A genomes from Chad exhibited allelic variation in 0 to 5 rMLST loci in pairwise comparisons, with an average of 1.4 loci different. Phylogenetic comparison with other *Nm*A:cc5 isolates, available through PubMLST.org/neisseria (174) (Supplemental Table 2), was performed including isolates from: a global collection of *Nm* isolates (n=12) (120); the African meningitis belt (n=99) (251); and other publically available isolates (n=30)(249, 326). The Neighbor-Joining Tree generated showed that most of the Chadian 2011 *Nm*A (21/23, 91%) formed a distinct branch (bootstrap value of 66); however, two isolates were found to cluster separately with a bootstrap value of a 100 (Figure 1). Isolates most closely related to the 21 Chadian *Nm*A isolates were from South Africa, Niger, Bangladesh, USA and Burkina

Faso, between 2001 and 2010 and exhibited several rSTs (rST-7, rST-8428 and rST-2859).




## Figure 1. rMLST Neighbor-Joining Tree of cc5 *Nm*A

The relationship from the concatenated nucleotide sequences of the ribosomal genes between the *Nm*A isolates from Chad (n=23) and other publically available cc5 *Nm*A genomes from the PubMLST database is represented in this tree. The label on each node indicates: the PubMLST ID number, the country, the date and the rST for each isolate represented. A total of 141 other cc5 *Nm*A isolates were found in PubMLST but only one representative of each unique strain (defined as isolates sharing the same alleles at all 53 ribosomal locus) was included in the tree alongside all the Chadian *Nm*A from the 2011 meningitis epidemic; the full list of publically available cc5 *NmA* isolates is shown in supplemental table 2. The seven-locus MLST profiles of the isolates are indicated by different colored boxes. The position of the reference genome used in this study (WUE 2594) is represented by a black star.

### *Whole genome MLST (wgMLST) clusters isolates into 3 groups*

Allelic comparison with the 2070 genes annotated in the reference genome (WUE2594) identified 1542 (74.5%) identical genes among all isolates, 1347 (65.1%) of which possessed the same allele as WUE2594. A total of 196 (9.5%) genes were identical in the Chad isolates but different from the reference. Sixty-six (3.2%) genes present in WUE2594 were absent in the Chadian isolates, while 242 (11.7%) were present in all but variable among the 23 *Nm*A isolates from Chad. A total of 221 (10.7%) of these loci had incomplete sequences, as a consequence of incomplete assembly and were not included in pairwise comparisons. Neighbor-Net analysis using a distance matrix based on 1849 (89.3%) genes (excluding the 221 incomplete loci) resolved three distinct clusters: Cluster 1, comprising 8 isolates; Cluster 2, 13 isolates; and, Cluster 3, 2 isolates (Table 2 and Figure 2A).

**Table 2. Epidemiological data associated with the host of the isolates and bacterial clusters**

| ID | Epidemiological data of the host | | | Bacterial Characteristic* | | |
|---|---|---|---|---|---|---|
| **PubMLST** | **Phenotype** | **Sex** | **Age (year/month)** | **ST** | **rST** | **Genomic clusters** |
| **34990** | Disease | F | 6 | ST-7 | rST-8263 | 2 |
| **34991** | Disease | M | 10 | ST-7 | rST-8296 | 1 |
| **34992** | Disease | M | 11 | ST-7 | rST-8303 | 1 |
| **34994** | Disease | F | 0/5 | ST-9021 | rST-8296 | 1 |
| **34995** | Disease | M | - | ST-7 | rST-8311 | 3 |
| **34996** | Disease | M | 15 | ST-7 | rST-8323 | 3 |
| **34997** | Disease | M | 15 | ST-7 | rST-8335 | 2 |

| | | | | | | |
|---|---|---|---|---|---|---|
| **34998** | Disease | - | - | ST-7 | rST-8335 | 2 |
| **34999** | Disease | - | - | ST-7 | rST-8335 | 2 |
| **35000** | Disease | M | 11 | ST-7 | rST-8335 | 2 |
| **35001** | Disease | M | 18 | ST-7 | rST-8335 | 2 |
| **35002** | Disease | M | 16 | ND | rST-8335 | 2 |
| **35003** | Disease | - | - | ST-7 | rST-8296 | 1 |
| **35004** | Carriage | M | 36 | ST-7 | rST-8263 | 2 |
| **35005** | Carriage | M | 14 | ST-7 | rST-8335 | 2 |
| **35006** | Carriage | F | 28 | ST-7 | rST-8263 | 2 |
| **35007** | Carriage | F | 4 | ST-7 | rST-8296 | 1 |
| **35008** | Carriage | M | 12 | ST-7 | rST-8296 | 1 |
| **35009** | Carriage | M | 7 | ST-7 | rST-8296 | 1 |
| **35010** | Carriage | M | 36 | ST-7 | rST-8263 | 2 |
| **35011** | Carriage | F | 22 | ST-7 | rST-8335 | 2 |
| **35012** | Carriage | F | 13 | ST-7 | rST-8263 | 2 |
| **35013** | Carriage | F | 6 | ST-7 | rST-8296 | 1 |

* All the isolates had the following strain designation: A: P1. 20,9: F3-1: ST: cc5; the variable STs are indicated in the table.

### *Differences among clusters*

As cluster 3 comprised only two invasive isolates from the same geographical location it was not included in further statistical analysis. A significant difference in the mean age of the individuals from whom the *Nm*A were isolated was observed between Clusters 1 and 2, with Cluster 1 exhibiting a mean age of 7.2 years and Cluster 2 a mean age of 19.5 years, *p=0.007.* No significant difference between the clusters was found for the gender or residence of individuals from whom the meningococci were isolated. Cluster-specific allelic differences were identified in nine loci for Cluster 1 and 10 loci for Cluster 2.

These allelic differences included non-synonymous mutations (NSMs) in seven genes. In Cluster 1, four of the NSMs led to changes in the chemical properties of the encoded amino acids (e.g. polar to non-polar; acidic to basic) and similarly, in Cluster 2 with six NSMs. In both clusters most of these genes were annotated as encoding components of metabolic pathways, however, this included enzymes, genes associated with antibiotic resistance, toxicity, and genetic information processing (Tables 3 and 4).

**Table 3. Genes with alleles specific to Cluster 1 isolates**

| Locus | Functional category | Number of mutation | Number of non-synonymous mutation |
|---|---|---|---|
| NEIS2150 (*alx/TerC*) | Integral membrane protein (tellurite resistance protein) | 1 (bp 676) | 1 (A → S)* |
| NMAA_0255 | Insertion element IS1016 transposase | 1 (bp 28) | 1 (T → A)* |
| NEIS0947 (*trpG*) | Amino acid metabolism (phenylalanine, tyrosine and tryptophan biosynthesis) | 1 (bp 414) | 0 |
| NMAA_0798 | Hypothetical protein | 1 (bp 400) | 1 (E → K)* |
| NEIS1071 | Hypothetical protein | 1 (bp 461) | 1 (Y → C) |
| NEIS1383 (*aroD*) | Amino acid metabolism (phenylalanine, tyrosine and tryptophan biosynthesis) | 1 (bp 418) | 1 (V → M) |
| NEIS1605 | Enzyme (TatD DNase family) | 1 (bp 186) | 0 |
| NEIS1742 (*murG*) | Glycan metabolism/ Vancomycin resistance | 1 (bp 632) | 1 (A → V) |
| NEIS2135 | Nicotinate and nicotinamide metabolism | 1 insertion (bp 155) | 15 stop codon* |

* Change in the chemistry properties of the AA side chains

**Table 4. Genes with alleles specific to cluster 2 isolates**

| Locus | Functional category | Number of mutation | Number of non-synonymous mutation |
|---|---|---|---|
| **NEIS0370 (*carA*)** | Metabolism (pyrimidine and alanine, aspartate and glutamate) | 1 (bp 1057) | 1 (T→A)* |
| **NEIS0422 (*metK*)** | Metabolism (cysteine and methionine metabolism) | 1 (bp 726) | 0 |
| **NEIS0529** | Metal ions transport (zinc/manganese) | 1 (bp 363) | 0 |
| **NEIS1091 (*cysI*)** | Metabolism (sulfite reductase) | 1 (bp 1021) | 1 (P → T)* |
| **NEIS1237 (*cmk*)** | Metabolism (pyrimidine) | 1 (bp 611) | 1 (I → T)* |
| **NEIS1379 (*dnaZX*)** | Metabolism/DNA processing | 1 (bp 1774) | 1 (G → S)* |
| **NEIS1460** | Putative metabolism (Glucose-6-Phosphate 1-Dehydrogenase_bact motif) | 1 (bp 402) | 0 |
| **NEIS1741 (*murC*)** | Metabolism (D-glutamine/D-Glutamate, peptidoglycan biosynthesis) | 1 (bp 397) | 1 (A→S)* |
| **NEIS1804** | putative role in toxicity (associated with Maf Genomic islands MGI-1 scheme pubmlst) | 1 (bp 868) | 1 (F → V) |
| **NEIS0132 (*rplC*)** | Genetic information processing (ribosomal protein) | 1 ( bp 22) | 1 ( C → R)* |

* Change in the chemistry properties of the AA side chains

Within cluster comparisons identified four genes that had alleles distinct to the 4 carried isolates from Cluster 1 (Table 5); however, one of these genes, NMAA_0123, was found to be identical to that found in the two invasive isolates in Cluster 3. All the other alleles were specific to the carried sub-cluster.

**Table 5. Genes with alleles specific to the carried isolates of Cluster 1**

| Locus | Functional category | Number of mutation | Number of non-synonymous mutation |
|---|---|---|---|
| **NMAA_0123** | Hypothetical protein | Difference in G polymeric track length | Preliminary stop Codon* |
| **NEIS1527** | Two component response regulator | Insertion of "GCGTT" | Frameshift leading to a longer coding sequence* |
| **NEIS2894** | Hypothetical protein | 1 (bp 65) | 1 (T → I)* |
| **NEIS0291 (lot)** | LOS O-acetyltransferase | 1 (bp 465) | 0 |

* Change in the chemistry properties of the AA side chains

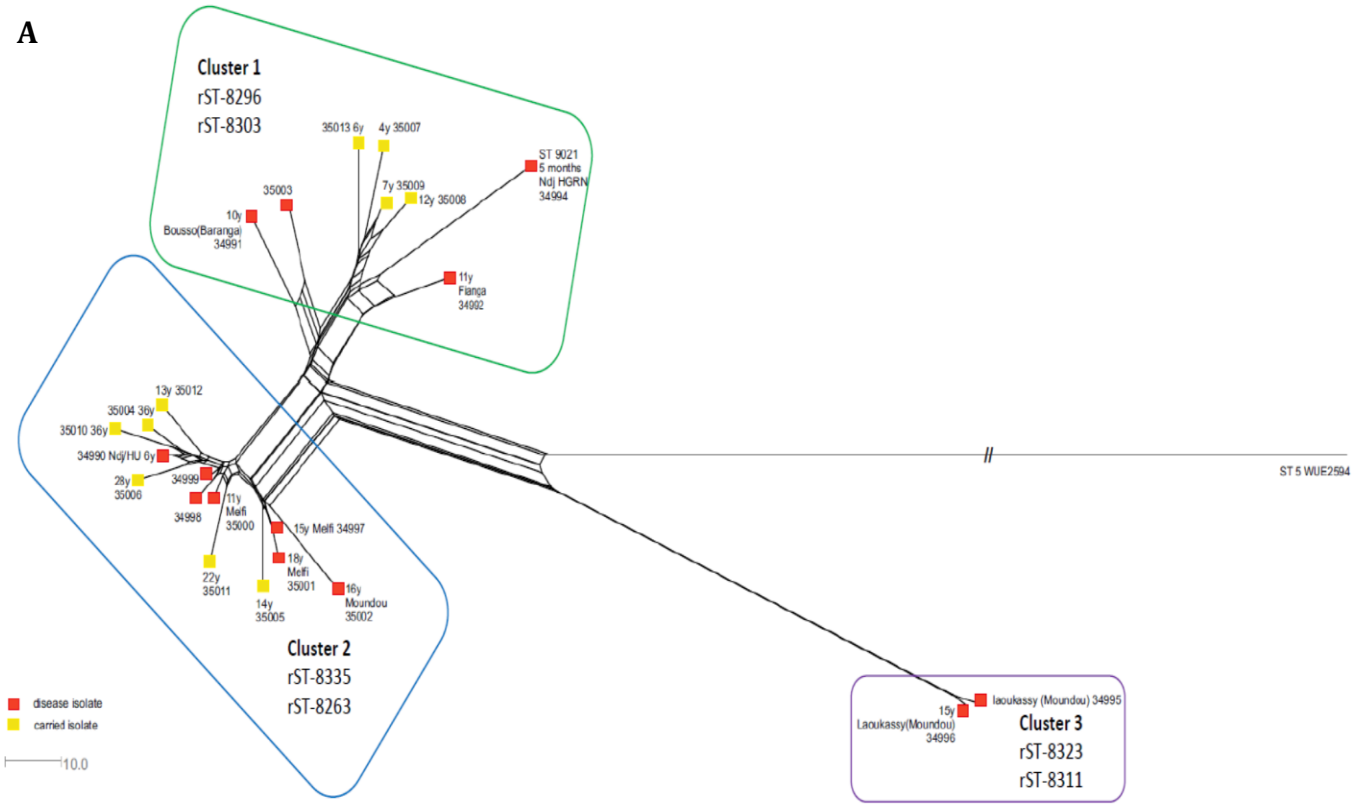
## *Whole genome Single Nucleotide Polymorphism (wgSNP) analysis of non-coding regions*

WgSNP comparison of the 23 *Nm*A genomes from Chad and the WUE2594 reference genome identified 1942 SNPs using assembled fasta sequences as input files, with 1924 SNPs identified when raw fastq files were used. Neighbor Net trees (Figure 2B and

Supplemental Figure 4) generated from the SNP matrix had a similar topology to those generated by wgMLST analysis (Figure 2A).

Using the annotations from the finished genome, WUE2594, enabled coding-regions, which had been included in wgMLST analysis, to be distinguished from non-coding regions, as well as other regions not found in the reference genome. There were 182 SNPs (assembled fasta files) and 181 SNPs (original fastq files) identified in non-coding regions: the majority of them 109 (fasta) and 112 (fastq) discriminated between the reference genome and the 23 Chadian *Nm*A; 26 SNPs were specific to Cluster 3; 6 SNPs were specific to Cluster 2 and 16 were specific to Cluster 1 by both methods. Within those 16 SNPs, only 3 were specific to the whole Cluster 1; a total of nine SNPs grouped six isolates (PubMLST ID: 34992, 34994, 35007, 35008, 35009 and 35013), three SNPs were specific to two isolates (PubMLST ID: 34991 and 35003) and one SNP was specific to the four carried isolates (PubMLST ID: 35007, 35008, 35009 and 35013). The other SNPs were unique, with 13 specific to PubMLST ID: 35007 by both methods (supplemental table 4). The SNP specific to the four carried isolates sub-cluster was mapped to a non-coding region between NEIS1544 and NEIS1545; an alignment of that region from all isolates of Cluster 1 allowed the identification of a nucleotide change from a G to an A, 132 base pairs upstream of the start codon of NEIS1545.

**A**


Cluster 1
rST-8296
rST-8303
35013 6y
4y 35007
ST 9021
5 months
Ndj HGRN
34994
35003
7y 35009
12y 35008
10y
Bousso(Baranga
34991
11y
Fiança
34992
13y 35012
35004 36y
35010 36y
34990 Ndj/HU 6y
28y
35006
34999
34998
11y
Meifi
35000
15y Meifi 34997
18y
Meifi
35001
22y
35011
14y
35005
16y
Moundou
35002
Cluster 2
rST-8335
rST-8263
ST 5 WUE2594
laoukassy (Moundou) 34995
15y
Laoukassy(Moundou)
34996
Cluster 3
rST-8323
rST-8311
disease isolate
carried isolate
10.0

**B**

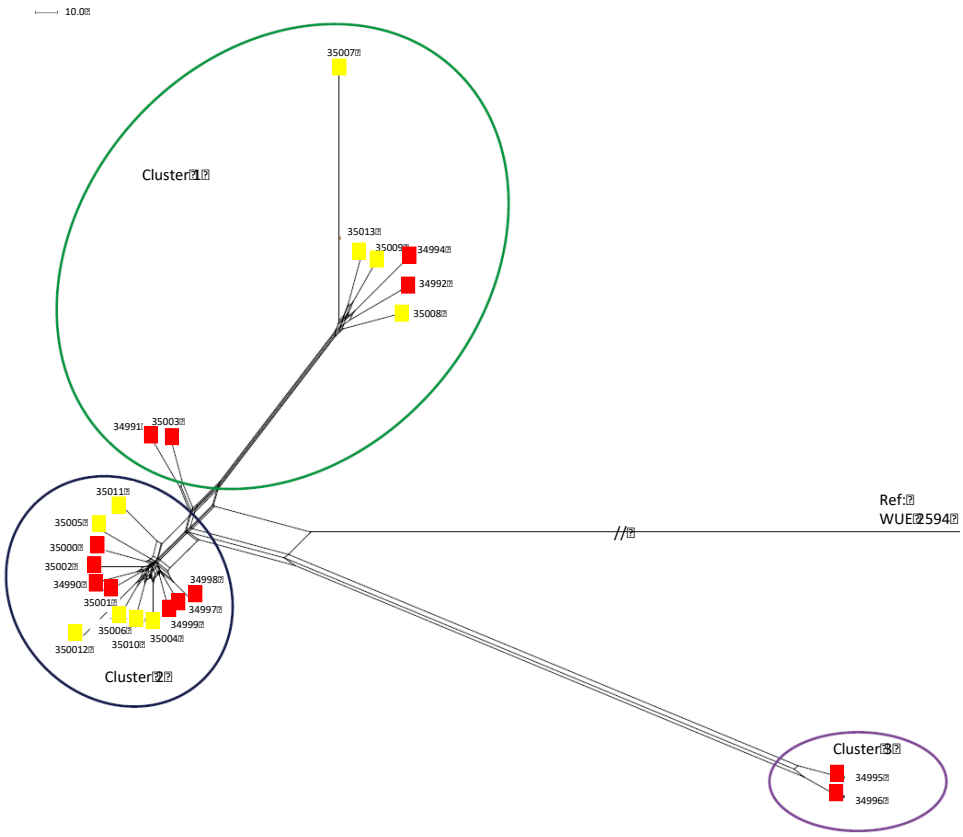

10.0
35007
Cluster 1
35013
34994
34992
35008
34991
35003
35011
35005
35000
35002
34990
35001
34998
34997
34999
35006
35004
35010
350012
Cluster 2
Ref:
WUE2594
Cluster 3
34995
34996

**Figure 2. wgMLST and wgSNP Neighbor Net Tree**

The genomic relationship based on wgMLST (2A) and wgSNP (2B) between the Chad *Nm*A isolates is depicted in relation to the reference genome WUE2594. Three clusters are observed and labeled on both trees. The invasive isolates are depicted in red and the carried ones in yellow. The rSTs contained in each cluster are also indicated as well as age and region of the patient/healthy volunteer are indicated when available, ND corresponds to the absence of any epidemiological information for the specific isolate (2A). The trees were produced based on a comparison in terms of n=2070 loci defined in the reference genome (2A) and the 1942 SNPs identified (2B).

## Discussion

In the absence of comprehensive vaccines, meningococcal meningitis epidemics remain a serious threat to public health in the African meningitis belt and elsewhere. Understanding the transition from the carried to the invasive phenotype will contribute to improved preventive measures in both epidemic and non-epidemic periods. The simultaneous collection of carried and invasive isolates during the 2011 epidemic in Chad enabled the comparison of closely related isolates obtained in the same temporal and geographic sampling frame. Such genomic comparisons rely on the availability of comprehensive collections of isolates, which are difficult to obtain and access from countries of the African meningitis belt. For example, isolate storage requires a -80°C freezer with a reliable electricity supply. While all of the Chadian isolates were appropriately stored at -80°C at the National Reference Laboratory of N'Djamena, the recovery rate was very low, perhaps a consequence of delays in the samples reaching the laboratory and/or difficulties in maintaining storage temperatures. The invasive isolates were mainly sourced from different areas around the capital N'Djamena, whilst the carried isolates were all obtained in the district of Mandelia, situated about 65 km away from N'Djamena (supplemental Figure 2). The carriage study involved an age-stratified randomly selected proportion of the population of the study area and so were likely to

be representative of those circulating in the community (111), whilst only a small proportion of disease cases were investigated microbiologically (77); nevertheless, these samples offer comparisons of meningococci from disease and carriage in the same region at the same time.

All of the *Nm*A isolates belonged to the hyper-invasive, pandemic, ST-5 clonal complex (cc5), with rMLST analysis placing the Chadian epidemic *Nm*A in the context of 141 other publically available *Nm*A:cc5 isolates (Supplemental Table 2), dating from 1963 to 2011 and from five continents allowing a global representation of *Nm*A:cc5. This confirmed the close genetic relatedness of members of this complex (327), but the clustering within cc5 was not entirely congruent with time and place. For example, the Chadian isolates occupied two different branches: one including the majority of isolates (n=21), comprised of 4 different rSTs; the other comprising the two remaining isolates with two different rSTs (Figure 1). These isolates did not cluster with other meningococci from the African meningitis belt; however, a global distribution of cc5 sub-variants spanning several years was apparent with isolates from Bangladesh, USA, and South Africa clustering with Chadian meningococci and isolates from Niger or Burkina.

Chadian isolates were present on branches of the phylogeny that were distinct from those which included the ST-7 and ST-2859 *Nm*A isolates from Ghana and Burkina Faso, which have also been analysed at the whole genome level (251), highlighting the need for the additional resolution obtained by rMLST in epidemiological studies (249). The two isolates from Cluster 3 were more distantly related, as were the two Chinese isolates, indicating that this relatively small sample contained much of the diversity seen in publically available isolates from different locations. The previous study (251) noted

potentially significant changes between ST-7 and ST-2859 *Nm*A isolates at: (i) the *pgl* locus, involved in glycosylation mechanisms; (ii) pilus regulation associated genes; and (iii) the *maf3* locus. In the Chad isolates, which were mostly ST-7, Cluster 1 and Cluster 2 shared the same alleles as the Ghanaian ST-7 isolates at the *pglD, pglC* and *pglB* locus; Cluster 3 had a different allele which may represent the acquisition of Deoxyribonucleic acid (DNA) from another source by homologous genetic transfer. The *pglH* locus was located at the beginning or the end of a contig in the majority of the draft genomes obtained and consequently its diversity could not be assessed in this analysis. The pilus genes were also variable in the Chad isolates but their variation did not correlate with the Clusters identified. On the other hand, all the Chadian isolates shared the same *maf3* alleles as the Ghanaian ST-7 isolates. Whole genome comparison of the *Nm*A:cc5 isolates clearly showed that the Chadian isolates were distinct at multiple loci from the Burkina Faso and Ghanaian isolates (Supplemental figure 3); additional whole genome comparisons are required, however, to elucidate further differences between these two isolate collections.

This study is the first description of a meningococcus lacking the *gdh* gene, encoding glucose-6-phosphate 1-dehydrogenase, making it impossible to define its sequence type by seven-locus MLST and reiterating the usefulness of whole genome analysis. The deleted region also included loci encoding a 6-phosphogluconolactonase, a glucokinase, and *pgi1* (a glycose-6-phophate isomerase) which are involved in glucose metabolism. Glucose being an essential source of energy for *Nm* in blood and CSF (328), such an invasive isolate would be at a disadvantage during an infection. This deletion probably occurred during sub-cultivation and is unlikely to be of biological relevance.

Whole genome gene-by-gene analysis identified three different *Nm*A clusters circulating during the epidemic in Chad. Isolates were very similar, with 74.5% of the genes identical in all genomes and 242 (11.6%) genes confirmed as variable. No clustering by disease phenotype was evident, with Clusters 1 and 2 containing both disease and carried isolates in similar proportions, indicating that the invasive and carried isolates circulating during the epidemic were part of the same bacterial population. This was consistent with previous genomic comparisons among more diverse carried and disease isolates, which found no distinct monophyletic groups by gene content (313) or SNP analysis (251, 329).

Previously proposed "virulence-associated" genes were not systematically clustered on the basis of disease phenotype (134, 330) among these isolates. Within-cluster analysis identified two genes that had alterations specific to the four carried isolates of Cluster 1: NEIS1527 encodes a two-component response regulator member of the ActR/RegA family that is involved in signal transduction mechanism and transcription (331) and NEIS2894 encodes a hypothetical protein of unknown function. The impact of these genetic mutations on the biological function of these bacteria would need to be assessed further.

The use of wgSNP analysis to detect nucleotide changes in non-coding regions that discriminated carried and invasive isolates identified 9.4% of SNPs in non-coding regions (Supplemental Table 4). Only one SNP was found to discriminate carried from invasive isolates of Cluster 1, this SNP was found within the proximal promoter region of the gene NEIS1545, which is known to include transcription regulatory elements, but is located away from the -10 and -35 region which are part of the core promoter required

for initiation of transcription (332); additional analyses is necessary to determine the impact of this particular SNP on the transcription of NEIS1545. The wgSNP Neighbor Net trees (Figure 2B and Supplemental Figure 4) showed identical phylogenetic clustering to that found with the wgMLST tree (Figure 2A), with the same nodes; however, Cluster 1 appeared to be more diverse than observed with wgMLST analysis. SNPs found in the non-coding regions specific to sub-clusters and single isolates within Cluster 1 led to the observed diversity (28 SNPs in total, Supplemental table 4). The wgSNP analysis based on the assembled fasta file and the original fastq files gave similar results.

Gene presence does not always correlate with expression and it is possible that despite both disease and carriage isolates possessing the same complement of genes, their expression levels might vary (333). A study comparing two serogroup B *Nm* (*Nm*B) from different clonal complexes, a carried ST-41/44 isolate and an invasive ST-32 isolate, identified eight putative virulence-associated genes missing or non-functional from the carried isolate and considerable differences in their expression patterns (334). *Nm* are highly variable bacteria and it is difficult to determine whether changes are due to the different phenotype or to inherent differences between the two clonal complexes. Analyses with additional genomes from the same clonal complexes are therefore essential for such comparisons. The results of the wgSNP analysis did not identify any changes at the nucleotide sequence level that could predict a change in gene expression between the carried and invasive isolates of this study except for one SNP found in the proximal promoter upstream of NEIS1545 that differentiated carried and invasive isolates of Cluster 1. A study applying similar methods to those presented here compared 172 carried and invasive *Nm*Y collected in the UK between 1997 and 2011,

with an overlapping collection of both phenotypes obtained only in 2010. As found in this study, clusters of isolates contained both carried and invasive isolates; however, these investigators were able to identify a disease-associated clone within their clonal complex 23 *Nm*Y, which included 90 % of invasive isolates (224).

The genetic differentiation between Clusters 1 and 2, and their strong association with host age, may represent bacterial adaptation to a particular niche and the change in the ecology of the nasopharynx from children to young adults in Chad. This is supported by the fact that most of the allelic variations found between the clusters were identified in metabolic genes (Tables 3 and 4). A previous study of the pharyngeal carriage of members of the *Neisseria* genus found that there was an inverse relationship between carriage of *Nm* and other non-pathogenic *Neisseria* species by age group which indicate a potential role that other microbes may play in modulating *Nm* carriage and could explain the age difference seen in this study (178). Further studies, similar to those undertaken on the gut microbiota (335, 336), might address this issue. DNA microarray studies have identified a bacteriophage that was mostly found in genomes from the hyper-invasive clonal complexes (226). This "meningococcal disease associated island" (MDA island) phage is associated with disease in young adults (227). The MDA island genes were present in both Clusters 1 and 2 with the same alleles and thus could not explain the differentiation seen in this collection of isolates. Host genetic polymorphisms affecting the susceptibility of an individual to invasive meningococcal disease have been described, such as those in complement components such as factor H (337) or C6 deficiencies known to vary depending on the racial group and described as more

common in African-American in the USA (338), interleukin-1 gene cluster (339) or the plasminogen activator inhibitor 1 (340). Differences in host genetics could also explain our clusters; however, such studies have yet to be undertaken in African subjects.

## Conclusion

During the epidemic in and around N'Djamena, carriers and cases were infected by meningococci that were indistinguishable at the whole genome level, an observation which is consistent with host factors playing a major role in determining whether an infected person remains a carrier or becomes a case. Potential factors include the ability of the host immune response to contain the meningococcus in the pharynx or to eliminate it rapidly if invasion does occur, an ability which is at least partly genetically determined (337). Gene expression among the isolates has not been directly compared in this work, and this may also play a role in the differentiation between carried and invasive isolates; one interesting SNP was identified in this study, upstream of a gene encoding a hypothetical protein, both the SNP and function of the gene should be investigated further to determine their role, if any, in meningococcal colonization and disease. In addition, it is possible that other bacteria within the pharyngeal microbiome influence the ability of a meningococcus to invade. Further bacterial genetic and protein expression studies, microbiome and human genetic studies comparing carriers and cases from similar backgrounds would help elucidate the role played by each factor in isolation and understand their interactions and the mechanisms driving *Nm* from a carried commensal to an invasive pathogen.

# C- Chapter 5: Genomic characterisation of novel *Neisseria* species

## Abstract

**Objectives.** Among the ten defined human-associated *Neisseria* species, only *Neisseria meningitidis* (*Nm*) and *Neisseria gonorrhoeae* (*Ng*) have been implicated as major causes of disease. The others have mostly been identified in the naso- and oro-pharynx of asymptomatic individuals. The role of non-pathogenic *Neisseria* (NPNs) in modulating carriage and invasive disease caused by *Nm* is unknown; however, comprehensive characterization of their diversity will further our understanding of this process. Genomic analyses were used to study previously unclassified *Neisseria* isolates, in the context of the three most closely-related defined species.

**Methods.** Whole genome sequence (WGS) data from 181 *Neisseria* isolates, sampled from distinct geographical locations, were studied. Those included three defined *Neisseria* species: *Nm; Ng;* and *Neisseria polysaccharea* (*Np*), and the genomes of isolates identified as belonging to the genus *Neisseria* but not further characterized (*Neisseria spp.; Nspp)*. Hierarchical multi locus sequence analysis of the *f_rplF* locus, the 53 ribosomal genes comprising the rMLST scheme, and a newly defined core genome MLST (cgMLST) scheme were undertaken and phylogenetic relationships inferred. Average Nucleotide Identity (ANI) calculations were used to distinguish different species clusters and species-specific allelic variation of the core genes was assessed. Phenotypic analyses were also undertaken to identify morphological and metabolic differences among members of different clusters.

**Results.** Phylogenetic trees generated from nucleotide sequences of the *f_rplF* and rMLST loci displayed two polyphyletic clusters: *Np* and *Nspp*. The other species, *Nm* and *Ng,* formed distinct monophyletic groups. The higher resolution obtained with cgMLST clustered the *Nspp* isolates into nine genetically distinct groups (*Nspp* 1- *Nspp* 9) and identified at least 3 *Np* clusters (*Np* 1- *Np* 3). Pairwise comparison of the allelic diversity of core genes revealed that genetically distinct clusters did not share many alleles. ANI results classified the *Nspp* clusters into seven distinct species and indicated that at least three putative *Np* species could be distinguished. Morphological and biochemical analyses undertaken did not provide useful additional discrimination.

**Conclusion.** Seven novel *Neisseria* species were identified, using a combination of cgMLST and ANI. This novel genomic approach provides a consistent methodology for the species characterization of distinct phylogenetic clusters. Each species had unique allelic profiles at their core loci, with few shared alleles. Phenotypic methods used did not distinguish the different species reiterating the importance of genomic studies in the characterization of the genus *Neisseria*.

## Introduction

The genus *Neisseria*, part of the *Neisseriaceae* family, is composed of multiple species that colonise the epithelium of various animals (127). All the defined human-associated species are Gram-negative, oxidase and catalase positive bacteria, but two different morphologies have been described: two rod shaped species have been characterized (*Neisseria elongata* (*Ne*) and *Neisseria bacilliformis* (*Nba*)); but all others are coccoid bacteria (*Neisseria cinerea* (*Nc*), *Neisseria gonorrhoeae* (*Ng*), *Neisseria polysaccharea* (*Np*), *Neisseria lactamica* (*Nl*), *Neisseria meningitidis* (*Nm*), *Neisseria mucosa* (*Nmu)*, *Neisseria oralis* (*No*) *and Neisseria subflava* (*Ns*)). All these species are asymptomatic commensal inhabitants of the mucosa they infect; however, *Nm* which colonises the nasopharynx and *Ng*, which is mostly found in the genitourinary tract, are the only two species with pathogenic potential. *Nm* causes invasive meningococcal disease (IMD) while *Ng* is responsible for the sexually transmitted disease gonorrhoea. The remaining eight human-associated species are also harmless inhabitants of the oro- and nasopharynx, sharing broadly the same body location as *Nm.*

Conventional *Neisseria* taxonomy, based on the phenotypic properties of the bacterial isolates, has been very accurate in identifying the most studied species such as *Nm*, *Ng* and *Nl*; however, it has led to a number of misclassifications among the other species (131). This has led to an increased use of molecular based approaches such as DNA-DNA hybridisation (DDH) (167, 169) and phylogenetic analyses of nucleotide sequence data of a fragment of the 16S ribosomal gene (177) to study the relatedness of collected isolates. The use of a single locus such as 16S, however, lacked the resolution needed to

differentiate all *Neisseria* species, at least in part due to horizontal genetic transfer events (HGT) which have distorted their phylogenetic relationships (341). Phylogenies based on multi-locus sequence analysis (MLSA) (342), such as the seven loci used in multi locus sequence typing (MLST) (120, 343), the 53 ribosomal genes of ribosomal MLST (rMLST) (241), and the 246 loci of the *Neisseria* genus core genome MLST (cgMLST) (131) greatly improved the classification of the different species. These new approaches led to the reclassification of some *Neisseria* species with the integration of *Ns* biovar *sublfava*, *perflava* and *flava*, and of *Neisseria* flavescens into a single species named *Neisseria subflava.* Isolates previously classified as *Neisseria sicca* were found to be variant of the *Nmu* species (131). Similar MLSA methods led to the renaming of "*Neisseria mucosa var. heidelbergensis*", which was found to be genetically identical to *Neisseria oralis* (243). In 2014, Bennett and collaborators proposed a new single locus sequence analysis for the rapid identification of *Neisseria* species based on a 413 base pair (bp) sequence of the ribosomal gene *rplF*, which was able to discriminate among the different species and generate phylogenies congruent with cgMLST (132). The development of the measure of average nucleotide identity (ANI) between pairs of genomes has also facilitated bacterial taxonomic endeavours; ANI was suggested as an alternative to DDH (176, 344), which was labour intensive, and difficult to standardise and compare among laboratories (345).

Non-pathogenic *Neisseria* (NPN) have not been intensively investigated because they are rarely involved in invasive disease, except rare reports, usually in immunocompromised individuals, and have therefore never represented a public health priority (127).

However, their abundance in the human microbiome (346), combined with the possibility that nasopharyngeal colonisation by *Nl* could be protective against *Nm* infection (135, 347, 348) and that *Nl* could be used for outer-membrane vesicle (OMV) vaccine design against *Nm* (349), have increased the interest in the role of these NPNs in modulating oropharyngeal carriage of *Nm* and reinforced the importance of understanding the diversity of this genus. This was exemplified by the finding that the risk factors for carrying *Nm* in the African Meningitis Belt (AMB) were inversely related to those of carrying NPNs, suggesting that carrying NPNs could protect against carriage of *Nm* (178); and the increasing recognition of the role of the microbiota in influencing other diseases like pneumonia (350) or cystic fibrosis (351, 352).

*Np* has previously been described as polyphyletic, potentially containing more than one species. In particular, isolate 15883, identified by Berger in 2005 in Germany (353), was proposed as a potential new species (131, 354). The higher number of carried isolates collected in previously under-sampled and geographically distinct regions of the world (178) and the concomitant decrease in the cost of whole genome sequencing have allowed a great number of NPN isolates to be sequenced; however, the numbers remain, low compared to *Nm*. Indeed, the *Neisseria* pubMLST database (174), which hosts the largest collection of *Neisseria* isolate data, contained 43301 isolates records, at the time of writing (August 2017), but these were not all genome sequenced and only included 937 NPN records. Isolates genetically close to isolate 15883, based on the *rplF* phylogeny, were identified in MenAfriCar carriage studies undertaken in seven countries of the AMB (178). Similar non-characterized isolates were also identified in other studies

conducted in and outside of the belt countries (354-357) and in the recent UKMenCar4 carriage study in the UK (358).

In this study, the phylogenetic relationship of close members of the human-associated *Neisseria* species was examined at the genomic level. The analyses included representative genomes from the species *Nm*, *Ng* and available genomes of *Np* and unclassified *Neisseria* (*Nspp*) in order to better characterise their diversity and these putative new species.

## Materials and Methods

### *Isolates and genomes*

#### Isolate collection

A total of 107 *Neisseria* isolates unclassified to species level (*Nspp*) were identified in the pubMLST *Neisseria* database; some of them had been recorded as "*Neisseria bergeri",* as suggested by preliminary analysis (178, 354, 357). The majority of the *Nspp* were isolated during carriage studies performed in Africa and included: (i) 57 isolates collected from Ndirande, Blantyre, Malawi, as part of a study into the acquisition of antibody to nontyphoidal *Salmonella* from October to December 2005 and September to November 2006 (357, 359) (356); (ii) 37 isolates collected in Mali and 9 from Chad as part of the MenAfriCar carriage surveys that took place between 2010 and 2012 (111, 178); and (iii) 2 isolates obtained in 1997, as part of a carriage study conducted in Basse, The Gambia alongside a serogroup A and C meningococcal vaccine follow up study (355).

Two additional isolates were collected in Europe: the first in Germany in 1984 (353); and the second in the United Kingdom as part of the UKMenCar4 carriage study undertaken between September 2014 and March 2015 (358).

**DNA preparation, Genome sequencing and assembly**

All of the African *Nspp* isolates were sequenced *de novo* using Illumina genome sequencing method. Isolates were cultured on blood agar plates (BAP) and incubated overnight, 16-24 hours, at 37˚C within an atmosphere containing 5% CO2. DNA was prepared in different laboratories: for 96 of the isolates, genomic DNA was extracted using the Wizard genomic DNA Purification kit (Promega) following the manufacturer's instructions; for the remaining nine isolates from Chad, DNA was extracted using the DNeasy Blood and Tissue kit (Quiagen), as previously described (249). DNA samples were sequenced by pair-end sequencing on an Illumina HiSeq, with read lengths of 100 (N=55), 125 (N=46) and 150 (N=4) base pairs at the Wellcome Trust Sanger Institute, using standard Illumina sequencing methods (217).

Resultant short reads were assembled using the Velvet genome assembly program (v1.2.08) (259): all odd-numbered kmer lengths between 21-99, 21-124 and 21-149 were sampled for read lengths of 100, 125, and 150 base pairs respectively, using the VelvetOptimiser software (v2.2.4) (320) to automatically establish the optimal assembly parameters for Velvet (default optimization functions used). The assembled contigs were deposited in the *Neisseria* PubMLST database (174) which uses the Bacterial Isolate Genome Sequence Database (BIGSdb) software (248). Draft genomes were automatically curated at all loci defined in the database using the BLAST algorithm (321) and a sequence similarity threshold of >98%, allowing rapid annotation of known alleles and

sequences which were very similar to defined loci (217). Manual verification was then performed for variable loci, such as those containing internal stop codons, frame shifts or those with sequence similarities lower than 98%. Incomplete gene sequences at the beginning or end of a contig were identified as such.

**Additional Genome selection**

In addition to the 105 African *Nspp* sequenced *de novo*, and the two European isolates previously sequenced and deposited into the pubMLST/Neisseria database, 74 other genomes deposited in the database were chosen to complete the genome collection analysed in this study. These represented three known human-associated *Neisseria* species and included all of the genomes available at the time of analysis for *Np* (N=45), all but one complete genomes of *Ng* (N=9) and representative genomes of the most common clonal complexes of *Nm* (N=20) (217), with a preference for complete genomes when available. Additional information and meta-data for each of the 181 genomes are available in Table 1.

## Table 1: List of genomes included in the aalysis and available meta-data

| PubMLST ID | Isolate ID | Country | Year | Disease | Age year | Age month | Gender | clusters |
|---|---|---|---|---|---|---|---|---|
| **2855** | FA1090 § | Unknown | Unknown | Unknown | Unknown | Unknown | Unknown | Ng |
| **13685** | NCCP11945 | South Korea | Unknown | Unknown | Unknown | Unknown | female | Ng |
| **21065** | TCDC-NG08107 | Unknown | 2008 | Unknown | Unknown | Unknown | Unknown | Ng |
| **46272** | 32867 | Canada | 2010 | Unknown | Unknown | Unknown | Unknown | Ng |
| **46273** | 34530 | Canada | 2012 | Unknown | Unknown | Unknown | Unknown | Ng |
| **46274** | 34769 | Canada | 2011 | Unknown | Unknown | Unknown | Unknown | Ng |
| **46275** | FA19 | Unknown | Unknown | Unknown | Unknown | Unknown | Unknown | Ng |
| **46276** | FA6140 | USA | Unknown | Unknown | Unknown | Unknown | Unknown | Ng |
| **46277** | 12816 | Sweden | 2002 | Unknown | Unknown | Unknown | Unknown | Ng |
| **30** | 14 | Germany | 1999 | No | 18 | Unknown | Unknown | Nm |
| **240** | MC58 | UK | 1983 | Unknown | Unknown | Unknown | Unknown | Nm |
| **410** | BZ 232 | The Netherlands | 1964 | Yes | Unknown | Unknown | Unknown | Nm |
| **613** | Z2491 § | The Gambia | 1983 | Yes | Unknown | Unknown | Unknown | Nm |
| **638** | G2136 | UK | 1986 | Yes | Unknown | Unknown | Unknown | Nm |
| **698** | FAM18 | USA | 1983 | Yes | Unknown | Unknown | Unknown | Nm |
| **1038** | 8013 | France | 1989 | Yes | Unknown | Unknown | male | Nm |
| **19261** | alpha710 | Germany | Unknown | No | Unknown | Unknown | Unknown | Nm |
| **31318** | NM3682 | UK | Unknown | Yes | Unknown | Unknown | Unknown | Nm |
| **34578** | 88050 | Chad | 1988 | Yes | Unknown | Unknown | Unknown | Nm |
| **34607** | 2004090 | Niger | 2004 | Yes | Unknown | Unknown | Unknown | Nm |
| **34610** | 2007056 | Burkina Faso | 2007 | Yes | Unknown | Unknown | Unknown | Nm |
| **34655** | NM3652 | Bangladesh | 2006 | Yes | Unknown | Unknown | Unknown | Nm |
| **36059** | M22276 | Mali | 1969 | Unknown | Unknown | Unknown | Unknown | Nm |
| **38695** | M22431 | Burkina Faso | 1978 | Unknown | Unknown | Unknown | Unknown | Nm |
| **39634** | 583-15 | Niger | 2015 | Unknown | Unknown | Unknown | Unknown | Nm |
| **39785** | 1947-15 | Niger | 2015 | Unknown | Unknown | Unknown | Unknown | Nm |
| **39854** | M05749 | Norway | 1987 | Unknown | Unknown | Unknown | Unknown | Nm |
| **39856** | M05729 | South Africa | 1990 | Unknown | Unknown | Unknown | Unknown | Nm |
| **39860** | M28679 | UK | 2014 | Unknown | Unknown | Unknown | Unknown | Nm |
| **19097** | CCUG 24846 | Unknown | Unknown | No | Unknown | Unknown | Unknown | Np 1 |
| **19098** | CCUG 27182 | Unknown | Unknown | Unknown | Unknown | Unknown | Unknown | Np 1 |
| **21047** | CCUG 4790 | Unknown | Unknown | No | Unknown | Unknown | Unknown | Np 1 |
| **36140** | 12015_2014 | Ireland | 2014 | No | 3 | Unknown | Unknown | Np 1 |
| **36142** | 12017_2014 | Ireland | 2014 | No | 1 | Unknown | Unknown | Np 1 |
| **36148** | 12024_2014 | Ireland | 2014 | No | 4 | Unknown | Unknown | Np 1 |

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|---|---|---|---|---|---|---|---|---|
| **36153** | 12030_2014 | Ireland | 2014 | No | 1 | Unknown | Unknown | Np 1 |
| **36167** | 12046_2014 | Ireland | 2014 | No | 0 | 2 | Unknown | Np 1 |
| **41652** | 2748 ₮ | Italy | 2015 | Unknown | Unknown | Unknown | Unknown | Np 1 |
| **43987** | LNP28609 | France | 2016 | No | Unknown | Unknown | Unknown | Np 1 |
| **45356** | LNP28667 | France | 2016 | No | Unknown | Unknown | Unknown | Np 1 |
| **14730** | ATCC 43768 | Belgium | Unknown | Unknown | Unknown | Unknown | Unknown | Np 1/ Np 3 |
| **19095** | CCUG 18031 * | Germany | 1984 | No | Unknown | Unknown | Unknown | Np 1/ Np 3 |
| **19096** | CCUG 24845 | Unknown | Unknown | No | Unknown | Unknown | Unknown | Np 1/ Np 3 |
| **38980** | LNP22706 | France | Unknown | Unknown | Unknown | Unknown | Unknown | Np 1/ Np 3 |
| **38981** | LNP24574 | France | Unknown | Unknown | Unknown | Unknown | Unknown | Np 1/ Np 3 |
| **43420** | 01_13564_XS3_1 | Mali | 2010 | No | 1 | Unknown | male | Np 1/ Np 3 |
| **44084** | ST41786 | UK | 2015 | No | 16 | Unknown | male | Np 1/ Np 3 |
| **44102** | BR40761 B | UK | 2014 | No | 16 | Unknown | male | Np 1/ Np 3 |
| **46136** | G97_6093 ₮ | The Gambia | 1997 | No | 3 | 9 | male | Np 1/ Np 3 |
| **46200** | G97_1061 | The Gambia | 1997 | No | 5 | 0 | female | Np 1/ Np 3 |
| **46409** | M-080 | Malawi | 2005 | No | 2 | 5 | female | Np 1/ Np 3 |
| **46417** | M-104 | Malawi | 2005 | No | 5 | 2 | female | Np 1/ Np 3 |
| **46418** | M-104A | Malawi | 2005 | No | 5 | 2 | female | Np 1/ Np 3 |
| **46428** | M-198 | Malawi | 2005 | No | 5 | 8 | female | Np 1/ Np 3 |
| **46437** | M-223 *§ | Malawi | 2005 | No | 5 | 6 | female | Np 1/ Np 3 |
| **46449** | M-264 | Malawi | 2005 | No | 4 | 10 | male | Np 1/ Np 3 |
| **46451** | M-286 | Malawi | 2005 | No | 1 | 9 | male | Np 1/ Np 3 |
| **46462** | M-442 | Malawi | 2005 | No | 0 | 8 | female | Np 1/ Np 3 |
| **46467** | M-571 | Malawi | 2006 | No | 16 | 8 | male | Np 1/ Np 3 |
| **46475** | M-856 | Malawi | 2007 | No | 2 | 5 | male | Np 1/ Np 3 |
| **46727** | PL40288 *₮ | UK | 2015 | No | 17 | Unknown | female | Np 1/ Np 3 |
| **43335** | 01_00098_XS1_1 | Mali | 2010 | No | 14 | Unknown | female | Np 2 |
| **43413** | 01_07665_XS1_1 | Mali | 2010 | No | 2 | Unknown | female | Np 2 |
| **43415** | 01_03967_XS1_1 | Mali | 2010 | No | 8 | Unknown | female | Np 2 |
| **43416** | 01_07343_XS1_1 | Mali | 2010 | No | 56 | Unknown | female | Np 2 |
| **43417** | 01_08009_XS1_1 | Mali | 2010 | No | 41 | Unknown | female | Np 2 |
| **43418** | 01_13553_XS3_1 | Mali | 2010 | No | 0 | 9 | male | Np 2 |
| **43419** | 01_13554_XS3_1 | Mali | 2010 | No | 3 | Unknown | male | Np 2 |

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|---|---|---|---|---|---|---|---|---|
| **46143** | G97_5907 | The Gambia | 1997 | No | 3 | 6 | male | Np 2 |
| **46173** | G97_2571 *§ | The Gambia | 1997 | No | 4 | 11 | male | Np 2 |
| **46186** | G97_1651 | The Gambia | 1997 | No | 3 | 10 | male | Np 2 |
| **46196** | G97_1162 | The Gambia | 1997 | No | 4 | 6 | male | Np 2 |
| **46197** | G97_1151 | The Gambia | 1997 | No | 4 | 6 | male | Np 2 |
| **46199** | G97_1072 | The Gambia | 1997 | No | 4 | 4 | male | Np 2 |
| **42909** | 02_11162_XS2_1 | Mali | 2011 | No | 8 | Unknown | female | Nspp 1 |
| **43020** | 02_11069_XS2_1 | Mali | 2011 | No | 12 | Unknown | male | Nspp 1 |
| **43021** | 02_11081_XS2_1 | Mali | 2011 | No | 5 | Unknown | female | Nspp 1 |
| **43022** | 02_11161_XS2_1 | Mali | 2011 | No | 2 | Unknown | female | Nspp 1 |
| **43023** | 02_11615_XS2_1 | Mali | 2011 | No | 21 | Unknown | male | Nspp 1 |
| **43024** | 02_11164_XS2_1 | Mali | 2011 | No | 2 | Unknown | female | Nspp 1 |
| **43025** | 02_11253_XS2_1 | Mali | 2011 | No | 2 | Unknown | female | Nspp 1 |
| **43026** | 02_11666_XS2_1 | Mali | 2011 | No | 17 | Unknown | male | Nspp 1 |
| **43027** | 02_11761_XS2_1 | Mali | 2011 | No | 34 | Unknown | female | Nspp 1 |
| **43028** | 02_11322_XS2_1 | Mali | 2011 | No | 4 | Unknown | male | Nspp 1 |
| **43029** | 02_11327_XS2_1 | Mali | 2011 | No | 14 | Unknown | male | Nspp 1 |
| **43030** | 02_11362_XS2_1 | Mali | 2011 | No | 7 | Unknown | male | Nspp 1 |
| **43031** | 02_11346_XS2_1 | Mali | 2011 | No | 4 | Unknown | female | Nspp 1 |
| **43032** | 02_11474_XS2_1 | Mali | 2011 | No | 3 | Unknown | female | Nspp 1 |
| **43033** | 02_11433_XS2_1 | Mali | 2011 | No | 5 | Unknown | male | Nspp 1 |
| **43034** | 02_13924_XS3_1 | Mali | 2012 | No | 6 | Unknown | male | Nspp 1 |
| **43035** | 02_13976_XS3_1 | Mali | 2012 | No | 11 | Unknown | male | Nspp 1 |
| **43036** | 02_14067_XS3_1 | Mali | 2012 | No | 4 | Unknown | male | Nspp 1 |
| **43037** | 02_13995_XS3_1 | Mali | 2012 | No | 11 | Unknown | female | Nspp 1 |
| **43038** | 02_14121_XS3_1 | Mali | 2012 | No | 6 | Unknown | male | Nspp 1 |
| **43039** | 01_13562_XS3_1 | Mali | 2012 | No | 7 | Unknown | female | Nspp 1 |
| **43040** | 01_13695_XS3_1 | Mali | 2012 | No | 6 | Unknown | female | Nspp 1 |
| **43041** | 01_13712_XS3_1 | Mali | 2012 | No | 5 | Unknown | male | Nspp 1 |
| **43042** | 01_12742_XS3_1 | Mali | 2012 | No | 23 | Unknown | female | Nspp 1 |
| **43043** | 01_13770_XS3_1 | Mali | 2012 | No | 13 | Unknown | male | Nspp 1 |
| **43421** | 01_00119_XS1_1 | Mali | 2010 | No | 11 | Unknown | male | Nspp 1 |
| **43422** | 01_03638_XS1_1 | Mali | 2010 | No | 2 | Unknown | female | Nspp 1 |
| **43423** | 01_03957_XS1_1 * | Mali | 2010 | No | 9 | Unknown | male | Nspp 1 |
| **43424** | 02_01070_XS1_1 | Mali | 2010 | No | 7 | Unknown | male | Nspp 1 |
| **43426** | 02_01287_XS1_1 *§ | Mali | 2010 | No | 41 | Unknown | female | Nspp 1 |
| **43427** | 02_07958_XS1_1 | Mali | 2010 | No | Unknown | Unknown | Unknown | Nspp 1 |
| **43428** | 01_00007_XS1_1 | Mali | 2010 | No | 4 | Unknown | male | Nspp 1 |
| **43429** | 01_03581_XS1_1 | Mali | 2010 | No | 5 | Unknown | male | Nspp 1 |
| **43430** | 01_07472_XS1_1 | Mali | 2010 | No | 16 | Unknown | female | Nspp 1 |
| **43431** | 01_07795_XS1_1 | Mali | 2010 | No | 4 | Unknown | female | Nspp 1 |
| **43432** | 02_01039_XS1_1 | Mali | 2010 | No | 10 | Unknown | female | Nspp 1 |

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|---|---|---|---|---|---|---|---|---|
| **46230** | M_676M | Malawi | 2006 | No | 22 | 3 | female | Nspp 2 |
| **46400** | M-037 | Malawi | 2005 | No | 7 | Unknown | female | Nspp 2 |
| **46401** | M-038 | Malawi | 2005 | No | 2 | 10 | male | Nspp 2 |
| **46404** | M-052 *§ | Malawi | 2005 | No | 4 | 9 | female | Nspp 2 |
| **46406** | M-065 | Malawi | 2005 | No | 0 | 1 | male | Nspp 2 |
| **46421** | M-129 | Malawi | 2005 | No | 4 | 4 | male | Nspp 2 |
| **46422** | M-130 | Malawi | 2005 | No | 0 | 8 | male | Nspp 2 |
| **46424** | M-161 | Malawi | 2005 | No | 11 | 1 | male | Nspp 2 |
| **46427** | M-190 | Malawi | 2005 | No | 7 | 1 | female | Nspp 2 |
| **46434** | M-214 | Malawi | 2005 | No | 5 | 6 | female | Nspp 2 |
| **46443** | M-250 | Malawi | 2005 | No | 11 | 8 | female | Nspp 2 |
| **46444** | M-252 | Malawi | 2005 | No | 8 | 7 | female | Nspp 2 |
| **46445** | M-256C * | Malawi | 2005 | No | 8 | Unknown | male | Nspp 2 |
| **46448** | M-262 | Malawi | 2005 | No | 4 | 5 | female | Nspp 2 |
| **46450** | M-274 | Malawi | 2005 | No | 12 | 9 | female | Nspp 2 |
| **46452** | M-290 | Malawi | 2005 | No | 13 | 4 | female | Nspp 2 |
| **46459** | M-357 | Malawi | 2005 | No | 1 | 1 | male | Nspp 2 |
| **46460** | M-366 | Malawi | 2005 | No | 0 | 2 | female | Nspp 2 |
| **46469** | M-718M | Malawi | 2007 | No | 21 | 1 | female | Nspp 2 |
| **46470** | M-760 | Malawi | 2007 | No | 13 | Unknown | male | Nspp 2 |
| **43128** | 12_12795_XS2_1 | Chad | 2011 | No | 9 | Unknown | female | Nspp 3 |
| **43129** | 12_13955_XS2_1 * | Chad | 2011 | No | 10 | Unknown | female | Nspp 3 |
| **43130** | 12_14141_XS2_1 | Chad | 2011 | No | 1 | Unknown | female | Nspp 3 |
| **43131** | 12_23282_XS3_1 | Chad | 2011 | No | 6 | Unknown | male | Nspp 3 |
| **43132** | 12_13996_XS2_1 | Chad | 2011 | No | 4 | Unknown | female | Nspp 3 |
| **43133** | 12_13835_XS2_1 | Chad | 2011 | No | 12 | Unknown | female | Nspp 3 |
| **43134** | 12_13988_XS2_1 *§ | Chad | 2011 | No | 6 | Unknown | male | Nspp 3 |
| **43135** | 12_17465_XS2_1 | Chad | 2011 | No | 1 | Unknown | male | Nspp 3 |
| **43136** | 12_14600_XS2_1 | Chad | 2011 | No | 4 | Unknown | female | Nspp 3 |
| **46231** | M_700M | Malawi | 2006 | No | 32 | 2 | female | Nspp 4 |
| **46402** | M-041 * | Malawi | 2005 | No | 1 | 4 | male | Nspp 4 |
| **46403** | M-046 | Malawi | 2005 | No | 0 | 2 | female | Nspp 4 |
| **46410** | M-089 | Malawi | 2005 | No | 9 | 10 | female | Nspp 4 |
| **46423** | M-131 | Malawi | 2005 | No | 1 | 7 | male | Nspp 4 |
| **46425** | M-173 | Malawi | 2005 | No | 2 | Unknown | male | Nspp 4 |
| **46426** | M-174 | Malawi | 2005 | No | 4 | 4 | male | Nspp 4 |
| **46435** | M-216 | Malawi | 2005 | No | 7 | 7 | female | Nspp 4 |
| **46441** | M-244 | Malawi | 2005 | No | 8 | 7 | male | Nspp 4 |
| **46447** | M-261 | Malawi | 2005 | No | 3 | 9 | female | Nspp 4 |
| **46455** | M-318 | Malawi | 2005 | No | 2 | 3 | male | Nspp 4 |
| **46456** | M-337 | Malawi | 2005 | No | 2 | 8 | male | Nspp 4 |

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|---|---|---|---|---|---|---|---|---|
| **46457** | M-338 *§ | Malawi | 2005 | No | 0 | 6 | female | Nspp 4 |
| **46458** | M-345 | Malawi | 2005 | No | 1 | 5 | male | Nspp 4 |
| **46405** | M-064 | Malawi | 2005 | No | 2 | 1 | male | Nspp 5 |
| **46408** | M-079 | Malawi | 2005 | No | 4 | 2 | female | Nspp 5 |
| **46415** | M-101 *§ | Malawi | 2005 | No | 1 | 9 | female | Nspp 5 |
| **46416** | M-102 | Malawi | 2005 | No | 4 | 8 | male | Nspp 5 |
| **46429** | M-200 | Malawi | 2005 | No | 3 | 4 | male | Nspp 5 |
| **46431** | M-210 | Malawi | 2005 | No | 4 | 11 | male | Nspp 5 |
| **46432** | M-211 | Malawi | 2005 | No | 11 | 5 | female | Nspp 5 |
| **46438** | M-225 | Malawi | 2005 | No | 6 | 6 | female | Nspp 5 |
| **46439** | M-226 * | Malawi | 2005 | No | 9 | 11 | male | Nspp 5 |
| **46442** | M-249 | Malawi | 2005 | No | 13 | 2 | female | Nspp 5 |
| **46461** | M-384 | Malawi | 2005 | No | 1 | 7 | male | Nspp 5 |
| **46463** | M-448 | Malawi | 2005 | No | 1 | Unknown | male | Nspp 5 |
| **46464** | M-456 | Malawi | 2005 | No | 1 | 11 | female | Nspp 5 |
| **46465** | M-457 | Malawi | 2005 | No | 1 | 7 | male | Nspp 5 |
| **46468** | M-672M | Malawi | 2006 | No | 23 | 11 | female | Nspp 5 |
| **46471** | M-784 | Malawi | 2007 | No | 7 | 11 | male | Nspp 5 |
| **46472** | M-786 | Malawi | 2007 | No | 3 | 11 | male | Nspp 5 |
| **46473** | M-802 | Malawi | 2007 | No | 5 | 5 | male | Nspp 5 |
| **46476** | M-872 | Malawi | 2007 | No | 2 | 5 | male | Nspp 5 |
| **46477** | M-875 | Malawi | 2007 | No | 2 | 6 | male | Nspp 5 |
| **46478** | M-879 | Malawi | 2007 | No | 1 | 5 | female | Nspp 5 |
| **44518** | OX40911 * | UK | 2015 | No | 16 | Unknown | female | Nspp 6 |
| **46411** | M-091 *§ | Malawi | 2005 | No | 1 | 9 | male | Nspp 6 |
| **46412** | M-092 | Malawi | 2005 | No | 4 | 7 | female | Nspp 6 |
| **46192** | G97_1403 *§ | The Gambia | 1997 | No | 4 | 10 | male | Nspp 7 |
| **46193** | G97_1402 | The Gambia | 1997 | No | 4 | 10 | male | Nspp 7 |
| **43425** | 02_01105_XS1_1 *§ | Mali | 2010 | No | 8 | Unknown | female | Nspp 8 |
| **5193** | 15883 *§ | Germany | 1984 | No | 2 | Unknown | Unknown | Nspp 9 |

*Nm*: *N. meningitidis*; *Ng*: *N. gonorrhoeae*; *Np*: *N. polysaccharea* and *Nspp*: *Neisseria spp*
* Isolates used for the phenotypic analysis
§ Isolates used for the first average nucleotide identity analysis
ᵀ additional *Np* 1 isolates for second average nucleotide identity analysis

## *Genomic diversity*

### Phylogenetic analysis

A hierarchical gene-by-gene approach to Whole Genome Sequence (WGS) characterisation was adopted to analyse all 181 genomes. This included:

*i)* *F_rplF*: the 413 base pair fragment of the ribosomal gene *rplF* (132) was extracted and aligned using MAFFT in pubMLST (174, 360).

*ii)* Ribosomal MLST (rMLST): The sequences of 51 of the 53 ribosomal loci were extracted from each genome and aligned using MAFFT. The loci BACT0060 (*rpmE*) and BACT0065 (*rpmI*) were excluded, as they are known to be paralagous in *Neisseria* species.

*iii)* Core genome MLST (cgMLST): A core genome specific to this isolate collection was created, and included all loci present in at least 95% of isolates. Two methods where used in parallel to generate this:

- The Genome Comparator tool of PubMLST was used to compare all genomes, using the *Nm* finished genome FAM18 (Accession number: AM421808) as a reference with parameters set at a minimum identity of 70%, a minimum alignment length of 50%, a BLASTN word size of 20 base pair and a core threshold of 95%. Paralogous loci were excluded from the analysis and variable loci aligned using MAFFT and concatenated into a single sequence for each genome (174).
- Proteinortho: Assembled draft genomes were downloaded from PubMLST for each isolate and used as input files for the annotation program Prokka,

using default settings with the option "--addgenes" and "--compliant" (265). The protein sequence outputs of Prokka were used as input files for Proteinortho, with default settings, to detect orthologous group of genes (273).

Both methods generated a list of core loci present in 95% of the genomes included in the analysis; 1421 loci were identified by Genome comparator and 1366 by Proteinortho. An inclusive list of 1441 loci including any that were considered core to 95% of isolates by both methods was generated and used in the phylogenetic analysis. Within these 1441 loci, 1114 had complete sequences in all the genomes, whereas the remaining 327 fell at the beginning or the end of a contig in at least one genome and were classified as incomplete genes and excluded from the phylogenetic analysis (Supplemental Table 1).

Phylogenetic analyses were performed for *f_rplF*, rMLST and cgMSLT loci using a complete genome of *Neisseria lactamica* (pubMLST ID: 8851/isolate ID: 020-06) as an out-group. Neighbor-Joining Phylogenies (NJP) were generated in MEGA6 using 100 bootstrap replications with the Kimura 2-parameter model. Tree annotations were performed in MEGA6 (269).

Pairwise allelic variations at the core genes, between each identified clusters, were assessed using the allele-overlap script comparing alleles of each gene between two defined sets of genomes (361).

## *Statistical methods*

### Average Nucleotide Identity

The Average Nucleotide Identity (ANI) was calculated by comparing concatenated sequences of the complete cgMLST loci of representative isolates of each phylogenetic cluster of interest. An online ANI tool, " the ANI calculator" developed by Rodriguez-R, LM (362, 363) was used, from May to August 2017, to calculate a two-way ANI between each pair of selected isolates using the method described by Goris, J and collaborators (176); briefly, pairwise comparison between two genomic sequence data was made using the BLASTN algorithm (321), and the ANI was calculated as the mean identity of all BLASTN matches that displayed a minimum sequence identity of 30% and a minimum alignment length of 70%. Pairs of isolates with ANI values higher than 95% were considered as indistinguishable at the species level as suggested by the program. The analysis was also repeated using the draft genomes of the same isolates.

## *Phenotypic analyses*

Representative isolates from cluster *Nspp1-9*, *Np1-2*, and three positive controls: *Nm* (pubMLST ID: 35956/isolate ID: Z1318)(184), *Np* (pubMLST ID: 19095/isolate ID: CCUG 18031)(309) and *Nl* (pubMLST ID: 8851/isolate ID: 020-06)(309) were used to evaluate phenotypic characteristics of the clusters identified (see Table 1). Each isolate was cultured on Columbia Horse Blood Agar plates (Oxoid) and incubated at 37˚C in an atmosphere containing 5% of CO2, between 16 and 24 hours. A single isolated colony

was then sub-cultured in the same conditions for 20 hours before carrying the tests described below.

**Microbiological analysis**

Macroscopic assessment. Cell morphology was determined, and the colour, texture, shape and colony contour were visually assessed after 20h of incubation. The size of individual colonies was measured using a graduated ruler.

Scanning electron microscopy (SEM). Sub-cultured isolates were also prepared for SEM after 20 hours of incubation, following an adaptation of a protocol previously described (364). Briefly, a piece of agar with bacterial cells was excised and fixed within a 2.5% glutaraldehyde solution and incubated at room temperature for 1 hour. Specimens were then transferred to the Electron Microscopy Facility of the Sir William Dunn School of Pathology (University of Oxford) where they were rinsed in 0.1M Phosphate Buffer solution and fixed with 1% Osmium tetroxide ($OsO4$) for 1 hour. Specimens were then rinsed in Mili-Q water and dehydrated using an Ethanol series: 50% for 10 min, 70% overnight (stored at 4˚C), 90% for 10 min, 95% for 10 min, 100% for 20 min and in pure ethanol three time for 20 min each. Ethanol was removed, and the samples were dried by incubating specimens in a 50% hexamethyldisilazane (HMDS) and 50% ethanol solution for 15 min, followed by incubation in pure HMDS for an additional 15 min. Once HMDS was removed, samples were left in a fume hood overnight to allow HMDS fumes to evaporate. Samples were mounted on SEM stubs with a conductive carbon adhesive, then coated with 10-15 nm of gold using a Quorum Technologies Q150R ES sputter

coater and were imaged with a Zeiss Sigma 300 field emission gun SEM at an accelerating voltage of 2kV.

**Sugars degradation and other biochemical tests**

Oxidase tests were conducted with the oxidase test disks (Sigma-Aldrich) following the manufacturer's instructions and a blue stain following contact between the bacteria and the paper disk was considered as a positive reaction. The catalase test was done by adding a drop of hydrogen peroxide to a bacterial colony; the formation of bubbles was considered a positive reaction. Haemolysis was assessed for each sample by visual inspection of the cells on BAP: a dark coloration of the agar around the colonies corresponds to alpha haemolysis; a clear agar around the colonies to beta haemolysis; and no changes in the colour of the agar represents gamma haemolysis.

Diatabs™ (Rosco Diagnostica) were used according to manufacturer instructions to test for sugar degradation of glucose, maltose, sucrose and lactose, and other selected microbial enzymatic properties such as: the ability to enzymatically hydrolyse aminopeptidase substrates like gamma glutamil aminopeptidase (GGA), leucine aminopeptidase and proline aminopeptidase; the hydrolysis activity of the enzyme β-galactosidase on the orthonitrophényl-β-galactoside (ONPG) substrate; and the enzymatic hydrolysis of tributyrin into butyric acid and glycerol often used for the differentiation of *Moraxella catarrhalis* from *Neisseria* species. Briefly, a dense bacterial suspension of at least 4 McFarland standard was prepared in 1x PBS, 0.25 ml of solution was added to nine different tubes, a single tablet was added to each tube and incubated

at 37˚C for 4h for the aminopeptidases and overnight for the remaining tests. The results were assessed following the instructions of the test noting the appropriate changes in colour (Supplemental Table 2).

The API-NH® kit (Biomerieux) for *Neisseria* characterisation was also tested in parallel, following the manufacturer's instructions. Briefly, a solution of McFarland 4 standard was prepared in the buffer solution provided with the kit for each isolate and added to the strip following the instruction guidelines; the first seven tubes were covered with mineral oil. The strips were incubated at 37˚C for 2 hours and the results of the test were read according to the manual of interpretation of the colour changes for each reaction (Supplemental Table 3).

## Results

### *Hierarchical gene by gene analysis reveals polyphyletic groups of isolates*

The increased resolution obtained from the larger number of loci included in the hierarchical analyses resolved distinct clusters of isolates (Figure 1). Four distinct clusters were identified in the NJP generated from the analysis of the *f_rplF* locus; the *Nm* and *Ng* clusters represented monophyletic groups; however, *Np* and *Nspp* isolates showed more diversity at this single locus (Figure 1A). Eighteen *f_rplF* alleles were identified: two among the *Ng* isolates (*f_rplF* 5 and 7), five among the *Nm* isolates (*f_rplF 1*, 2, 3, 4 and 8), six among the *Np* isolates (*f_rplF* 9, 39, 44, 63, 90 and 120) and six among the *Nspp* isolates (*f_rplF* 16, 62, 69, 70, 79 and 146).

The phylogeny inferred from the 51 ribosomal loci identified distinct clusters in the *Nspp* isolates with long branches and confirmed the polyphyletic relationship of the *Np* isolates (Figure 1B). A total of 115 rMLST profiles were identified: 9 among the *Ng*; 18 among the *Nm* isolates, with an additional isolate missing two loci and for which an rMLST profile could not be defined; 39 among the *Np* isolates; and 49 among the *Nspp* isolates.

Nine distinct clusters were observed in the NJP derived from the 1114 cgMLST loci with complete sequences. These were provisionally designated *Nspp* 1 to *Nspp* 9. At least two clusters could be differentiated among the *Np* isolates, designated *Np* 1 and *Np* 2 (Figure 1 C). Phylo-geographical clustering was observed in both *Nspp* and *Np* groups: (i) all the isolates from *Nspp* 1 (N=36) and *Nspp* 8 (N=1) were collected in Mali; (ii) *Nspp* 2 (N=20), *Nspp* 4 (N=14) and *Nspp* 5 (N=21) were collected in Malawi; (iii) *Nspp* 3 (N=9) came from Chad; (iv) *Nspp* 7 (N=2) from The Gambia; and (v) *Nspp* 9 (N=1) from Germany. The only cluster with isolates from different locations was *Nspp* 6 collected in Malawi (N=2) and in the UK (N=1). Similarly, all *Np* 2 isolates were collected in The Gambia (N=6) and Mali (N=7), two countries of the AMB, whereas *Np* 1 included isolates both from Europe and Africa. Even within the *Np* 1 cluster, which remained polyphyletic with deep branches, the ten isolates from Malawi (N=10) formed a divergent branch and the remaining three African isolates, from Mali (N=1) and The Gambia (N=2), clustered more closely together compared to the European derived isolates (Figure 1C).

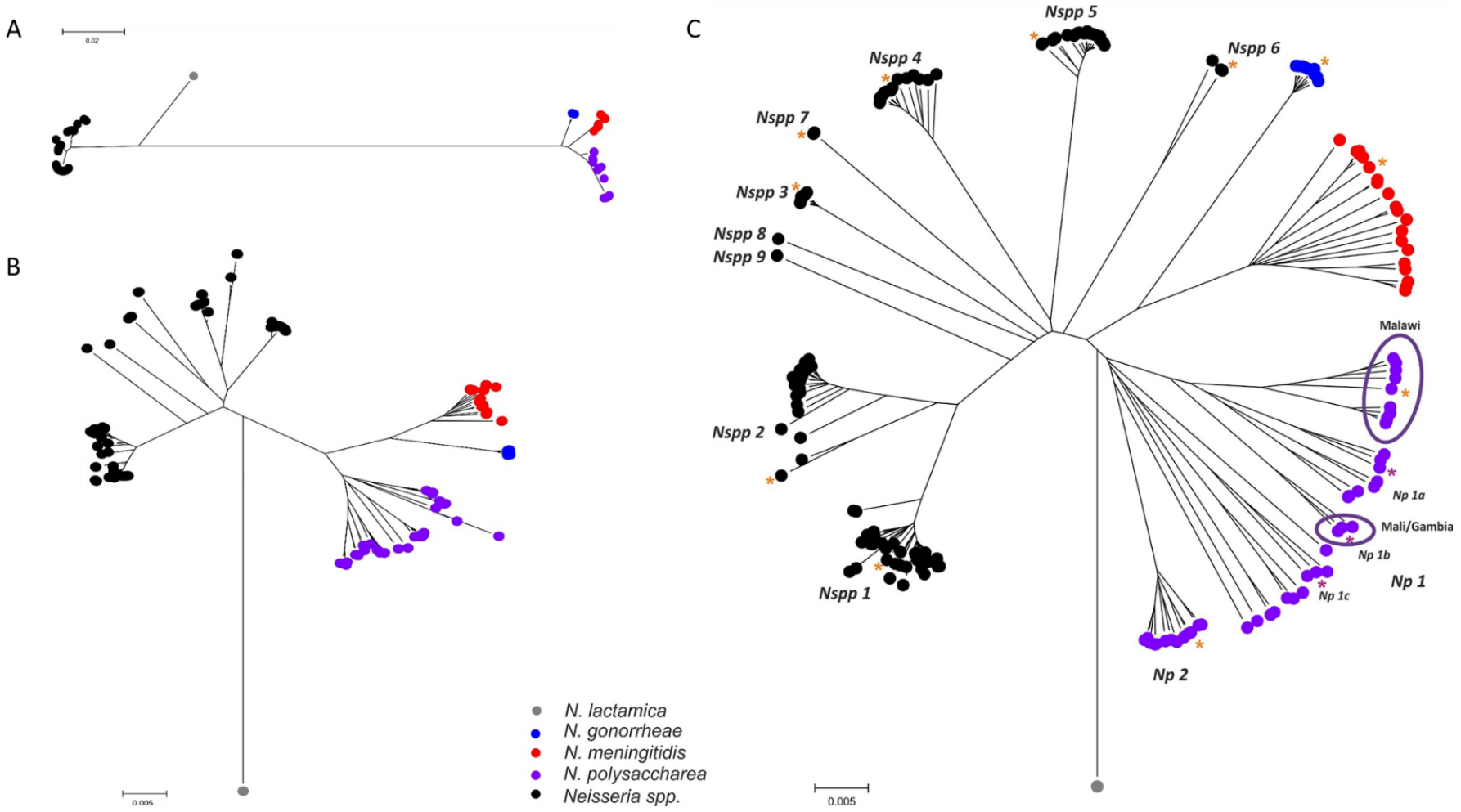


**Figure 1: Neighbor-Joining Trees.**

Trees generated from the aligned sequences of *f_rplF* (A); the concatenated sequences of 51 rMLST loci (B) and the concatenated sequences of the complete 1114 cgMLST loci (C). The orange stars correspond to the isolates selected in the first ANI analysis (Table2) and the purple stars to those added in the ANI analysis done only among the *N. polysaccharea* clusters (Table 4). Np: *N. polysaccharea* and Nspp: *Neisseria spp.*

### *Average Nucleotide Identity identified seven novel Neisseria species*

The cgMLST ANI varied from 93.1% between *Ng* and *Nspp* 6, and *Ng* and *Nspp* 7 to 96.6% between *Nspp* 1 and *Nspp* 2*.* Only three pairwise comparisons yielded values >95% between: (i) *Nspp* 1 and *Nspp* 2; (ii) *Nspp* 1 and *Nspp* 9; and (iii) *Nspp* 2 and *Nspp* 9. These results indicated that the three clusters were indistinguishable at the species level by ANI, using the 95% threshold. All the remaining ANI values were lower than 95% (Table 2). Similar results were obtained using draft WGS (supplemental table 4).

**Table 2: Two-way average nucleotide identity (ANI) using concatenated cgMLST loci sequences**

| | *Nm* | *Ng* | *Np 1* | *Np 2* | *Nspp 1* | *Nspp 2* | *Nspp 3* | *Nspp 4* | *Nspp 5* | *Nspp 6* | *Nspp 7* | *Nspp 8* | *Nspp 9* |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***Nm*** | | | | | | | | | | | | | |
| ***Ng*** | 94.5 | | | | | | | | | | | | |
| ***Np 1*** | 93.7 | 93.2 | | | | | | | | | | | |
| ***Np 2*** | 94.0 | 93.3 | 94.6 | | | | | | | | | | |
| ***Nspp 1*** | 93.7 | 93.5 | 93.7 | 93.8 | | | | | | | | | |
| ***Nspp 2*** | 93.9 | 93.6 | 93.8 | 93.9 | 96.6 | | | | | | | | |
| ***Nspp 3*** | 93.6 | 93.4 | 93.8 | 93.9 | 94.6 | 94.7 | | | | | | | |
| ***Nspp 4*** | 93.5 | 93.2 | 93.8 | 93.7 | 94.4 | 94.3 | 94.4 | | | | | | |
| ***Nspp 5*** | 93.5 | 93.2 | 93.8 | 93.8 | 94.3 | 94.3 | 94.2 | 94.6 | | | | | |
| ***Nspp 6*** | 93.6 | 93.1 | 93.8 | 93.9 | 94.1 | 94.1 | 93.9 | 94.3 | 93.9 | | | | |
| ***Nspp 7*** | 93.4 | 93.1 | 93.9 | 93.9 | 94.3 | 94.3 | 94.3 | 94.1 | 94.0 | 94.1 | | | |
| ***Nspp 8*** | 93.5 | 93.4 | 93.7 | 93.8 | 94.7 | 94.7 | 94.7 | 94.2 | 94.1 | 93.9 | 94.3 | | |
| ***Nspp 9*** | 93.5 | 93.4 | 93.6 | 93.6 | 95.5 | 95.4 | 94.7 | 94.3 | 94.1 | 94.1 | 94.1 | 94.8 | |


ANI measured in percentage are presented with a colour gradient, yellow for values <94 and red for values >95%, which is the threshold above which genomes are considered to be from the species. *Nm*: *N. meningitidis*; *Ng*: *N. gonorrhoeae*; *Np*: *N. polysaccharea* and *Nspp*: *Neisseria spp.*

ANI analysis classified *Nspp* isolates into seven distinct clusters, which were given species name. The first comprised 57 isolates and included clusters *Nspp* 1, *Nspp* 2 and *Nspp* 9; the name *Neisseria bergeri sp. nov.* is proposed for these strains, after the late Ulrich Berger who isolated the first strain (type strain: 15883; pubMLST ID: 5193) in Germany in 1984 (353). The *Nspp* 8 cluster comprised a single isolate collected in Mali in 2010; the name "*Neisseria maigaei*" is suggested, after the late Aziz Maiga who played an important role in the isolate characterisation of the MenAfriCar study in Mali. The name *Neisseria uirgultaei sp. nov.* is proposed for the nine isolates from cluster *Nspp* 3 (type strain: 12_13955_XS2_1; pubMLST ID: 43129), after Sir Brian Greenwood, the director of the MenAfriCar project (greenwood= uirgulta in Latin). As only two isolates have been identified in *Nspp* 7, the name "*Neisseria basseii*" is suggested, after the city Basse in The Gambia, where the isolates were collected. The name *Neisseria blantyrii sp. nov.* is proposed for the 14 *Nspp* 4 isolates (type strain: M-041; pubMLST ID: 46402), after the city Blantyre in Malawi where the isolates were collected. *Neiseria viridiae sp. nov.* is proposed for the 21 *Nspp 5* isolates (type strain: M-226; pubMLST ID: 46439), after Jenny Green MacLennan who did the microbiological characterisation of all the isolates from Malawi included in this study (green=viridi in Latin). Finally, the name "*Neisseria benedictiae*" is suggested for the three *Nspp* 6 isolates, after Julia Bennett (bennet=benedictus in Latin) who started the genomic work on the *N. bergeri* (Figure 2).

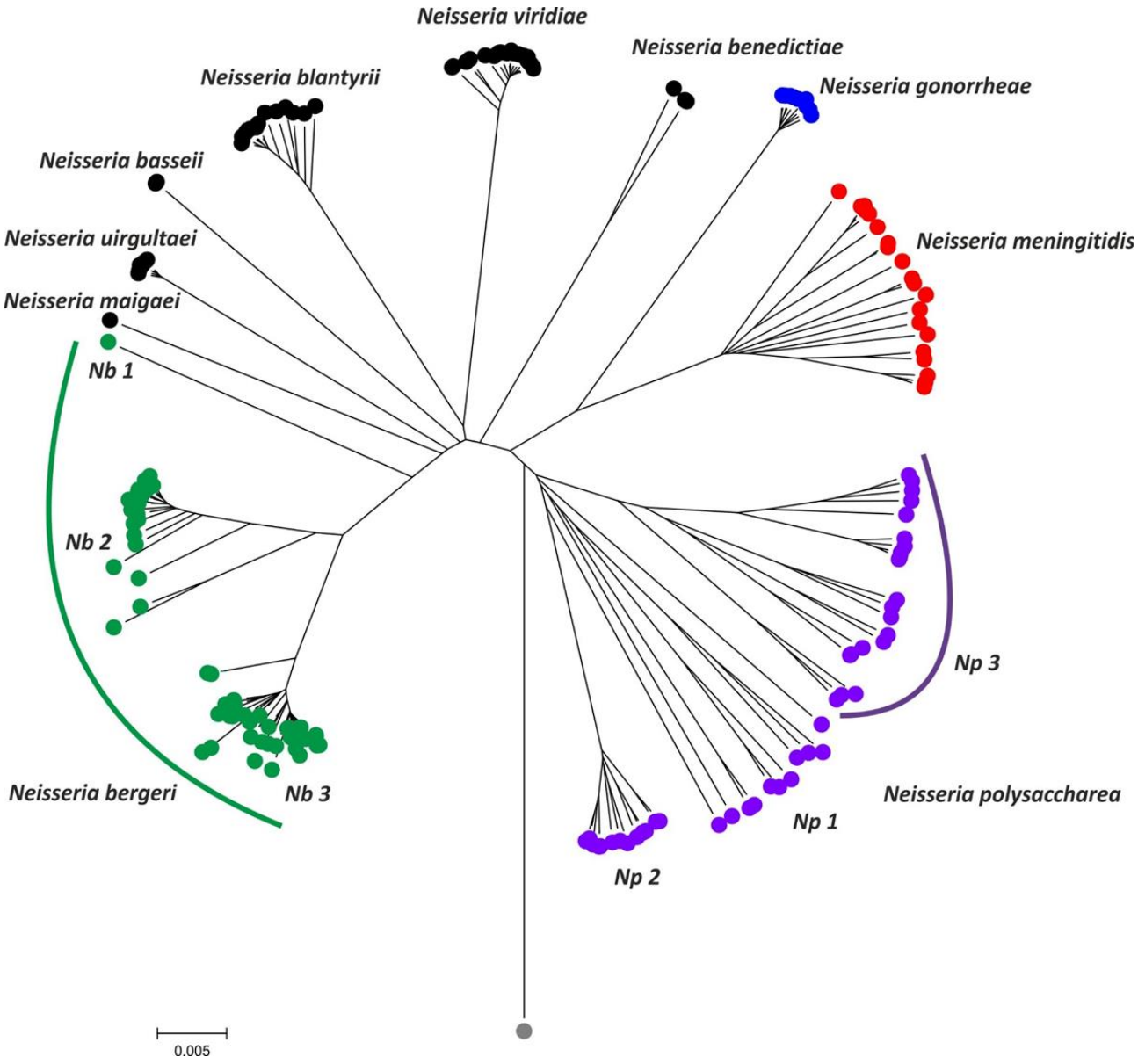


**Figure 2: Novel *Neisseria* species defined following 95% cgMLST ANI**

The pairwise allelic comparison of the 1441 core loci between each defined cluster identified that, despite sharing the same loci, the majority of clusters had cluster-specific alleles, with only small numbers of loci sharing at least one allele between clusters. *Nspp* 1 and *Nspp* 2, however, had the largest number of loci (N=693), sharing at least one allele, and similarly for *Nspp* 1 and *Nspp* 9 (N=145) and *Nspp* 2 and *Nspp* 9 (N=134) (Table 3), consistent with the ANI results grouping them into a single species.

**Table 3: Pairwise allelic comparison of the 1441 cgMLST loci**

| | ***Nm*** | ***Ng*** | ***Np 1*** | ***Np 2*** | ***Nspp 1*** | ***Nspp 2*** | ***Nspp 3*** | ***Nspp 4*** | ***Nspp 5*** | ***Nspp 6*** | ***Nspp 7*** | ***Nspp 8*** | ***Nspp 9*** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***Nm*** | | | | | | | | | | | | | |
| ***Ng*** | 9 | | | | | | | | | | | | |
| ***Np 1*** | 75 | 7 | | | | | | | | | | | |
| ***Np 2*** | 18 | 2 | 191 | | | | | | | | | | |
| ***Nspp 1*** | 15 | 1 | 120 | 44 | | | | | | | | | |
| ***Nspp 2*** | 25 | 1 | 177 | 27 | 643 | | | | | | | | |
| ***Nspp 3*** | 7 | 1 | 54 | 23 | 68 | 38 | | | | | | | |
| ***Nspp 4*** | 15 | 0 | 113 | 17 | 35 | 68 | 30 | | | | | | |
| ***Nspp 5*** | 12 | 1 | 122 | 15 | 26 | 55 | 30 | | | | | | |
| ***Nspp 6*** | 7 | 1 | 123 | 22 | 20 | 28 | 15 | 51 | 22 | | | | |
| ***Nspp 7*** | 8 | 0 | 48 | 18 | 23 | 23 | 22 | 22 | 21 | 13 | | | |
| ***Nspp 8*** | 3 | 0 | 26 | 19 | 55 | 27 | 20 | 17 | 15 | 8 | 11 | | |
| ***Nspp 9*** | 8 | 0 | 54 | 10 | 145 | 134 | 36 | 23 | 22 | 11 | 18 | 16 | |


Number of loci with at least one allele shared are displayed with a colour gradient, pink for values < 50 and purple for values > 500. *Nm*: *N. meningitidis*; *Ng*: *N. gonorrhoeae*; *Np*: *N. polysaccharea* and *Nspp*: *Neisseria spp*

## *Neisseria polysaccharea form a polyphyletic cluster*

The two *Np* clusters originally designated *Np* 1 and *Np 2* had an ANI value of 94.7% confirming that they might be considered as two distinct species (Table 2). The pairwise allelic comparison based on the two clusters found that *Np* 1 also had a large number of loci sharing at least one allele with various clusters (*Np* 2*; Nspp* 1, *Nspp* 2, *Nspp* 4, *Nspp* 5 and *Nspp* 6), suggesting that the cluster was not homogeneous and

probably included more than one species. Three additional genomes of the *Np 1* cluster were selected to attempt to dissect it further (Figure 1C). 95% cgMLST and WGS ANI (Table 4 and Supplemental Table 5) comparison among those isolates identified another distinct cluster, *Np 3* (Figure 2).

**Table 4: Two-way ANI among the *N. polysaccharea* isolates using concatenated cgMLST loci sequences**

| | *Np 1* | *Np 1a* | *Np 1b* | *Np 1c* | *Np 2* |
|---|---|---|---|---|---|
| *Np 1* | | | | | |
| *Np 1a* | 96.1 | | | | |
| *Np 1b* | 95.4 | 96.0 | | | |
| *Np 1c* | 94.3 | 94.5 | 94.2 | | |
| *Np 2* | 94.6 | 94.4 | 94.6 | 94.3 | |

<94

<95

ANI measured in percentage are presented with a colour gradient, yellow for values <94 and red for values >95%. *Np*: *N. polysaccharea*

## *Phenotypic analysis of the clusters*

The macroscopic analysis of the bacterial cell morphology (Table 6) established that all isolates tested had a grey colour, exhibited γ-hemolysis, indicating an absence of hemolysis, and had a round shape on BAP. All the novel species had edges with regular shape and smooth texture; however, *Neisseria blantyrii* (*Nspp* 4) was found to be moister than the others. The size range of the colonies varied from 0.1 mm to 1 mm; the *Nm* size range went up to 2 mm (Table 5).

**Table 5: morphological results**

| morphology | haemolysis | colour | texture | size | shape | shape of edges |
|---|---|---|---|---|---|---|
| ***Neisseria bergeri (Nspp9)*** | gamma | grey | smooth | 0.1-1 mm | round | regular |
| ***Neisseria bergeri (Nspp1)*** | gamma | grey | smooth | 0.5-1 mm | round | regular |
| ***Neisseria bergeri (Nspp2)*** | gamma | grey | smooth | 0.5-1 mm | round | regular |
| ***Neisseria maigaei (Nspp8)*** | gamma | grey | smooth | 0.2-0.5 mm | round | regular |
| ***Neisseria uirgultaei (Nspp3)*** | gamma | grey | smooth | 0.5-1 mm | round | regular |
| ***Neisseria basseii (Nspp7)*** | gamma | grey | smooth | 0.5 mm | round | regular |
| ***Neisseria blantyrii (Nspp4)*** | gamma | grey | smooth/moist | 0.2- 0.5 mm | round | regular |
| ***Neisseria viridiae (Nspp5)*** | gamma | grey | smooth | 0.5-1 mm | round | regular |
| ***Neisseria benedictiae (Nspp6)*** | gamma | grey | smooth | 0.5-1 mm | round | regular |
| ***Neisseria meningitidis*** | gamma | grey | moist | 0.5-2 mm | round | irregular/merging |
| ***Neisseria polysaccharea*** | gamma | grey | moist | 0.2 mm | round | regular |
| ***Neisseria lactamica*** | gamma | grey | smooth | 1 mm | round | regular |

SEM of isolates from each species identified that they were all cocoid bacteria with a mix of completely formed diplococci and slightly "heart-shaped" morphology (Figure 3). Variation over the extracellular structures observed around the cell membrane could be identified: for example, the isolates from the three sub-clusters of *Neisseria bergeri* (*Nspp* 1, 2, and 9) exhibited filaments covering their extracellular membranes, "pili-like" structures could also be seen connecting cells of "*Neisseria maigaei"* (*Nspp* 8), the cells of *Neisseria blantyrii* (*Nspp* 4) appeared covered in an intense filamentous network, *Neisseria viridiae* (*Nspp* 5) and "*Neisseria benedictiae"* (*Nspp* 6) had visible "bulbs" present on the surface of their extracellular membranes. *Neisseria uirgultaei* (*Nspp* 3); however, had a smooth surface with no visible extracellular elements and "*Neisseria basseii"* (*Nspp* 7) had few visible filaments and bulbs around their extracellular membranes (Figure 3).

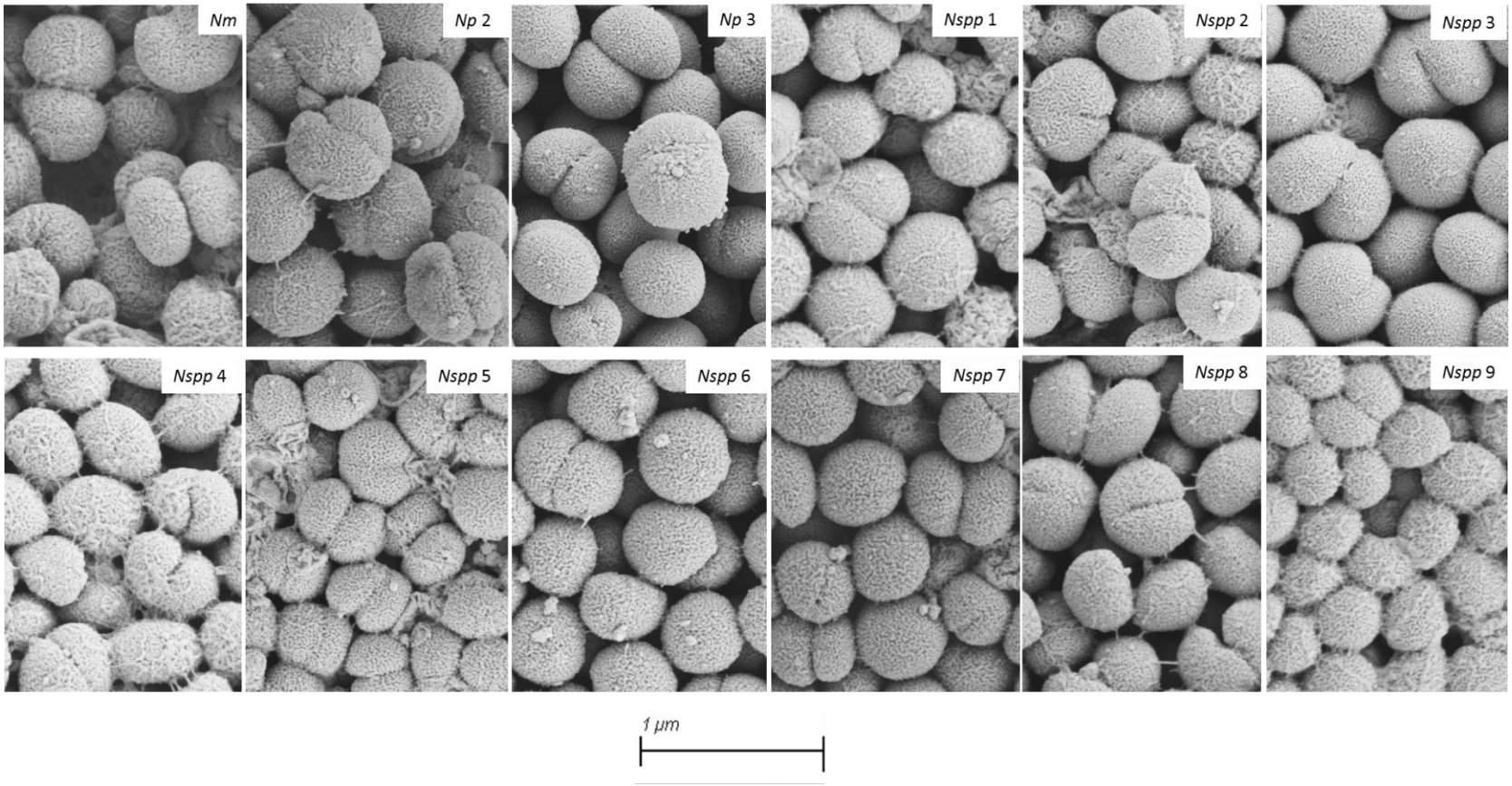


**Figure 3: Scanning electron microscopy images of the different clusters identified by genomic analysis.**

*Nspp* 1, 2 and 9: *N. bergeri*; *Nspp 3*: *N. uirgultaei*; *Nspp 4*: *N. blantyrii*; *Nspp* 5: *N. viridiae*; *Nspp* 6: *N. benedictiae*; *Nspp* 7: *N. bassei*; *Nspp* 8: *N. maigaei*

Biochemical results obtained using Diatabs™ identified the novel species as GGA, ONPG, and Tributyrin negative, Leucine and Proline Aminopeptidase positive. They were also positive for the degradation of Maltose and negative for Lactose. Results were variable for Glucose and Sucrose: *N. bergeri* subcluster 1 (*Nb1*; *Nspp* 9) and 2 (*Nb2*; *Nspp* 2), *N. uirgultaei* (*Nspp* 3), "*N. basseii*" (*Nspp* 7) and *N. viridiae* (*Nspp* 5) being on average positive for Glucose after at least 3 repeats; and *N. bergeri* subcluster 3 (*Nb3*; *Nspp* 1), "*N. maigaei*" (*Nspp* 8)*, N. blantyrii* (*Nspp* 4) and "*N. benedictiae"* (*Nspp* 6) being on average negative. Similarly, *N. viridiae* (*Nspp* 5) and "*N. benedictiae*" (*Nspp* 6) were on average positive for sucrose while all the other species were negative. The GGA, Proline Aminopeptidase and lactose/ONPG tests were useful for distinguishing the new species from *Nm* and *Nl*; however, none of the tests allowed a distinction from *Np* (Table 6).

**Table 6: Diatabs™ results**

| Diatabs | Glucose | Maltose | Sucrose | Lactose | GGA | LA | PA | ONPG | Tributyrin |
|---|---|---|---|---|---|---|---|---|---|
| ***Neisseria bergeri (Nspp9)*** | +* | + | - | - | - | + | + | - | - |
| ***Neisseria bergeri (Nspp1)*** | -* | + | - | - | - | + | + | - | - |
| ***Neisseria bergeri (Nspp2)*** | + | + | - | - | - | + | + | - | - |
| ***Neisseria maigaei* (*Nspp8)*** | - | + | - | - | - | + | + | - | - |
| ***Neisseria uirgultaei* (*Nspp3)*** | + | + | - | - | - | + | + | - | - |
| ***Neisseria basseii* (*Nspp7)*** | +* | + | - | - | - | + | + | - | - |
| ***Neisseria blantyrii (Nspp4)*** | -* | + | - | - | - | + | + | - | - |
| ***Neisseria viridiae (Nspp5)*** | + | + | +* | - | - | + | + | - | - |
| ***Neisseria benedictiae (Nspp6)*** | - | + | +* | - | - | + | + | - | - |
| ***Neisseria meningitidis*** | + | + | - | - | + | + | - | - | - |
| ***Neisseria polysaccharea*** | +* | + | - | - | - | + | + | - | - |
| ***Neisseria lactamica*** | + | + | - | + | - | + | + | + | - |

GGA: Gama-Glutamyl Aminopeptidase; LA: Leucine Aminopeptidase; PA: Proline Aminopeptidase; ONPG: Ortho-Nitrophenyl-β-galactoside; *Nspp*: *Neisseria spp*
* Variable results upon multiple repeats, the most common result is presented

Results obtained from the API®-NH tests showed that all the isolates were positive for the degradation of all four sugars tested on the strip (glucose, fructose, maltose and saccharose), which contradicted the pattern observed for glucose with the diatabs for some isolates. Similarly to the Diatabs, the β-galactosidase, Proline Aminopeptidase and Gamma-glutamyl transferase (GGT) reactions were useful to distinguish the novel species from *Nl* and *Nm* but no test could distinguish them from *Np* (Table 7).

**Table 7: API®-NH results**

| API®-NH | PEN | GLU | FRU | MAL | SAC | ODC | URE | LIP | PAL | βGAL | ProA | GGT | IND |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***Neisseria bergeri (Nspp9)*** | - | + | + | + | + | - | - | - | - | - | + | - | - |
| ***Neisseria bergeri (Nspp1)*** | - | + | + | + | + | - | - | - | - | - | + | - | - |
| ***Neisseria bergeri (Nspp2)*** | - | + | + | + | + | - | - | - | - | - | + | - | - |
| ***Neisseria maigaei* (*Nspp8)*** | - | + | + | + | + | - | - | - | - | - | + | - | - |
| ***Neisseria uirgultaei* (*Nspp3)*** | - | + | + | + | + | - | - | - | - | - | + | - | - |
| ***Neisseria basseii* (*Nspp7)*** | - | + | + | + | + | - | - | - | - | - | + | - | - |
| ***Neisseria blantyrii (Nspp4)*** | - | + | + | + | + | - | - | - | - | - | + | - | - |
| ***Neisseria viridiae (Nspp5)*** | - | + | + | + | + | - | - | - | - | - | + | - | - |
| ***Neisseria benedictiae (Nspp6)*** | - | + | + | + | + | - | - | - | - | - | + | - | - |
| ***Neisseria meningitidis*** | - | + | + | + | + | - | - | - | - | - | - | + | - |
| ***Neisseria polysaccharea*** | - | + | + | + | + | - | - | - | - | - | + | - | - |
| ***Neisseria lactamica*** | - | + | + | + | + | - | - | - | - | + | + | - | - |

PEN: Penicilinase; GLU: glucose; FRU: fructose; MAL: maltose; SAC: saccharose; URE: urea; LIP: Lipase; PAL: Alkaline Phosphatase; βGAL: β-Galactosidase; ProA: Proline Arylamidase; GGT: Gamma-Glutamyl Transferase; IND: Indole; *Nspp*: *Neisseria spp*

## Discussion

The concept and definition of species in prokaryotes and the methods used to identify them continue to be debated (365, 366). Many bacterial species have been solely defined based on the disease they cause without taking into consideration broader evolutionary aspects (342). For example, the two species of the genus *Neisseria*, *Nm* and *Ng*, were named after and characterised by the diseases they caused, which are clinically important phenotypic differences, despite hybridization studies indicating that both species were very closely related and did not meet the 70% DDH criterion necessary to distinguish them into two species (170). Although species definitions were initially based on phenotypic characteristics, the integration of ecological and genetic data has greatly improved classifications. MLSA has been the approach of choice in recent studies to characterise new species among the genus *Neisseria* and the analysis of the seven MLST loci has proven to be sufficient to distinguish *Nm, Ng* and *Nl* (367), which sequence data from the single locus 16S RNA failed to do (131). Although housekeeping genes have mostly been used, there have been no specific guidelines on the loci or the number of loci to be chosen for MLSA. The increase in availability of whole or nearly complete genome sequence data allows species characterisation at a higher resolution, with the inclusion of a larger number of loci as demonstrated through the use of the *Neisseria* genus cgMLST analysis, which successfully identified multiple *Neisseria* species, for taxonomic purposes (131).

Here, a novel genomic-phylogenetic approach (368) to the definition and characterisation of *Neisseria* species was developed. This combined use of MLSA and ANI scores, using nucleotide sequence data of core genes, allowed phylogenetic

relationships to be inferred among the collection of isolates under study (Figure 1C), supplemented with a quantitative measure of genetic relatedness (Tables 2 and 4). The broadly accepted threshold of 95% ANI was used, as previously proposed by Goris et al. (176). This threshold, which corresponds to the accepted 70% DDH standard has been considered arbitrary, chosen to fit with previously existing species definitions. Some studies have proposed that a higher range of threshold could be used; however, they were based on the comparison of only a few genomes which more than likely underestimated the overall species diversity (171).

The 95% cgMLST ANI cut-off applied in this study allowed the classification of previously unclassified *Nspp* isolates into seven distinct species groups, providing a systematic method of species definition based on the clusters identified by phylogenetic analysis (Figure 2). Indeed, three of the clusters originally identified were indistinguishable by ANI and were grouped into a single species named *N. bergeri sp. nov.*; these three clusters may be considered as subspecies (*Nb* Subspecies 1, 2, and 3). Three *Neisseria* species found in other clusters were assigned names, as they contained more than three representative isolates: *N. uirgultaei sp. nov.; N. blantyrii sp. nov.;* and *N. viridiae sp. nov.* The type strains of these novel species will be deposited in an appropriate culture collection, following the regulations of the bacteriological code. The remaining clusters had fewer than three isolates and therefore will not be formally named and deposited; however, the species names ("*N. maigaei*", "*N. basseii*" and "*N. benedictiae*") are proposed for future reference. Identical ANI results were obtained from the analysis using the full draft WGS (Supplemental Tables 4), confirming that the cgMLST provided optimal genomic resolution and that the exclusion of the remaining part of the genomes, i.e. intergenic

regions and accessory genes, did not affect the clustering results into species groups. The consistency between the ANI results and the cgMLST allelic comparison (Table 3), suggest that allelic diversity play an important role in the speciation process, alongside gene presence/absence. The low number of shared alleles confirm the infrequency of cross-species recombination as previously observed in a study comparing *Nm, Nl* and *Ng* (201).

Distinct clusters were identified among the *Np* isolates included in this study; two phylogenetic clusters *Np* 2 and *Np* 3 could be reclassified as distinct species based on the 95% cgMLST ANI (Table 4 and Supplemental Table 5); however, a subset of the isolates (*Np* 1) remained polyphyletic and additional genomic comparison of a larger collection of isolates would be needed to fully determine the number of species present. For historical reasons it may be preferable to maintain these isolates as *Np* and the identified clusters as subspecies (*Np* Subspecies 1, 2, and 3) until more genomes are available to allow a complete reorganisation of the *Neisseria polysaccharea*.

A major limitation when undertaking speciation studies is in obtaining an appropriate sample of the bacteria that reflect the natural diversity of the population. Indeed, studies are often geographically limited, leading to an underestimation of the diversity. The different nasopharyngeal carriage studies undertaken in the UK (358, 369), countries of the AMB (111, 130, 355) and in Malawi (outside of AMB) (357) have led to the collection of a larger number of *Neisseria* isolates; however, the NPNs were not always characterised at the genomic level in those studies. Although the sequencing of the *f_rplF* locus provides phylogenetic distinction on previously

defined species, it was not designed to identify novel ones. Our study confirms that it does not provide enough resolution for the characterisation of the novel species defined here. Each of the clusters identified had distinct *f_rplF* alleles except *N. benedictiae* (*Nspp* 6) and *N. basseii* (*Nspp* 7) which shared allele 69, consistent with HGT or shared ancestry. The genomic results presented here indicate a phylogeographic clustering of genotypes, with isolates from the same countries clustering together on the cgMLST NJP tree. Despite the fact that the most recent carriage studies, done in the UK and in the AMB, used the same laboratory methodology, most of the previously non-speciated isolates were recovered in Africa with only one *Nspp* found in the UK, indicating the particularly high diversity of the *Neisseria* species in the African continent; however, differences in the age groups targeted, the whole population (AMB) vs 15-19 years old high school students (UK), may have played a role in the differences observed.

The genome sequencing of additional carried *Neisseria* isolates from various geographical regions are likely to improve the taxonomy of this genus. Isolates previously characterized as "*N. bergeri*" based on nucleotide sequences of the *rplF* locus (178) may in fact, with further cgMLST analysis, also include novel *Neisseria* species, such as those identified in this study. Genome sequences obtained from the Malian collection of the MenAfriCar project found that most of *Nspp* genomes were classified as *N. bergeri sp. nov.* using the 95% cgMLST ANI analysis presented here; however, one was found to form a distinct putative species, "*N. maigaei".*

The phenotypic tests included in this study were far from exhaustive and although few distinctive traits were identified for each of the novel species, it is possible that additional tests such as other biochemical tests, pH, or chemotaxonomy (the analysis

of chemical composition of the cell) could identify differences which may have been missed (370). All the novel species and the *Np* isolates were indistinguishable using most biochemical tests, despite being clearly distinct by 95% cgMLST ANI. Phenotypic tests were labour intensive, and the results were difficult to interpret and often based on subjective distinction of colour changes. The Diatabs™ tests were overall more straightforward than the API®-NH tests, which require a strict McFarland Standard concentration, making results more sensitive to small concentration changes. The assessment of sugars degradation by the Diatabs™ were accurate for the *Nm* and *Nl* control, but were unstable for some of the species with multiple repeats giving different results. On the other hand, the degradation of sugars assessed by the API®-NH were highly repeatable but failed to give the expected results for *Nm,* which is usually characterised as able to metabolise glucose and maltose but not the other sugars. This was probably due to inadequate McFarland concentrations, despite the use of a standard for comparison during the preparation of the inoculum, as the same isolates gave the expected results with the Diatabs™ test.

The SEM allowed the visualisation of the coccoid cells and of distinct structures on the extracellular membranes. “Heart-shaped” cells were visible among most of the novel species after 20h of incubation; these could be intermediate shapes of coccoid cells or a distinctive cell shape, these cells were still visible after 48h of incubation (data no shown) but additional time points would help clarify this. Overall the phenotypic tests included in this analysis provided very little distinctive information and led to many challenges, indicating the usefulness of genomic approaches.

The high resolution genomic analysis presented here allowed the identification of novel *Neisseria* species that were predominantly carried in African countries, indicating the high diversity of the *Neisseria* genus in that region. The implications of these findings are, however, difficult to determine as more sampling, genomic characterisations and analysis of the interactions of these different species in the oropharynx will be needed to determine the role they play, if any, in modulating carriage and invasion of *Nm*. Future microbiome and immunological studies will be crucial and are likely to shed more light onto the dynamics of carriage and help answer those very important questions; however, genomic characterisation of the isolates will be necessary to adequately assess the diversity of that microbiome.

Overall, the results of this study suggest that more *Neisseria* diversity is found outside of the AMB, in Malawi, than within the belt, which could have important implications regarding the impact of those species in modulating the carriage and invasiveness of *Nm* as the disease epidemiology is known to be very different between these two regions of Africa. However, it is not unlikely that the analysis of more genome sequences of the *Neisseria* isolates from the AMB, such as those from the other countries sampled alongside Mali and Chad during the MenAfriCar project (178), will improve our understanding of the diversity seen within the AMB and allow more adequate hypothesis to be formulated. The analysis method developed here provides a framework for future speciation endeavours, and could be easily repeated to incorporate additional genomes when available. It is now evident that the diversity of human restricted *Neisseria* has been underestimated and more carriage studies using genomic methods should be encouraged to define a more accurate picture of the genus.

# III- Discussion and Conclusion

## Chapter 6: Concluding remarks and future work

### Initial hypotheses

*Neisseria meningitidis* (*Nm*), mostly known for its ability to cause invasive meningococcal disease (IMD), is a frequent commensal inhabitant of the oropharynx, spending the majority of its life cycle colonizing and spreading among healthy individuals. *Nm* does not benefit from causing disease, as the death of an infected individual leads to a disruption of its transmission chain (3). Factors encouraging a change in phenotype from harmless commensal to invasive pathogen remain unclear, and it has been suggested that complex multifactorial mechanisms are involved. Among these hypothetical factors, two have been investigated in this thesis: (i) the existence of differences in the bacterial genetic make-up of carried and invasive isolates that could explain pathogenicity; and (ii) the possibility that dynamic changes in the immediate environment of the meningococcus, focusing on other members of the *Neisseria* genus, could trigger the invasion process and thus pathogenicity.

Understanding the mechanisms driving this change is essential for prevention and better control of IMD (115), especially when, despite adequate treatment, the fatality rate remains around 10%. It is even more important for countries of the African meningitis belt (AMB), which suffer large and currently unpredictable epidemics that are often disruptive to the whole health system, due to their scale (371). It is also important to study the carriage state and the diversity among *Neisseria* strains in order to better understand the evolution of the bacteria at a population level.

The nasopharynx is a complex environment and *Nm* does not live in isolation. Indeed, the meningococcus shares its ecological niche with multiple organisms in a dynamic way (372). The other members of the genus *Neisseria* are of particular interest as they have been shown to exchange genetic information among themselves and with *Nm* (133, 373). Data available on *Neisseria lactamica* (*Nl*), one of the most studied non-pathogenic *Neisseria* (NPN), also suggest that it could play a role in protecting against carriage of *Nm*; indeed, a recent human challenge study has shown that inoculation of healthy volunteers with *Nl* was protective against *Nm* acquisition (135). The knowledge that other *Neisseria* species, such as *Neisseria polysaccharea*, were genetically more closely related to *Nm* than *Nl*, raises questions over the potential protective role of other species (131).

### Findings and future work

Previous carriage studies conducted in the AMB used different protocols and time points making comparisons difficult (112). Additionally, most of them focused on the characterisation of *Nm*, and reports of NPNs were almost non-existent, except for a few studies that collected *Nl* (129). The more recent collection of all putative *Neisseria* species by the MenAfriCar consortium, in seven countries of the belt between 2010 and 2012, using standardized methods, provided the first opportunity to characterise the diversity of carried *Neisseria* species on the African continent (111). The molecular methods applied to the collection of isolates in Chapter 3; sequencing of a fragment of the *rplF* gene to determine the species, and of the variable region of an outer membrane protein common to all *Neisseria* species, *fetA*, to assess species diversity; allowed efficient characterisation of 4694 *Neisseria* isolates and the identification of five distinct species at that single locus resolution

(178). These results were the first evaluation of the species sharing the *Nm* niche in the AMB and demonstrated the large diversity of *Neisseria* strains isolated, with more than six hundred strain types defined. The culture dependant and low resolution genetic methods used, however, are likely to have led to an underestimation of diversity in that study both at the strain and species level.

Significant risk factors forf carrying *Nm* were inversely related to those of carrying NPNs in terms of age group, gender and season, indicating that the individuals with higher risk of carrying a NPN were at lower risk of carrying *Nm*, and suggesting that carriage of a NPN could be protective against *Nm* carriage. Unfortunately, the investigation of only single colonies per nasopharyngeal swab prevented an analysis of co-carriage of those species in this particular dataset, and this remains an important question that warrants further investigations by future carriage studies or *in vitro* co-infection analysis. The impact of such protection against *Nm* carriage will also require additional investigations to determine whether these NPNs are able to elicit protective immunity through cross reactive bactericidal antibodies, which would provide useful protection against invasive *Nm*; however, if they don't offer cross-reactive immunity, the mere physical prevention of *Nm* carriage could have the detrimental effect of depriving individuals from developing an immunity that could be protective upon infection with an hyper-virulent *Nm* strain (374).

The application of higher resolution genomic approaches was impractical for the analysis of the 4694 *Neisseria* collected by the MenAfriCar project. The genomic analysis presented in Chapter 5, of a subset of *Neisseria* species that had not been fully characterised at the lower resolutions used in previous studies, has, however, shed light on the complexity of the genus *Neisseria*. Moreover, whole genome

sequence analyses of these previously unclassified isolates led to the identification of seven novel species, which were not distinguishable using the phenotypic methods applied in this study; these methods remain, however, clinically relevant, as they did distinguish them from *Nm* and *Nl,* but not from *Neisseria polysaccharea*. The innovative combination of a core genome phylogenetic analysis (cgMLST) with a measure of sequence relatedness between phylogenetic clusters, through the 95% Average Nucleotide Identity (ANI), presented in this thesis provides a simple and reproducible approach for future speciation endeavours. The computational demands of calculating ANI has made it difficult to apply this to multiple sequences, which is one of the drawback of the approach that relies on pairwise comparison of representative isolates. But the rapid advances in technologies and development of new bioinformatics tools are likely to facilitate the use of ANI for the comparison of large collections of genetic data. Alternative tools like MASH, which also yields a measure of sequence dissimilarities using a kmer approach, need to be further validated to determine the best parameters to use in order to obtain ANI analogous values for speciation purposes (242).

It is interesting to note that the large majority of the novel species were collected in Africa, in and out of the AMB, suggesting again that the diversity of the genus was more substantial there than in high-income countries; however, this could also be due to sampling bias. The sequencing of additional *Neisseria* genomes from variable geographical regions and comparable demographic populations will be necessary to confirm these results. More importantly, the genomic characterisation of additional isolates from within and outside of the belt, will help determine whether changes in

the carriage dynamic of these species, by season, age group, regions or other factors, could influence carriage of *Nm* and the epidemiology of IMD.

Results presented in Chapter 4, obtained from the genomic comparison of carried and invasive *NmA* isolates, indicate that the change of phenotype is not driven by a particular genetic factor (225), although further gene expression studies will be needed to confirm that result. Instead, the carried and invasive *NmA* isolates formed clusters associated with different age groups, which suggests that age-related changes in the nasopharynx are likely to play a role in allowing a particular *Nm* strain to infect a particular individual. The changes could be due to many different factors such as diet, exposure to different environmental climates, living conditions or changes in the composition of the microbiome, all of which are interlinked. Appropriately designed studies evaluating the impact of those factors on carriage are going to be necessary to fully understand the mechanisms underlying the invasiveness of *Nm.* Similar studies, at a larger scale, allowing genome wide association analysis to be performed, will also be helpful in confirming these results for other serogroups, during epidemics as well as in intermediate periods.

Very little is known about the link between the microbiota of the nasopharynx and diseases caused by some of the members of the flora (375). Studies of the throat microbiota have identified multiple operational taxonomic units (372, 376) present within different proportions. Links between the microbiota in the respiratory system and certain respiratory diseases have been studied, for example for cystic fibrosis (377) and pneumonia (350). In the case of meningococcal meningitis, no studies, at the time of writing had looked at the changes in the general microbiota and the potential role it could play in modulating carriage of *Nm* and therefore the disease.

With the technological advances, metagenomic sequencing methods are being elaborated to allow such studies to be performed and this represents a promising area of research in the meningitis field (378).

## Conclusion

This thesis presents a comprehensive analysis of members of the human restricted *Neisseria* genus obtained from carriage studies undertaken in the AMB. The molecular and genomic analysie applied to the different sample sets identified multiple species and strains colonizing the oropharynx with *Nm*, including novel species indistinguishable at lower resolutions. The role of these NPNs remains unclear, but results suggest they may participate in modulating carriage of *Nm.* Further studies will be needed to establish the exact mechanisms.

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# The Molecular Epidemiology and Ecology of *Neisseria* Species in the African Meningitis Belt

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# Appendices

# V- Appendices

## Appendix 1: Supplemental material for Chapter 3

### Supplementary methods

### General Sanger Sequencing protocol

A reaction mixture of 50µl was prepared for the PCR amplification step containing 10µl of Q Solution Buffer (Quiagen), 5µl of 10X Buffer (Quiagen), 1µl of dNTPs (Quiagen), 1µl of each primer (10uM stocks), 0.25µl Taq DNA polymerase (Quiagen) and 2µl of DNA, with the following reaction conditions: one cycle at 95 °C for 3 min, followed by 35 cycles of a sequence of three temperatures, 95°C for 30 s, 55°C for 30 s and 72°C for 1 min and a final incubation of one cycle at 72 °C for a further 10 min. The amplified reactions were purified using the PEG-NaCl precipitation method (379). Sequencing of the cleaned DNA precipitate was done in a 10µl reaction mix containing the following: 0.5µl BigDye ready reaction mix (Life Technologies), 1.75µl of 5X dilution buffer (Life Technologies), 4µl of primer (10µM 1:15) and 2µl of DNA, with cycling condition as follow: 30 cycles of a sequence of tree temperatures, 96°C for 10 s, 50°C for 5 s and 60°C for 2 min. Sequence reactions were cleaned before sequencing on an Applied Biosystems 3730 DNA analyzer (Life Technologies).

### *fetA_VR* sequencing protocol

Primers S1 and S8 (121) were used for the PCR amplification with the following reaction conditions: one cycle at 95 °C for 3 min, followed by 30 cycles of a sequence of three temperatures, 94°C for 1 min, 55°C for 1 min and 72°C for 1 min and a final incubation of one cycle at 72 °C for a further 5 min. The cleaned amplicons were sequenced using primer S12 (forward sequencing) and primer S15 (reverse sequencing) (121).

### *fnl* sequencing protocol

Primers CM21 and CM24 were used for both amplification and sequencing; however, the reaction mixture was slightly different from the general method described above, in that it did not contain the Q Solution Buffer (Quiagen) and the cycling conditions were as follows: one cycle at 95°C for 3 min, followed by 35 cycles of a sequence of three temperatures, 95°C for 30 s, 56°C for 30 s and 72°C for 5 minutes and a final incubation at 72 °C for a further 10 minutes. Sequencing was done as for the other targets

## Supplementary Tables

### Table S1: Number of isolates identified as a *Neisseria* species per country

| | *N meningitidis* | Prevalence [CI] | *N lactamica* | Prevalence [CI] | *N polysaccharea* | Prevalence [CI] | *N bergeri* | Prevalence [CI] | *N subflava* | Prevalence [CI] | **Total** | Prevalence [CI] |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Chad N=13396 | 131 | 0.9 [0.8-1.1] | 467 | 3.5 [3.1-3.8] | 40 | 0.3 [0.2-0.4] | 47 | 0.3 [0.2-0.5] | 10 | 0.1 [0.03-0.1] | **695** | 5.3 [4.9-5.7] |
| Ethiopia N=5970 | 388 | 6.3 [5.6-7.1] | 268 | 4.4 [3.8-5.0] | 179 | 3.0 [2.5-3.5] | 0 | - | 3 | 0.05 [-0.01-0.1] | **838** | 13.8 [12.8-14.8] |
| Ghana N=5209 | 193 | 3.7 [3.1-4.3] | 217 | 4.1 [3.5-4.7] | 10 | 0.2 [0.1-0.3] | 26 | 0.5 [0.3-0.7] | 0 | - | **446** | 8.5 [7.6-9.4] |
| *Mali N=8837 | 79 | 0.9 [0.7-1.1] | 170 | 1.9 [1.6-2.2] | 9 | 0.1 [0.03-0.2] | 37 | 0.4 [0.3-0.6] | 3 | 0.03 [-0.004-0.] | **298** | 3.4 [2.9-3.9] |
| *Niger N=8213 | 532 | 6.4 [5.8-7.0] | 1094 | 13.3 [12.5-14.1] | 13 | 0.2 [0.1-0.2] | 3 | 0.04 [-0.005-0.01] | 2 | 0.02 [-0.01-0.05] | **1644** | 19.9 [18.9-20.9] |
| Senegal N=4409 | 356 | 8.0 [7.1-9.0] | 372 | 8.4 [7.4-9.3] | 39 | 0.9 [0.6-1.2] | 0 | - | 6 | 0.1 [0.03-0.2] | **773** | 17.5 [16.1418.8] |
| **Total** | **1679** | **3.6 [3.4-3.8]** | **2588** | **5.6 [5.3-5.8]** | **290** | **0.6 [0.5-0.7]** | **113** | **0.2 [0.2-0.3]** | **24** | **0.05 [0.03-0.1]** | **4694** | **10.2 [9.8-10.5]** |

N corresponds to the total number of subject studied; CI: Confidence Interval
*Countries that received the serogroup A conjugate vaccine (MenAfriVac) during the study

**Table S2: Frequency of *f_rplf* alleles by species**

| *f_rplF* | *Neisseria bergeri* | *Neisseria lactamica* | *Neisseria meningitidis* | *Neisseria polysaccharea* | *Neisseria subflava* | Total |
|---|---|---|---|---|---|---|
| 6 | - | 1453 | - | - | - | 1453 |
| 2 | - | - | 749 | - | - | 749 |
| 1 | - | - | 707 | - | - | 707 |
| 52 | - | 453 | - | - | - | 453 |
| 33 | - | 318 | - | - | - | 318 |
| 9 | - | - | - | 207 | - | 207 |
| 32 | - | 186 | - | - | - | 186 |
| 34 | - | 132 | - | - | - | 132 |
| 67 | - | - | 83 | - | - | 83 |
| 63 | - | - | - | 72 | - | 72 |
| 4 | - | - | 62 | - | - | 62 |
| 62 | 57 | - | - | - | - | 57 |
| 69 | 46 | - | - | - | - | 46 |
| 88 | - | - | 41 | - | - | 41 |
| 3 | - | - | 15 | - | - | 15 |
| 43 | - | - | - | - | 15 | 15 |
| 8 | - | - | 10 | - | - | 10 |
| 112 | 9 | - | - | - | - | 9 |
| 51 | - | 8 | - | - | - | 8 |
| 80 | - | 7 | - | - | - | 7 |
| 86 | - | 6 | - | - | - | 6 |
| 90 | - | - | - | 6 | - | 6 |
| 18 | - | - | 5 | - | - | 5 |
| 65 | - | 5 | - | - | - | 5 |
| 81 | - | 5 | - | - | - | 5 |
| 96 | - | - | - | 5 | - | 5 |
| 113 | - | 4 | - | - | - | 4 |
| 64 | - | - | 3 | - | - | 3 |
| 82 | - | - | - | - | 3 | 3 |
| 91 | - | - | 3 | - | - | 3 |
| 92 | - | 3 | - | - | - | 3 |
| 94 | - | 3 | - | - | - | 3 |
| 97 | - | - | - | - | 2 | 2 |
| 111 | - | 2 | - | - | - | 2 |
| 0 | - | - | 1 | - | - | 1 |
| 16 | 1 | - | - | - | - | 1 |
| 31 | - | - | - | - | 1 | 1 |
| 38 | - | - | - | - | 1 | 1 |
| 58 | - | - | - | - | 1 | 1 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 85 | - | 1 | - | - | - | 1 |
| 89 | - | 1 | - | - | - | 1 |
| 93 | - | 1 | - | - | - | 1 |
| 95 | - | - | - | - | 1 | 1 |
| Total | 113 | 2588 | 1679 | 290 | 24 | 4694 |

**TableS3: Frequency of *feta_VR* alleles by countries**

| *fetA_VR* | Chad | Ethiopia | Ghana | Mali | Niger | Senegal | Total |
|---|---|---|---|---|---|---|---|
| ND | 92 | 109 | 48 | 80 | 278 | 36 | 643 |
| *fnl* | 31 | 135 | 2 | 10 | 321 | 20 | 519 |
| F1-1 | 2 | 4 | 77 | 6 | 132 | 239 | 460 |
| F1-31 | 15 | 15 | 2 | 1 | 199 | 3 | 235 |
| F5-1 | 13 | 1 | 95 | 8 | 17 | 4 | 138 |
| F1-62 | 10 | - | 79 | 9 | 30 | 2 | 130 |
| F1-72 | 2 | 5 | 1 | 9 | 34 | 42 | 93 |
| F1-29 | 14 | 26 | 3 | 2 | 25 | 21 | 91 |
| F1-3 | 4 | 42 | 3 | 6 | 4 | 30 | 89 |
| F1-21 | 37 | 24 | - | - | 19 | - | 80 |
| F4-5 | 7 | 4 | 13 | 3 | 23 | 16 | 66 |
| F4-6 | 15 | 1 | 1 | 4 | 32 | 12 | 65 |
| F1-100 | 3 | - | 7 | 1 | 16 | 32 | 59 |
| F5-133 | 6 | 3 | - | 2 | 2 | 44 | 57 |
| F2-24 | 2 | 42 | 4 | 2 | 1 | 5 | 56 |
| F5-34 | 20 | 14 | 1 | 6 | 10 | 3 | 54 |
| F3-1 | 44 | 1 | - | - | - | 7 | 52 |
| F6-3 | 1 | - | - | 30 | 5 | 16 | 52 |
| F7-3 | 2 | 44 | - | - | 3 | - | 49 |
| F3-60 | - | 47 | - | - | - | - | 47 |
| F6-2 | 12 | 3 | 1 | 2 | 20 | 8 | 46 |
| F4-17 | 14 | - | 9 | - | 19 | 3 | 45 |
| F1-24 | 8 | 11 | - | - | 25 | - | 44 |
| F5-84 | 4 | - | 2 | 22 | 2 | 13 | 43 |
| F1-120 | 14 | - | 1 | 3 | 22 | 1 | 41 |
| F5-12 | 8 | 2 | 3 | 9 | 13 | 3 | 38 |
| F2-17 | - | - | - | 1 | 34 | 2 | 37 |
| F3-22 | 5 | 10 | - | 4 | 14 | 2 | 35 |
| F1-155 | 10 | - | 4 | 17 | - | 3 | 34 |
| F5-5 | 1 | 27 | 2 | - | - | 4 | 34 |
| F2-23 | 3 | - | 6 | 1 | 20 | 3 | 33 |
| F1-101 | 16 | - | 3 | 2 | 11 | - | 32 |
| F1-153 | 12 | 17 | - | - | 1 | 1 | 31 |
| F1-160 | 15 | - | 1 | 1 | 11 | 2 | 30 |
| F4-19 | 21 | 4 | - | - | 4 | - | 29 |
| F1-7 | - | 20 | 1 | - | 3 | 4 | 28 |
| F5-66 | 14 | - | 6 | 1 | 5 | 2 | 28 |
| F1-145 | 9 | 9 | 1 | 2 | 6 | - | 27 |
| F1-38 | - | - | - | 3 | 1 | 23 | 27 |
| F5-18 | 10 | - | 9 | - | 8 | - | 27 |
| F4-23 | 14 | 9 | 2 | - | 1 | - | 26 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| F5-88 | 6 | - | 1 | - | 13 | 6 | 26 |
| F1-104 | 3 | - | 11 | 2 | - | 9 | 25 |
| F1-58 | - | - | - | 6 | 3 | 16 | 25 |
| F1-84 | 2 | 11 | - | 1 | 11 | - | 25 |
| F11-4 | - | 25 | - | - | - | - | 25 |
| F1-156 | 5 | - | 2 | 4 | 6 | 4 | 21 |
| F1-46 | - | - | - | - | 21 | - | 21 |
| F1-49 | 7 | 6 | - | - | 6 | 2 | 21 |
| F3-57 | - | - | - | 2 | 17 | 1 | 20 |
| F4-28 | 3 | 2 | 1 | - | 11 | 3 | 20 |
| F1-186 | 3 | 10 | - | - | 6 | - | 19 |
| F5-127 | 2 | 4 | 1 | 1 | 5 | 6 | 19 |
| F4-2 | - | - | - | 1 | - | 17 | 18 |
| F5-25 | 1 | - | - | - | 17 | - | 18 |
| F3-3 | 6 | 6 | 1 | 3 | - | 1 | 17 |
| F5-69 | 4 | 1 | 6 | - | 5 | 1 | 17 |
| F5-8 | - | 14 | 2 | - | - | - | 16 |
| F6-7 | - | 16 | - | - | - | - | 16 |
| F1-173 | 10 | - | - | - | 4 | - | 14 |
| F1-35 | - | 8 | - | - | 6 | - | 14 |
| F1-81 | - | - | - | - | - | 14 | 14 |
| F3-56 | - | - | 2 | - | 12 | - | 14 |
| F4-1 | 1 | 7 | - | 1 | - | 5 | 14 |
| F1-89 | 1 | - | - | - | 10 | 1 | 12 |
| F3-43 | 4 | 4 | - | 1 | 1 | 2 | 12 |
| F5-101 | - | - | - | 1 | 8 | 2 | 11 |
| F5-140 | 6 | - | 1 | - | 4 | - | 11 |
| F6-6 | 1 | 4 | - | - | 6 | - | 11 |
| F1-28 | - | 8 | 1 | - | 1 | - | 10 |
| F3-18 | - | 9 | - | 1 | - | - | 10 |
| F5-77 | 1 | - | - | - | 8 | 1 | 10 |
| F1-197 | - | - | - | - | 6 | 3 | 9 |
| F4-51 | 2 | - | - | 2 | 5 | - | 9 |
| F5-24 | - | - | - | 8 | 1 | - | 9 |
| F1-22 | 8 | - | - | - | - | - | 8 |
| F3-12 | 2 | 1 | - | - | - | 5 | 8 |
| F5-149 | - | - | 4 | - | 4 | - | 8 |
| F5-9 | 1 | 5 | 2 | - | - | - | 8 |
| F1-174 | 7 | - | - | - | - | - | 7 |
| F1-192 | - | - | - | - | 6 | 1 | 7 |
| F2-14 | - | 6 | - | - | - | 1 | 7 |
| F2-6 | - | - | - | - | - | 7 | 7 |
| F4-38 | 5 | - | 1 | - | 1 | - | 7 |
| F5-70 | 4 | - | 1 | - | 2 | - | 7 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| F5-87 | 1 | - | - | - | 6 | - | 7 |
| F1-170 | 6 | - | - | - | - | - | 6 |
| F1-172 | 4 | - | - | - | 2 | - | 6 |
| F1-5 | 2 | 2 | 1 | - | - | 1 | 6 |
| F2-32 | - | - | - | - | - | 6 | 6 |
| F7-2 | 5 | - | - | - | 1 | - | 6 |
| F1-183 | - | - | 2 | - | 2 | 1 | 5 |
| F1-20 | - | 5 | - | - | - | - | 5 |
| F1-209 | - | - | 4 | - | 1 | - | 5 |
| F1-55 | - | 5 | - | - | - | - | 5 |
| F3-28 | - | - | - | - | 4 | 1 | 5 |
| F5-132 | 3 | - | - | 1 | 1 | - | 5 |
| F5-17 | 1 | 2 | - | - | - | 2 | 5 |
| F5-71 | - | - | - | 3 | 1 | 1 | 5 |
| F6-4 | - | - | - | 1 | - | 4 | 5 |
| F1-152 | 4 | - | - | - | - | - | 4 |
| F1-177 | 4 | - | - | - | - | - | 4 |
| F1-189 | - | - | 4 | - | - | - | 4 |
| F1-47 | - | 1 | - | - | 3 | - | 4 |
| F1-51 | - | 4 | - | - | - | - | 4 |
| F1-80 | - | 1 | - | - | - | 3 | 4 |
| F1-96 | 4 | - | - | - | - | - | 4 |
| F11-3 | 1 | - | 3 | - | - | - | 4 |
| F2-9 | - | 4 | - | - | - | - | 4 |
| F5-137 | - | - | - | - | - | 4 | 4 |
| F5-145 | 4 | - | - | - | - | - | 4 |
| F5-4 | - | 1 | - | - | 2 | 1 | 4 |
| F5-59 | - | 4 | - | - | - | - | 4 |
| F5-91 | 2 | 2 | - | - | - | - | 4 |
| F1-176 | 1 | - | - | - | 2 | - | 3 |
| F1-181 | 3 | - | - | - | - | - | 3 |
| F1-182 | 3 | - | - | - | - | - | 3 |
| F1-184 | - | 3 | - | - | - | - | 3 |
| F1-187 | - | 1 | - | - | 2 | - | 3 |
| F1-196 | - | - | - | - | 2 | 1 | 3 |
| F1-37 | - | - | - | 1 | - | 2 | 3 |
| F1-52 | - | - | - | - | - | 3 | 3 |
| F11-1 | 1 | - | - | 2 | - | - | 3 |
| F11-7 | 2 | - | - | - | 1 | - | 3 |
| F2-31 | - | 3 | - | - | - | - | 3 |
| F3-6 | - | - | - | - | - | 3 | 3 |
| F3-9 | 1 | 2 | - | - | - | - | 3 |
| F5-134 | - | 3 | - | - | - | - | 3 |
| F5-142 | 1 | - | - | - | 2 | - | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| F5-146 | 3 | - | - | - | - | - | 3 |
| F5-95 | - | - | - | 1 | - | 2 | 3 |
| F1-158 | - | - | - | 2 | - | - | 2 |
| F1-175 | 2 | - | - | - | - | - | 2 |
| F1-178 | 2 | - | - | - | - | - | 2 |
| F1-18 | - | 2 | - | - | - | - | 2 |
| F1-190 | - | - | 2 | - | - | - | 2 |
| F1-199 | - | - | - | - | 2 | - | 2 |
| F1-2 | 2 | - | - | - | - | - | 2 |
| F1-200 | - | - | - | - | 2 | - | 2 |
| F1-64 | - | 2 | - | - | - | - | 2 |
| F1-90 | - | - | - | 2 | - | - | 2 |
| F11-2 | - | - | 1 | - | 1 | - | 2 |
| F11-5 | - | - | - | - | 1 | 1 | 2 |
| F11-8 | 2 | - | - | - | - | - | 2 |
| F2-12 | 2 | - | - | - | - | - | 2 |
| F2-13 | 2 | - | - | - | - | - | 2 |
| F3-13 | - | 2 | - | - | - | - | 2 |
| F3-59 | 2 | - | - | - | - | - | 2 |
| F4-57 | - | - | 2 | - | - | - | 2 |
| F4-60 | - | 2 | - | - | - | - | 2 |
| F4-63 | - | - | - | - | 2 | - | 2 |
| F4-64 | - | - | - | - | 2 | - | 2 |
| F4-65 | - | - | - | - | 2 | - | 2 |
| F4-66 | - | - | - | - | 2 | - | 2 |
| F5-143 | 2 | - | - | - | - | - | 2 |
| F5-151 | - | 2 | - | - | - | - | 2 |
| F5-154 | - | - | - | - | - | 2 | 2 |
| F5-155 | - | - | - | - | - | 2 | 2 |
| F5-160 | - | - | - | - | 2 | - | 2 |
| F5-19 | - | - | - | - | - | 2 | 2 |
| F1-119 | - | - | - | - | - | 1 | 1 |
| F1-15 | 1 | - | - | - | - | - | 1 |
| F1-157 | - | - | - | 1 | - | - | 1 |
| F1-159 | - | - | - | 1 | - | - | 1 |
| F1-167 | - | - | - | 1 | - | - | 1 |
| F1-169 | 1 | - | - | - | - | - | 1 |
| F1-171 | 1 | - | - | - | - | - | 1 |
| F1-179 | 1 | - | - | - | - | - | 1 |
| F1-180 | 1 | - | - | - | - | - | 1 |
| F1-185 | - | 1 | - | - | - | - | 1 |
| F1-188 | - | 1 | - | - | - | - | 1 |
| F1-19 | - | - | 1 | - | - | - | 1 |
| F1-191 | - | - | - | - | - | 1 | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| F1-193 | - | - | - | - | - | 1 | 1 |
| F1-194 | - | - | - | - | - | 1 | 1 |
| F1-195 | - | - | - | - | - | 1 | 1 |
| F1-198 | - | - | - | - | 1 | - | 1 |
| F1-201 | - | - | - | - | 1 | - | 1 |
| F1-202 | - | - | - | - | 1 | - | 1 |
| F1-203 | - | - | - | - | 1 | - | 1 |
| F1-204 | - | - | - | - | 1 | - | 1 |
| F1-205 | - | - | - | - | 1 | - | 1 |
| F1-206 | - | - | - | - | 1 | - | 1 |
| F1-207 | - | - | - | - | 1 | - | 1 |
| F1-208 | - | - | - | - | 1 | - | 1 |
| F1-33 | - | - | - | - | - | 1 | 1 |
| F1-68 | - | 1 | - | - | - | - | 1 |
| F1-94 | - | - | - | - | - | 1 | 1 |
| F1-99 | - | 1 | - | - | - | - | 1 |
| F10-1 | 1 | - | - | - | - | - | 1 |
| F11-6 | - | - | - | - | 1 | - | 1 |
| F2-33 | - | - | - | - | 1 | - | 1 |
| F2-7 | - | - | - | - | 1 | - | 1 |
| F3-5 | - | 1 | - | - | - | - | 1 |
| F3-61 | - | 1 | - | - | - | - | 1 |
| F3-62 | - | 1 | - | - | - | - | 1 |
| F3-63 | - | - | - | - | - | 1 | 1 |
| F3-64 | - | - | - | - | - | 1 | 1 |
| F3-65 | - | - | - | - | 1 | - | 1 |
| F3-66 | - | 1 | - | - | - | - | 1 |
| F4-12 | - | - | - | - | 1 | - | 1 |
| F4-21 | - | - | - | - | - | 1 | 1 |
| F4-24 | 1 | - | - | - | - | - | 1 |
| F4-25 | - | - | - | - | - | 1 | 1 |
| F4-58 | - | - | 1 | - | - | - | 1 |
| F4-59 | - | 1 | - | - | - | - | 1 |
| F4-61 | - | - | - | - | - | 1 | 1 |
| F4-62 | - | - | - | - | - | 1 | 1 |
| F5-115 | - | - | - | - | 1 | - | 1 |
| F5-118 | 1 | - | - | - | - | - | 1 |
| F5-13 | - | - | - | - | - | 1 | 1 |
| F5-131 | - | - | - | 1 | - | - | 1 |
| F5-139 | 1 | - | - | - | - | - | 1 |
| F5-141 | 1 | - | - | - | - | - | 1 |
| F5-144 | 1 | - | - | - | - | - | 1 |
| F5-147 | 1 | - | - | - | - | - | 1 |
| F5-150 | - | 1 | - | - | - | - | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| F5-152 | - | - | 1 | - | - | - | 1 |
| F5-153 | - | - | - | - | - | 1 | 1 |
| F5-156 | - | - | - | - | - | 1 | 1 |
| F5-157 | - | - | - | - | 1 | - | 1 |
| F5-158 | - | - | - | - | 1 | - | 1 |
| F5-159 | - | - | - | - | 1 | - | 1 |
| F5-161 | 1 | - | - | - | - | - | 1 |
| F5-162 | - | - | - | - | 1 | - | 1 |
| F5-163 | - | - | - | - | 1 | - | 1 |
| F5-164 | 1 | - | - | - | - | - | 1 |
| F5-165 | 1 | - | - | - | - | - | 1 |
| F5-166 | 1 | - | - | - | - | - | 1 |
| F5-2 | - | - | - | - | - | 1 | 1 |
| F5-67 | 1 | - | - | - | - | - | 1 |
| F5-68 | - | 1 | - | - | - | - | 1 |
| F5-81 | - | 1 | - | - | - | - | 1 |
| F6-5 | - | - | - | 1 | - | - | 1 |
| F7-4 | 1 | - | - | - | - | - | 1 |
| Total | 715 | 841 | 446 | 299 | 1645 | 773 | 4699 |

**Table S4: Frequency of *fetA_VR* alleles by survey**

| *fetA_VR* | survey 1 | survey 2 | survey 3 | Total |
|---|---|---|---|---|
| ND | 247 | 221 | 175 | 643 |
| *fnl* | 280 | 104 | 130 | 514 |
| F1-1 | 56 | 61 | 342 | 459 |
| F1-31 | 122 | 65 | 48 | 235 |
| F5-1 | 26 | 68 | 44 | 138 |
| F1-62 | 27 | 67 | 36 | 130 |
| F1-72 | 36 | 42 | 15 | 93 |
| F1-29 | 32 | 34 | 25 | 91 |
| F1-3 | 28 | 43 | 18 | 89 |
| F1-21 | 19 | 39 | 22 | 80 |
| F4-5 | 25 | 22 | 19 | 66 |
| F4-6 | 30 | 18 | 17 | 65 |
| F1-100 | 16 | 25 | 18 | 59 |
| F5-133 | 19 | 22 | 16 | 57 |
| F2-24 | 9 | 27 | 19 | 55 |
| F5-34 | 15 | 27 | 12 | 54 |
| F3-1 | 10 | 40 | 2 | 52 |
| F6-3 | 9 | 14 | 29 | 52 |
| F7-3 | 15 | 13 | 20 | 48 |
| F3-60 | 6 | 24 | 17 | 47 |
| F6-2 | 18 | 12 | 16 | 46 |
| F4-17 | 11 | 17 | 17 | 45 |
| F1-24 | 9 | 23 | 12 | 44 |
| F5-84 | 22 | 9 | 12 | 43 |
| F1-120 | 16 | 17 | 8 | 41 |
| F2-17 | 26 | 4 | 7 | 37 |
| F5-12 | 20 | 9 | 8 | 37 |
| F3-22 | 18 | 9 | 8 | 35 |
| F1-155 | 15 | 14 | 5 | 34 |
| F5-5 | 16 | 11 | 7 | 34 |
| F2-23 | 12 | 15 | 6 | 33 |
| F1-101 | 5 | 18 | 9 | 32 |
| F1-153 | 4 | 17 | 10 | 31 |
| F1-160 | 5 | 11 | 14 | 30 |
| F4-19 | 2 | 23 | 4 | 29 |
| F1-7 | 12 | 9 | 7 | 28 |
| F5-66 | 4 | 15 | 9 | 28 |
| F1-145 | 6 | 13 | 8 | 27 |
| F1-38 | 8 | 16 | 3 | 27 |

| | | | | |
|---|---|---|---|---|
| F5-18 | 3 | 13 | 11 | 27 |
| F4-23 | 7 | 10 | 9 | 26 |
| F5-88 | 7 | 5 | 14 | 26 |
| F1-104 | 2 | 11 | 12 | 25 |
| F1-58 | 11 | 10 | 4 | 25 |
| F1-84 | 8 | 5 | 12 | 25 |
| F11-4 | 12 | 7 | 6 | 25 |
| F1-156 | 7 | 12 | 2 | 21 |
| F1-46 | 11 | 2 | 8 | 21 |
| F1-49 | 7 | 8 | 6 | 21 |
| F3-57 | 10 | 9 | 1 | 20 |
| F4-28 | 8 | 9 | 3 | 20 |
| F5-127 | 8 | 7 | 4 | 19 |
| F1-186 | 5 | 8 | 5 | 18 |
| F4-2 | 5 | 13 | - | 18 |
| F5-25 | 13 | 5 | - | 18 |
| F3-3 | 4 | 11 | 2 | 17 |
| F5-69 | 2 | 13 | 2 | 17 |
| F5-8 | 12 | 4 | - | 16 |
| F6-7 | 7 | 5 | 4 | 16 |
| F1-173 | 1 | 9 | 4 | 14 |
| F1-35 | 7 | 3 | 4 | 14 |
| F1-81 | 4 | 8 | 2 | 14 |
| F3-56 | 5 | 4 | 5 | 14 |
| F4-1 | 6 | 5 | 3 | 14 |
| F1-89 | 9 | 3 | - | 12 |
| F3-43 | 6 | 6 | - | 12 |
| F5-101 | 6 | 4 | 1 | 11 |
| F5-140 | 3 | 5 | 3 | 11 |
| F6-6 | 1 | 4 | 6 | 11 |
| F1-28 | - | 8 | 2 | 10 |
| F3-18 | 3 | 5 | 2 | 10 |
| F5-77 | 3 | 3 | 4 | 10 |
| F1-197 | 6 | 1 | 2 | 9 |
| F4-51 | 4 | 4 | 1 | 9 |
| F5-24 | 5 | 4 | - | 9 |
| F1-22 | 1 | 6 | 1 | 8 |
| F3-12 | 1 | 5 | 2 | 8 |
| F5-149 | 3 | 4 | 1 | 8 |
| F5-9 | 2 | 4 | 2 | 8 |
| F1-174 | - | 3 | 4 | 7 |
| F1-192 | 5 | - | 2 | 7 |
| F2-14 | 1 | 2 | 4 | 7 |
| F2-6 | 1 | 4 | 2 | 7 |

| | | | | |
|---|---|---|---|---|
| F4-38 | - | 5 | 2 | 7 |
| F5-70 | - | 6 | 1 | 7 |
| F5-87 | 3 | 3 | 1 | 7 |
| F1-170 | 1 | 5 | - | 6 |
| F1-172 | 2 | 3 | 1 | 6 |
| F1-5 | - | 4 | 2 | 6 |
| F2-32 | 3 | 2 | 1 | 6 |
| F7-2 | - | 4 | 2 | 6 |
| F1-183 | 2 | 2 | 1 | 5 |
| F1-20 | - | 3 | 2 | 5 |
| F1-209 | 1 | - | 4 | 5 |
| F1-55 | 3 | 2 | - | 5 |
| F3-28 | 2 | - | 3 | 5 |
| F5-132 | - | 4 | 1 | 5 |
| F5-17 | 2 | 2 | 1 | 5 |
| F5-71 | 2 | 2 | 1 | 5 |
| F6-4 | 2 | - | 3 | 5 |
| F1-152 | - | 1 | 3 | 4 |
| F1-177 | - | 2 | 2 | 4 |
| F1-189 | - | 1 | 3 | 4 |
| F1-47 | - | 1 | 3 | 4 |
| F1-51 | - | 3 | 1 | 4 |
| F1-80 | 2 | 2 | - | 4 |
| F1-96 | - | 2 | 2 | 4 |
| F11-3 | - | 4 | - | 4 |
| F2-9 | 2 | 2 | - | 4 |
| F5-137 | - | 1 | 3 | 4 |
| F5-145 | - | 2 | 2 | 4 |
| F5-4 | 2 | 1 | 1 | 4 |
| F5-59 | - | - | 4 | 4 |
| F5-91 | - | 2 | 2 | 4 |
| F1-176 | 1 | 2 | - | 3 |
| F1-181 | - | 3 | - | 3 |
| F1-182 | - | 3 | - | 3 |
| F1-184 | 1 | - | 2 | 3 |
| F1-187 | 2 | 1 | - | 3 |
| F1-196 | - | 1 | 2 | 3 |
| F1-37 | 1 | 2 | - | 3 |
| F1-52 | - | 3 | - | 3 |
| F11-1 | 1 | 1 | 1 | 3 |
| F11-7 | - | 2 | 1 | 3 |
| F2-31 | - | 2 | 1 | 3 |
| F3-6 | 3 | - | - | 3 |
| F3-9 | 1 | 1 | 1 | 3 |

| | | | | |
|---|---|---|---|---|
| F5-134 | 1 | 1 | 1 | 3 |
| F5-142 | - | 2 | 1 | 3 |
| F5-146 | - | 2 | 1 | 3 |
| F5-95 | - | - | 3 | 3 |
| F1-158 | - | 2 | - | 2 |
| F1-175 | - | 2 | - | 2 |
| F1-178 | - | 1 | 1 | 2 |
| F1-18 | 2 | - | - | 2 |
| F1-190 | - | - | 2 | 2 |
| F1-199 | 2 | - | - | 2 |
| F1-2 | 1 | 1 | - | 2 |
| F1-200 | 1 | - | 1 | 2 |
| F1-64 | 1 | 1 | - | 2 |
| F1-90 | - | 1 | 1 | 2 |
| F11-2 | - | - | 2 | 2 |
| F11-5 | - | 1 | 1 | 2 |
| F11-8 | - | 2 | - | 2 |
| F2-12 | - | 1 | 1 | 2 |
| F2-13 | - | - | 2 | 2 |
| F3-13 | 2 | - | - | 2 |
| F3-59 | - | 2 | - | 2 |
| F4-57 | - | 2 | - | 2 |
| F4-60 | - | 1 | 1 | 2 |
| F4-63 | 2 | - | - | 2 |
| F4-64 | 2 | - | - | 2 |
| F4-65 | 1 | 1 | - | 2 |
| F4-66 | - | 2 | - | 2 |
| F5-143 | - | 1 | 1 | 2 |
| F5-151 | - | - | 2 | 2 |
| F5-154 | - | 2 | - | 2 |
| F5-155 | - | 1 | 1 | 2 |
| F5-160 | 1 | - | 1 | 2 |
| F5-19 | - | 2 | - | 2 |
| F1-119 | - | 1 | - | 1 |
| F1-15 | 1 | - | - | 1 |
| F1-157 | - | 1 | - | 1 |
| F1-159 | 1 | - | - | 1 |
| F1-167 | 1 | - | - | 1 |
| F1-169 | 1 | - | - | 1 |
| F1-171 | - | 1 | - | 1 |
| F1-179 | - | - | 1 | 1 |
| F1-180 | - | - | 1 | 1 |
| F1-185 | - | 1 | - | 1 |
| F1-188 | - | - | 1 | 1 |

| | | | | |
|---|---|---|---|---|
| F1-19 | - | - | 1 | 1 |
| F1-191 | 1 | - | - | 1 |
| F1-193 | 1 | - | - | 1 |
| F1-194 | 1 | - | - | 1 |
| F1-195 | 1 | - | - | 1 |
| F1-198 | 1 | - | - | 1 |
| F1-201 | 1 | - | - | 1 |
| F1-202 | 1 | - | - | 1 |
| F1-203 | 1 | - | - | 1 |
| F1-204 | 1 | - | - | 1 |
| F1-205 | - | - | 1 | 1 |
| F1-206 | - | - | 1 | 1 |
| F1-207 | 1 | - | - | 1 |
| F1-208 | 1 | - | - | 1 |
| F1-33 | 1 | - | - | 1 |
| F1-68 | - | - | 1 | 1 |
| F1-94 | - | - | 1 | 1 |
| F1-99 | - | - | 1 | 1 |
| F10-1 | - | - | 1 | 1 |
| F11-6 | - | 1 | - | 1 |
| F2-33 | - | 1 | - | 1 |
| F2-7 | 1 | - | - | 1 |
| F3-5 | - | 1 | - | 1 |
| F3-61 | - | 1 | - | 1 |
| F3-62 | - | - | 1 | 1 |
| F3-63 | - | 1 | - | 1 |
| F3-64 | - | - | 1 | 1 |
| F3-65 | 1 | - | - | 1 |
| F3-66 | - | - | - | 1 |
| F4-12 | 1 | - | - | 1 |
| F4-21 | - | 1 | - | 1 |
| F4-24 | - | - | 1 | 1 |
| F4-25 | 1 | - | - | 1 |
| F4-58 | - | - | 1 | 1 |
| F4-59 | 1 | - | - | 1 |
| F4-61 | - | - | - | 1 |
| F4-62 | - | - | 1 | 1 |
| F5-115 | 1 | - | - | 1 |
| F5-118 | - | 1 | - | 1 |
| F5-13 | - | 1 | - | 1 |
| F5-131 | - | 1 | - | 1 |
| F5-139 | - | 1 | - | 1 |
| F5-141 | - | 1 | - | 1 |
| F5-144 | - | 1 | - | 1 |

| | | | | |
|---|---|---|---|---|
| F5-147 | - | - | 1 | 1 |
| F5-150 | - | 1 | - | 1 |
| F5-152 | - | 1 | - | 1 |
| F5-153 | 1 | - | - | 1 |
| F5-156 | - | - | 1 | 1 |
| F5-157 | 1 | - | - | 1 |
| F5-158 | 1 | - | - | 1 |
| F5-159 | - | 1 | - | 1 |
| F5-161 | 1 | - | - | 1 |
| F5-162 | 1 | - | - | 1 |
| F5-163 | 1 | - | - | 1 |
| F5-164 | - | 1 | - | 1 |
| F5-165 | - | 1 | - | 1 |
| F5-166 | - | - | 1 | 1 |
| F5-2 | 1 | - | - | 1 |
| F5-67 | - | 1 | - | 1 |
| F5-68 | - | 1 | - | 1 |
| F5-81 | - | - | 1 | 1 |
| F6-5 | - | 1 | - | 1 |
| F7-4 | - | - | 1 | 1 |
| *fnl*;F1-1 | 1 | - | - | 1 |
| *fnl*;F1-186 | - | 1 | - | 1 |
| *fnl*;F2-24 | - | 1 | - | 1 |
| *fnl*;F5-12 | - | - | 1 | 1 |
| *fnl*;F7-3 | - | 1 | - | 1 |
| Total | 1,573 | 1,660 | 1,461 | 4,694 |

**Table S5: Frequency of *fetA_VR* alleles by species**

| *fetA_VR* allele | *Neisseria bergeri* | *Neisseria lactamica* | *Neisseria meningitidis* | *Neisseria polysaccharea* | *Neisseria subflava* | Total |
|---|---|---|---|---|---|---|
| ND | 67 | 375 | 118 | 75 | 7 | 642 |
| *fnl* | - | 2 | 517 | - | - | 519 |
| F1-1 | - | 1 | 459 | - | - | 460 |
| F1-31 | 1 | 229 | 3 | - | 2 | 235 |
| F5-1 | - | - | 138 | - | - | 138 |
| F1-62 | 4 | 122 | 2 | 1 | 1 | 130 |
| F1-72 | - | 63 | 3 | 27 | - | 93 |
| F1-29 | - | 90 | 1 | - | - | 91 |
| F1-3 | - | 7 | 81 | 1 | - | 89 |
| F1-21 | - | 66 | 11 | 2 | 1 | 80 |
| F4-5 | 2 | 59 | 5 | - | - | 66 |
| F4-6 | - | 56 | 3 | 5 | 1 | 65 |
| F1-100 | - | 58 | - | - | 1 | 59 |
| F5-133 | - | 54 | 3 | - | - | 57 |
| F2-24 | 1 | 13 | 10 | 32 | - | 56 |
| F5-34 | - | 50 | 3 | 1 | - | 54 |
| F3-1 | - | - | 52 | - | - | 52 |
| F6-3 | - | 25 | 25 | 2 | - | 52 |
| F7-3 | - | 3 | 2 | 44 | - | 49 |
| F3-60 | - | 46 | 1 | - | - | 47 |
| F6-2 | 3 | 36 | 1 | 5 | 1 | 46 |
| F4-17 | - | 44 | 1 | - | - | 45 |
| F1-24 | - | 43 | 1 | - | - | 44 |
| F5-84 | - | 43 | - | - | - | 43 |
| F1-120 | - | 40 | - | - | 1 | 41 |
| F5-12 | - | 35 | 3 | - | - | 38 |
| F2-17 | - | 37 | - | - | - | 37 |
| F3-22 | 1 | 24 | 10 | - | - | 35 |
| F1-155 | - | 34 | - | - | - | 34 |
| F5-5 | - | - | 34 | - | - | 34 |
| F2-23 | 1 | 30 | 2 | - | - | 33 |
| F1-101 | 4 | 28 | - | - | - | 32 |
| F1-153 | - | 20 | 6 | 5 | - | 31 |
| F1-160 | 1 | 28 | - | - | 1 | 30 |
| F4-19 | - | 28 | - | - | 1 | 29 |
| F5-66 | - | 16 | 12 | - | - | 28 |
| F1-7 | - | 1 | 27 | - | - | 28 |
| F5-18 | - | 27 | - | - | - | 27 |

| | | | | | | |
|---|---|---|---|---|---|---|
| F1-38 | - | 25 | 2 | - | - | 27 |
| F1-145 | 2 | 18 | - | 7 | - | 27 |
| F5-88 | 1 | 25 | - | - | - | 26 |
| F4-23 | - | 2 | 24 | - | - | 26 |
| F1-84 | - | 22 | 2 | - | 1 | 25 |
| F1-58 | 2 | 20 | - | 3 | - | 25 |
| F1-104 | 7 | 16 | 1 | 1 | - | 25 |
| F11-4 | - | - | - | 25 | - | 25 |
| F1-46 | - | 21 | - | - | - | 21 |
| F1-49 | - | 19 | 2 | - | - | 21 |
| F1-156 | - | 16 | 2 | 3 | - | 21 |
| F3-57 | - | 20 | - | - | - | 20 |
| F4-28 | - | 13 | 4 | 3 | - | 20 |
| F1-186 | - | 18 | 1 | - | - | 19 |
| F5-127 | - | 14 | 4 | 1 | - | 19 |
| F4-2 | - | 18 | - | - | - | 18 |
| F5-25 | - | 18 | - | - | - | 18 |
| F3-3 | - | 15 | 2 | - | - | 17 |
| F5-69 | 3 | 11 | 3 | - | - | 17 |
| F5-8 | - | - | 16 | - | - | 16 |
| F6-7 | - | - | - | 16 | - | 16 |
| F3-56 | - | 14 | - | - | - | 14 |
| F1-81 | - | 12 | 1 | 1 | - | 14 |
| F1-173 | - | 11 | - | 3 | - | 14 |
| F1-35 | - | 11 | 3 | - | - | 14 |
| F4-1 | - | - | 14 | - | - | 14 |
| F1-89 | - | 12 | - | - | - | 12 |
| F3-43 | - | 10 | 1 | 1 | - | 12 |
| F5-101 | - | 11 | - | - | - | 11 |
| F5-140 | - | 11 | - | - | - | 11 |
| F6-6 | - | 9 | - | 2 | - | 11 |
| F1-28 | - | 10 | - | - | - | 10 |
| F3-18 | - | 10 | - | - | - | 10 |
| F5-77 | - | 10 | - | - | - | 10 |
| F1-197 | - | 9 | - | - | - | 9 |
| F5-24 | - | 8 | - | - | 1 | 9 |
| F4-51 | 2 | 7 | - | - | - | 9 |
| F1-22 | - | 8 | - | - | - | 8 |
| F3-12 | - | 8 | - | - | - | 8 |
| F5-149 | - | 5 | - | 3 | - | 8 |
| F5-9 | - | 3 | 5 | - | - | 8 |
| F1-192 | - | 7 | - | - | - | 7 |
| F2-6 | - | 7 | - | - | - | 7 |
| F5-70 | - | 7 | - | - | - | 7 |

| | | | | | | |
|---|---|---|---|---|---|---|
| F2-14 | - | 6 | 1 | - | - | 7 |
| F4-38 | - | 6 | - | - | 1 | 7 |
| F5-87 | - | 6 | 1 | - | - | 7 |
| F1-174 | - | 1 | - | 6 | - | 7 |
| F1-170 | - | 6 | - | - | - | 6 |
| F1-172 | - | 6 | - | - | - | 6 |
| F1-5 | - | - | 6 | - | - | 6 |
| F2-32 | - | 5 | 1 | - | - | 6 |
| F7-2 | 2 | 2 | - | 2 | - | 6 |
| F1-20 | - | 5 | - | - | - | 5 |
| F1-209 | - | 5 | - | - | - | 5 |
| F6-4 | - | 5 | - | - | - | 5 |
| F1-55 | - | - | 5 | - | - | 5 |
| F1-183 | - | 4 | 1 | - | - | 5 |
| F3-28 | - | 4 | 1 | - | - | 5 |
| F5-17 | - | 4 | - | 1 | - | 5 |
| F5-71 | - | 4 | - | - | 1 | 5 |
| F5-132 | - | 2 | - | 3 | - | 5 |
| F1-177 | - | 4 | - | - | - | 4 |
| F1-51 | - | 4 | - | - | - | 4 |
| F1-80 | - | 4 | - | - | - | 4 |
| F1-96 | - | 4 | - | - | - | 4 |
| F5-137 | - | 4 | - | - | - | 4 |
| F5-145 | - | 4 | - | - | - | 4 |
| F5-59 | - | 4 | - | - | - | 4 |
| F1-189 | 1 | 3 | - | - | - | 4 |
| F2-9 | - | - | 4 | - | - | 4 |
| F1-47 | - | 3 | 1 | - | - | 4 |
| F5-91 | - | 3 | - | - | 1 | 4 |
| F5-4 | - | 2 | 2 | - | - | 4 |
| F1-152 | - | 1 | 3 | - | - | 4 |
| F11-3 | 3 | 1 | - | - | - | 4 |
| F1-176 | - | 3 | - | - | - | 3 |
| F1-181 | - | 3 | - | - | - | 3 |
| F1-182 | - | 3 | - | - | - | 3 |
| F1-184 | - | - | 3 | - | - | 3 |
| F1-187 | - | 3 | - | - | - | 3 |
| F1-37 | - | 3 | - | - | - | 3 |
| F1-52 | - | 3 | - | - | - | 3 |
| F2-31 | - | 3 | - | - | - | 3 |
| F5-142 | - | 3 | - | - | - | 3 |
| F11-7 | 2 | - | - | 1 | - | 3 |
| F5-146 | - | 3 | - | - | - | 3 |
| F3-6 | - | - | 3 | - | - | 3 |

| | | | | | | |
|---|---|---|---|---|---|---|
| F3-9 | - | - | 3 | - | - | 3 |
| F5-95 | - | 3 | - | - | - | 3 |
| F1-196 | - | 2 | - | - | 1 | 3 |
| F5-134 | - | 2 | 1 | - | - | 3 |
| F11-1 | 2 | 1 | - | - | - | 3 |
| F1-158 | - | 2 | - | - | - | 2 |
| F1-175 | - | 2 | - | - | - | 2 |
| F1-178 | - | 2 | - | - | - | 2 |
| F1-18 | - | - | 2 | - | - | 2 |
| F1-190 | - | - | 2 | - | - | 2 |
| F1-199 | - | 2 | - | - | - | 2 |
| F1-2 | - | - | 2 | - | - | 2 |
| F1-200 | - | 2 | - | - | - | 2 |
| F1-64 | - | - | 2 | - | - | 2 |
| F1-90 | - | 2 | - | - | - | 2 |
| F2-12 | - | 2 | - | - | - | 2 |
| F11-5 | - | - | - | 2 | - | 2 |
| F11-8 | - | - | - | 2 | - | 2 |
| F2-13 | - | 2 | - | - | - | 2 |
| F3-59 | - | 2 | - | - | - | 2 |
| F4-57 | - | 2 | - | - | - | 2 |
| F4-63 | - | 2 | - | - | - | 2 |
| F4-64 | - | 2 | - | - | - | 2 |
| F4-60 | - | - | 2 | - | - | 2 |
| F4-65 | - | 2 | - | - | - | 2 |
| F4-66 | - | 2 | - | - | - | 2 |
| F5-143 | - | 2 | - | - | - | 2 |
| F5-151 | - | 2 | - | - | - | 2 |
| F5-154 | - | 2 | - | - | - | 2 |
| F5-155 | - | 2 | - | - | - | 2 |
| F5-160 | - | 2 | - | - | - | 2 |
| F11-2 | - | 1 | - | 1 | - | 2 |
| F3-13 | - | 1 | 1 | - | - | 2 |
| F5-19 | - | - | 2 | - | - | 2 |
| F1-119 | - | - | - | 1 | - | 1 |
| F1-15 | - | - | 1 | - | - | 1 |
| F1-157 | - | 1 | - | - | - | 1 |
| F1-159 | - | 1 | - | - | - | 1 |
| F1-167 | - | 1 | - | - | - | 1 |
| F1-169 | 1 | - | - | - | - | 1 |
| F1-171 | - | 1 | - | - | - | 1 |
| F1-179 | - | 1 | - | - | - | 1 |
| F1-180 | - | 1 | - | - | - | 1 |
| F1-185 | - | 1 | - | - | - | 1 |

| | | | | | | |
|---|---|---|---|---|---|---|
| F1-188 | - | 1 | - | - | - | 1 |
| F1-19 | - | 1 | - | - | - | 1 |
| F1-191 | - | 1 | - | - | - | 1 |
| F1-193 | - | - | - | - | 1 | 1 |
| F1-194 | - | 1 | - | - | - | 1 |
| F1-195 | - | 1 | - | - | - | 1 |
| F1-198 | - | 1 | - | - | - | 1 |
| F1-201 | - | 1 | - | - | - | 1 |
| F1-202 | - | 1 | - | - | - | 1 |
| F1-203 | - | 1 | - | - | - | 1 |
| F1-204 | - | 1 | - | - | - | 1 |
| F1-205 | - | 1 | - | - | - | 1 |
| F1-206 | - | 1 | - | - | - | 1 |
| F1-207 | - | 1 | - | - | - | 1 |
| F1-208 | - | 1 | - | - | - | 1 |
| F1-33 | - | 1 | - | - | - | 1 |
| F1-68 | - | 1 | - | - | - | 1 |
| F1-94 | - | - | 1 | - | - | 1 |
| F1-99 | - | 1 | - | - | - | 1 |
| F10-1 | - | 1 | - | - | - | 1 |
| F11-6 | - | 1 | - | - | - | 1 |
| F2-33 | - | 1 | - | - | - | 1 |
| F2-7 | - | 1 | - | - | - | 1 |
| F3-5 | - | - | 1 | - | - | 1 |
| F3-61 | - | - | - | 1 | - | 1 |
| F3-62 | - | 1 | - | - | - | 1 |
| F3-63 | - | 1 | - | - | - | 1 |
| F3-64 | - | - | 1 | - | - | 1 |
| F3-65 | - | 1 | - | - | - | 1 |
| F3-66 | - | - | 1 | - | - | 1 |
| F4-12 | - | 1 | - | - | - | 1 |
| F4-21 | - | - | 1 | - | - | 1 |
| F4-24 | - | 1 | - | - | - | 1 |
| F4-25 | - | 1 | - | - | - | 1 |
| F4-58 | - | 1 | - | - | - | 1 |
| F4-59 | - | - | 1 | - | - | 1 |
| F4-61 | - | 1 | - | - | - | 1 |
| F4-62 | - | 1 | - | - | - | 1 |
| F5-115 | - | 1 | - | - | - | 1 |
| F5-118 | - | - | 1 | - | - | 1 |
| F5-13 | - | - | 1 | - | - | 1 |
| F5-131 | - | 1 | - | - | - | 1 |
| F5-139 | - | 1 | - | - | - | 1 |
| F5-141 | - | 1 | - | - | - | 1 |

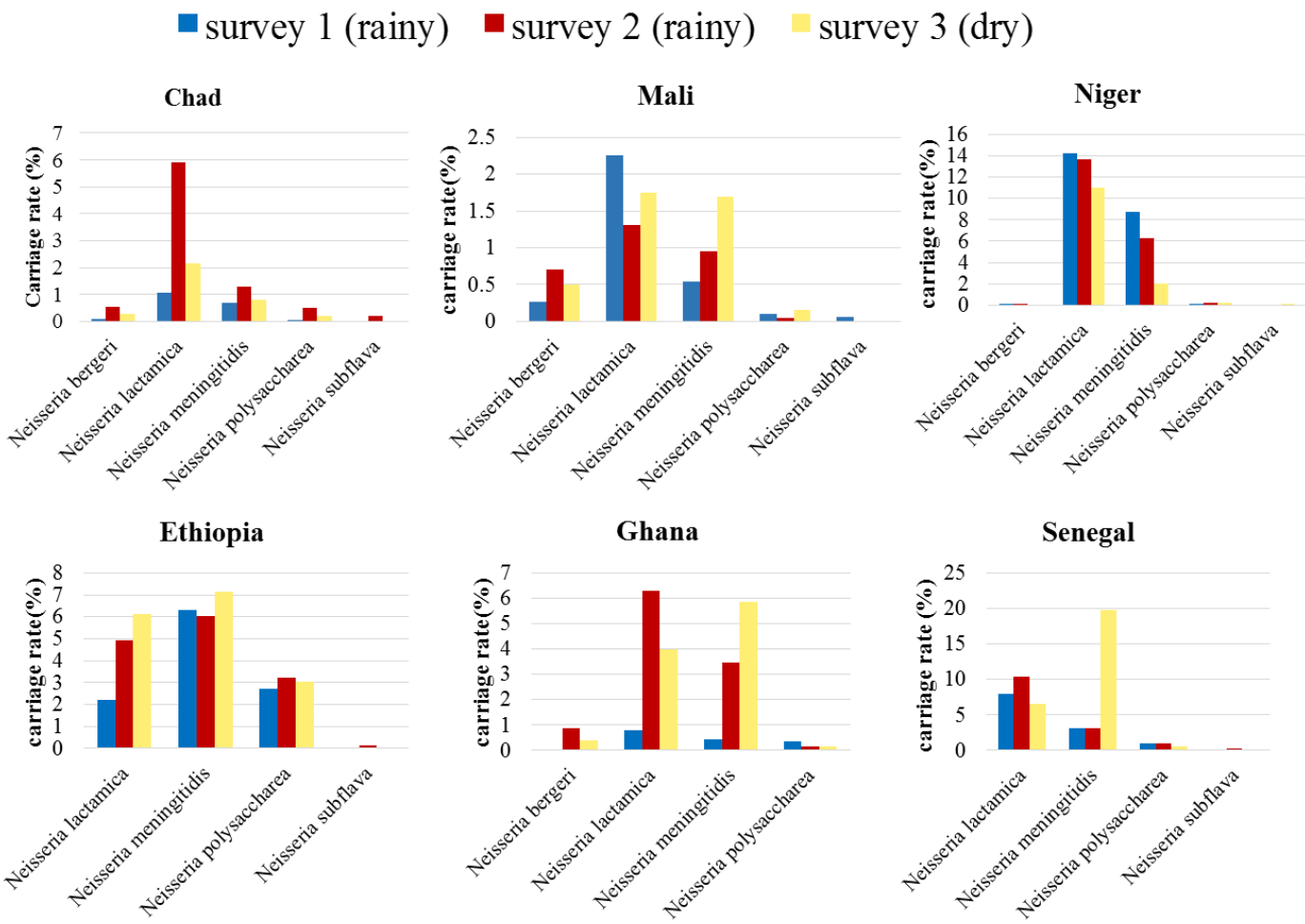
| | | | | | | |
|---|---|---|---|---|---|---|
| F5-144 | - | 1 | - | - | - | 1 |
| F5-147 | - | 1 | - | - | - | 1 |
| F5-150 | - | 1 | - | - | - | 1 |
| F5-152 | - | 1 | - | - | - | 1 |
| F5-153 | - | - | 1 | - | - | 1 |
| F5-156 | - | 1 | - | - | - | 1 |
| F5-157 | - | 1 | - | - | - | 1 |
| F5-158 | - | 1 | - | - | - | 1 |
| F5-159 | - | 1 | - | - | - | 1 |
| F5-161 | - | 1 | - | - | - | 1 |
| F5-162 | - | 1 | - | - | - | 1 |
| F5-163 | - | 1 | - | - | - | 1 |
| F5-164 | - | 1 | - | - | - | 1 |
| F5-165 | - | 1 | - | - | - | 1 |
| F5-166 | - | 1 | - | - | - | 1 |
| F5-2 | - | - | 1 | - | - | 1 |
| F5-67 | - | 1 | - | - | - | 1 |
| F5-68 | - | - | 1 | - | - | 1 |
| F5-81 | - | 1 | - | - | - | 1 |
| F6-5 | - | - | 1 | - | - | 1 |
| F7-4 | - | - | - | 1 | - | 1 |
| Total | 113 | 2588 | 1683 | 290 | 24 | 4698 |

**Table S6: Frequency of the most common meningococci strain types**

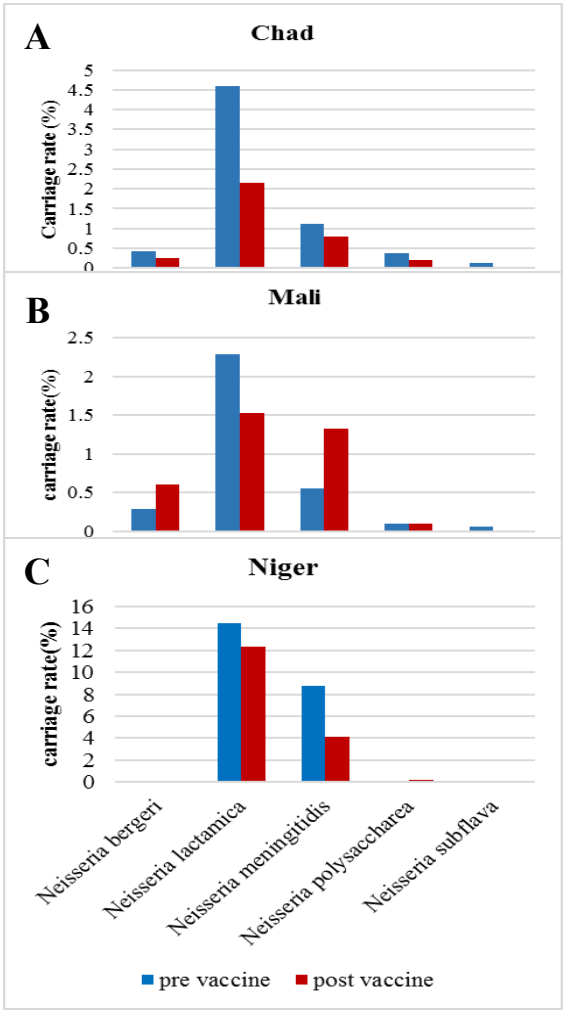
| meningo_strain_type | frequency |
|---|---|
| *cnl*:P1.18-11,42-1:*fnl* | 438 |
| W:P1.5,2:F1-1 | 432 |
| W:P1.5-1,2-36:F5-1 | 105 |
| A:P1.20,9:F3-1 | 38 |
| *cnl*:P1.18-11,42-1:ND | 36 |
| W:P1.5,2:F6-3 | 25 |
| Y:P1.5-1,10-62:F1-3 | 24 |
| *cnl*:P1.18-11,ND:*fnl* | 24 |
| ND:P1.18-11,42-1:*fnl* | 23 |
| *cnl*:P1.ND,ND:ND | 23 |
| X:P1.5-1,10-1:F4-23 | 21 |
| Y:P1.5-1,10-8:F1-3 | 21 |

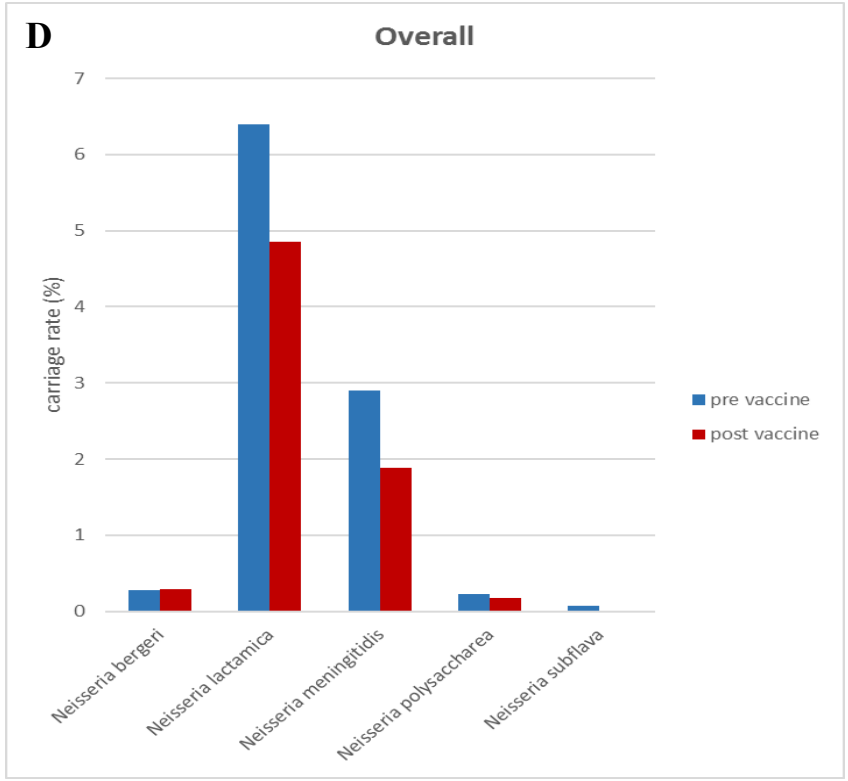
## Supplementary Figures

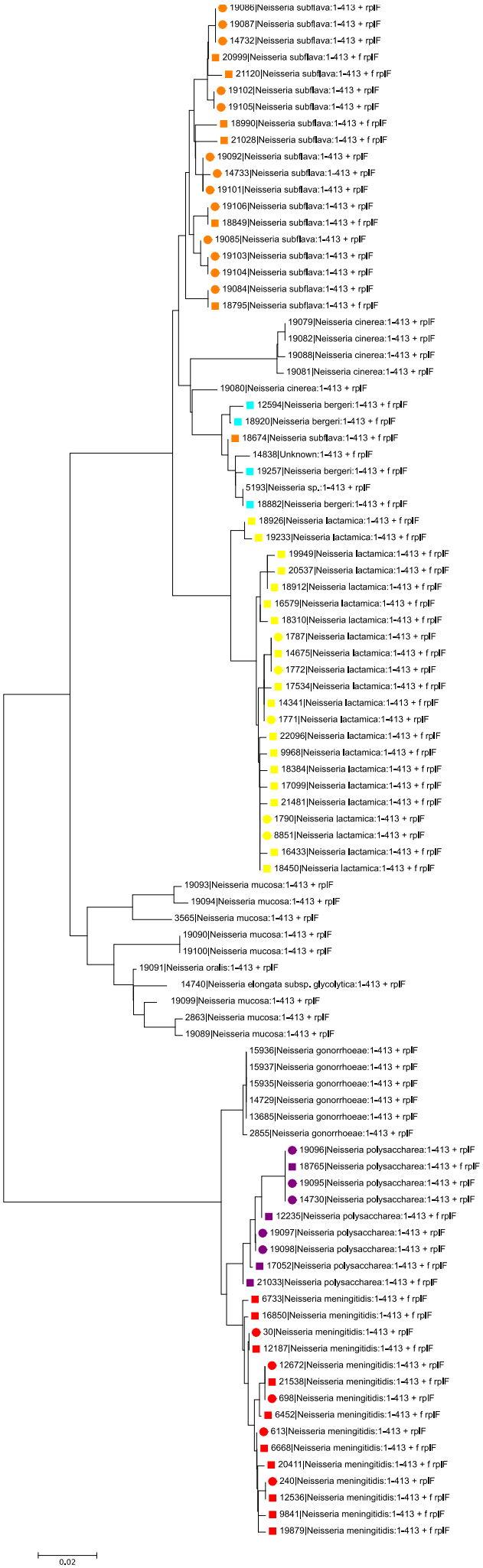
**Supplemental Figure 1. Prevalence of *Neisseria* species carriage per survey, for each country**



**Supplemental figure 2.** ***Neisseria*** **species carriage rate pre and post vaccine administration**



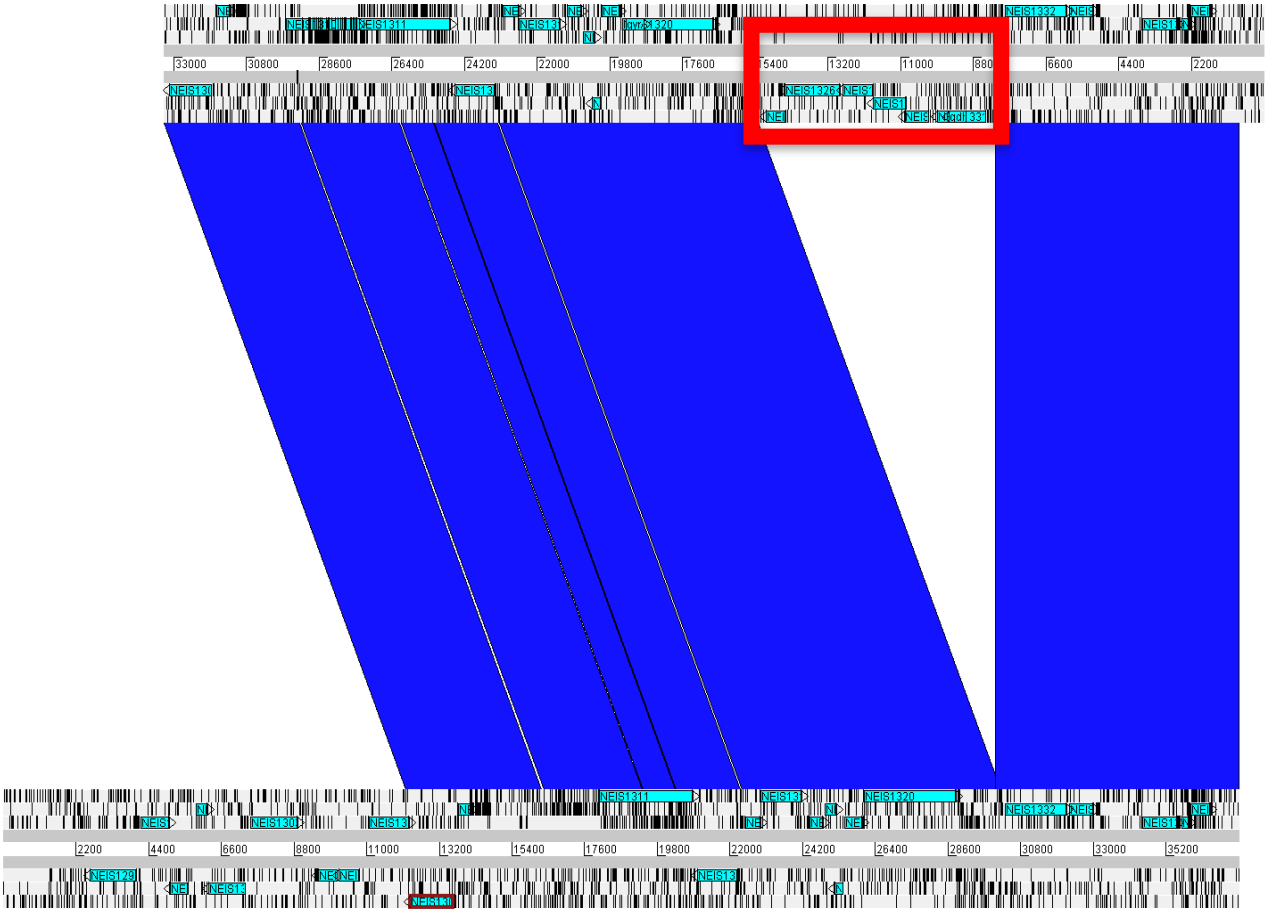



**Supplemental Figure 3: Evolutionary relationship of the *Neisseria* isolates based on *f_rplF***

Neighbor-Joining tree representing the phylogeny based on the different *f_rplF* allele. The colors correspond to each species covered in this study: *Nm* (red), *Nl* (yellow), *Np* (purple), *Nb* (blue) and *Ns* (orange). The circles correspond to the isolates used in the Bennett et al (2014) paper and the squares to the isolates described in this current work.

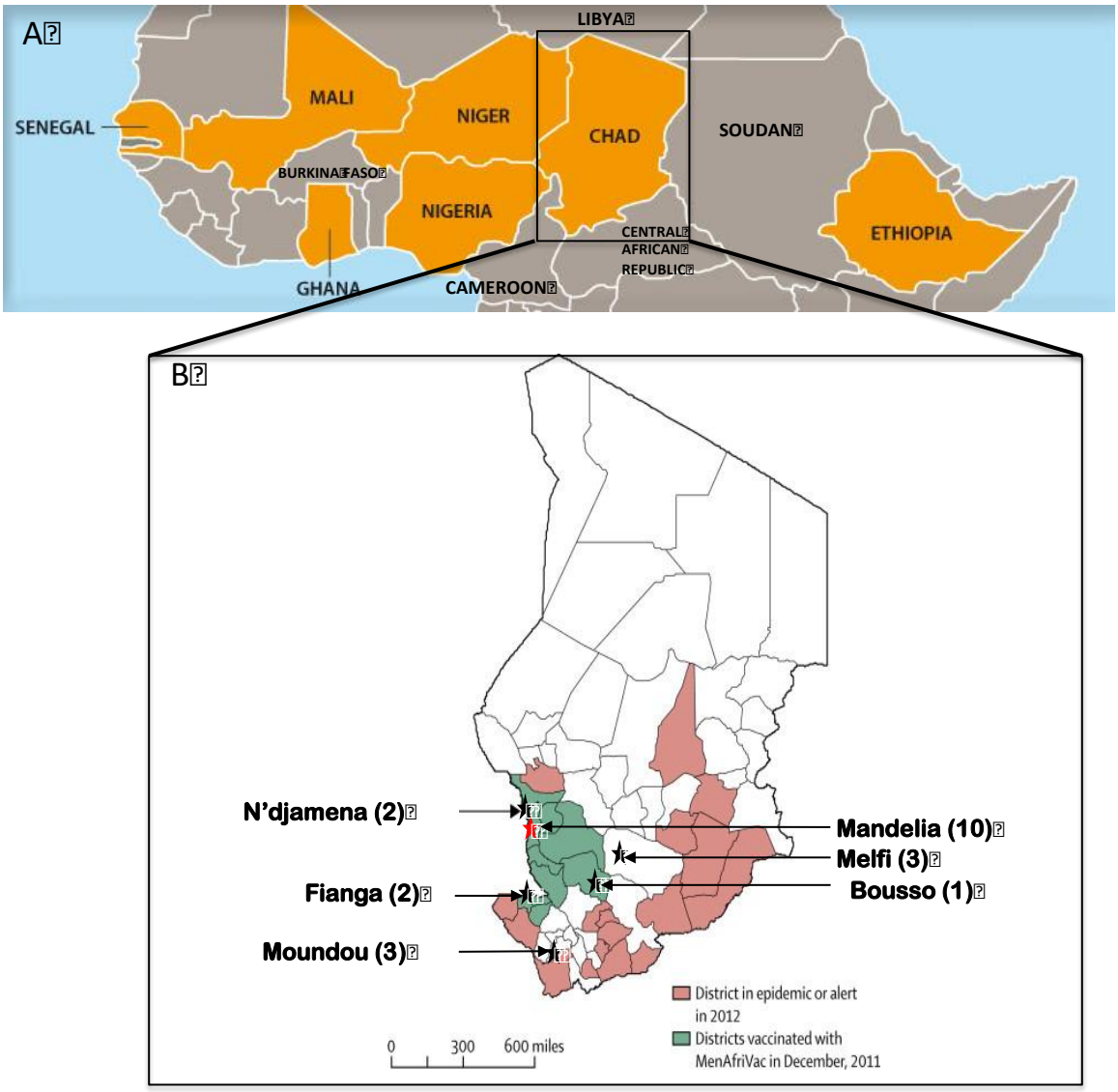
# Appendix 2: Supplemental material for Chapter 4

***Supplemental Figures***



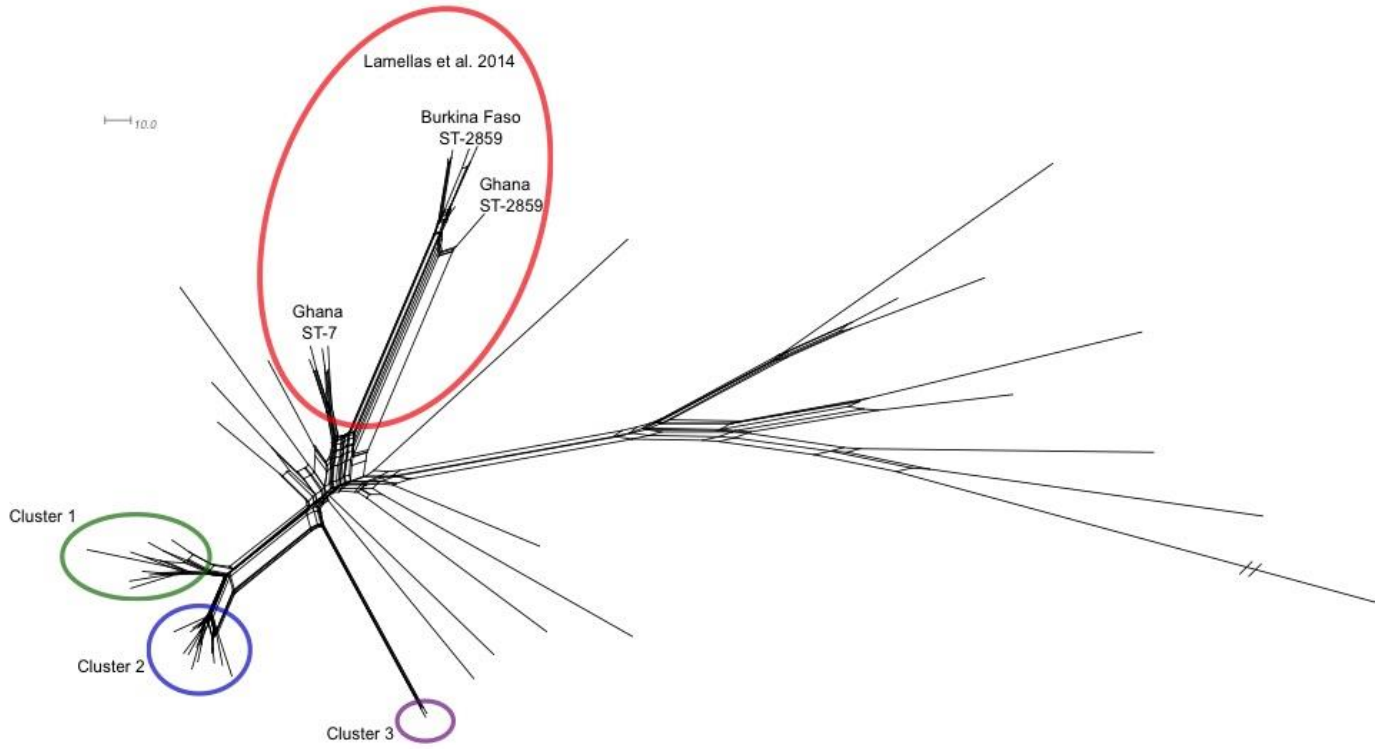
**Supplemental Figure 1. Deletion of six genes in isolate 120-2011**

ACT comparison of isolates 10-2011 (on the top) and 120-2011 (at the bottom). The blue blocks represent identical sequences in reversed orientation and the red box highlights the deleted genetic sequence.



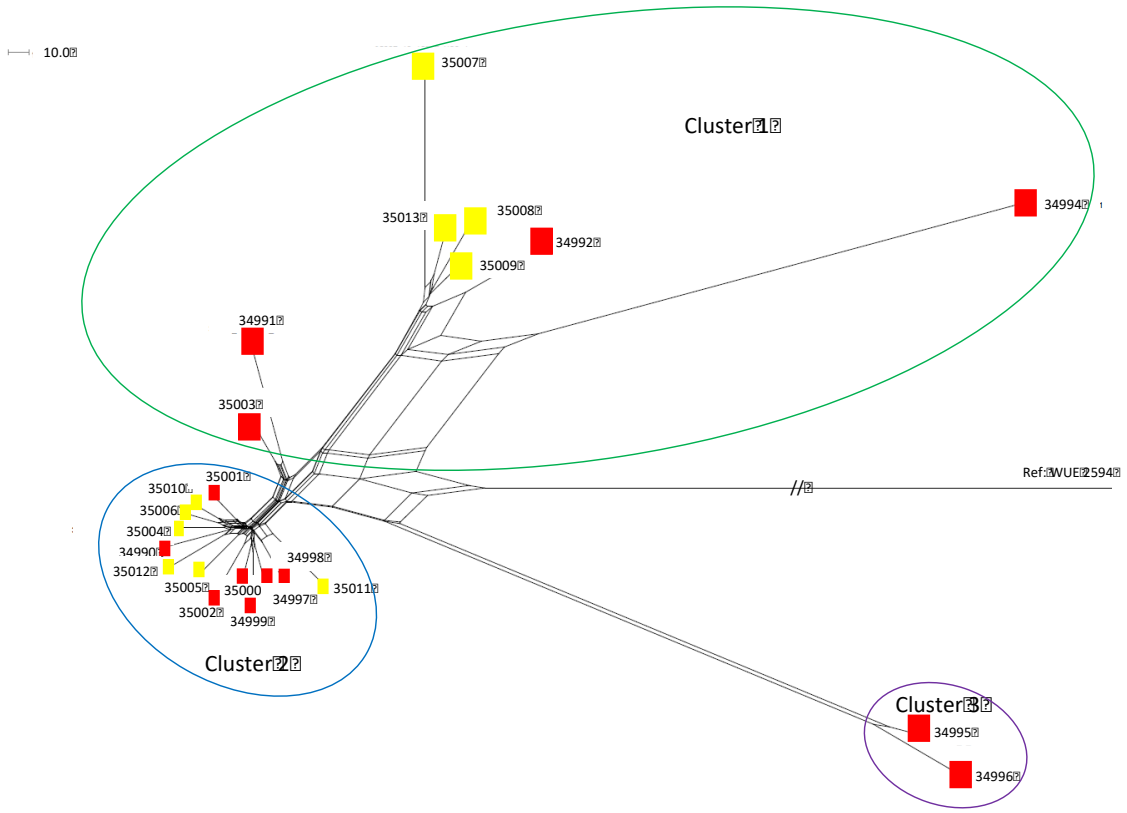

**Supplemental Figure 2. Geographical location of the *Nm*A isolates**

A map of the African meningitis belt showing Chad in relation its neighboring countries; countries of the MenAfriCar project are shown in orange and the name of the countries sharing borders with Chad. The map was adapted from the MenAfriCar website, http://www.menafricar.org (A). The provenance location of the 2011 *Nm*A isolates included in this study on a map of Chad adapted from Daugla, MD et al. 2014 (113) . The black stars represent the disease isolates and the red ones the carried isolates (B).




**Supplemental Figure 3. wgMLST relationship of the *Nm*A:cc5 isolates**

Whole genome analysis of the 50 isolates included in the rMLST analysis (all the Chadian isolates and a single representative of unique strain of the other *Nm*A:cc5 publically available isolate) is presented in this neighbor Net tree. The three clusters identified in this study are labeled as well as the isolates from the most recent publication on genomic of *Nm*A:cc5 in the African meningitis belt in Africa




**Supplemental Figure 4. wgSNP relationship of the 23 Chadian *Nm*A from their original fastq files**

Whole genome SNP analysis based on the 1924 SNPs identified in the kSNP3 analysis based on the processed fastq files is presented in this neighbor Net tree. The three clusters identified in this study are labeled. The same reference genome WUE 2504 was used in this analysis

*Supplemental Tables*

## Supplemental Table 1. Velvet assembly statistics

| PubMLST ID | Isolate ID | Number of contigs | N50 | Allele designated (%)* | Total length bp |
|---|---|---|---|---|---|
| **34990** | Tchad54/11 | 125 | 51921 | 1574 (98.1) | 2160120 |
| **34991** | Tchad78/11 | 171 | 40301 | 1575 (98.1) | 2163900 |
| **34992** | Tchad95/11 | 175 | 37578 | 1574 (98.1) | 2159198 |
| **34994** | Tchad106/11 | 185 | 35661 | 1561 (97.3) | 2174025 |
| **34995** | 8-2011 | 130 | 43934 | 1573 (98) | 2161554 |
| **34996** | 10-2011 | 113 | 51921 | 1577 (98.3) | 2159817 |
| **34997** | 39-2011 | 162 | 41190 | 1560 (97.2) | 2166409 |
| **34998** | 59-2011 | 126 | 51915 | 1573 (98) | 2165858 |
| **34999** | 63-2011 | 125 | 52444 | 1573 (98) | 2165886 |
| **35000** | 75-2011 | 134 | 40895 | 1571 (97.9) | 2162502 |
| **35001** | 76-2011 | 148 | 48158 | 1575 (98.1) | 2163115 |
| **35002** | 120-2011 | 156 | 38996 | 1558 (97.1) | 2155465 |
| **35003** | 403-2011 | 243 | 28533 | 1539 (95.9) | 2173410 |
| **35004** | 12-15398-XS2-1 | 135 | 52853 | 1567 (97.6) | 2165054 |
| **35005** | 12-13952-XS2-1 | 193 | 29845 | 1564 (97.4) | 2163657 |
| **35006** | 12-15317-XS2-1 | 173 | 39334 | 1562 (97.3) | 2166457 |
| **35007** | 12-15047-XS2-1 | 167 | 41374 | 1572 (97.9) | 2166917 |
| **35008** | 12-15661-XS2-1 | 134 | 44112 | 1574 (98.1) | 2163800 |
| **35009** | 12-15657-XS2-1 | 164 | 41379 | 1567 (97.6) | 2165755 |
| **35010** | 12-17186-XS2-1 | 145 | 45919 | 1568 (97.7) | 2161231 |
| **35011** | 12-17194-XS2-1 | 132 | 48170 | 1570 (97.8) | 2164552 |
| **35012** | 12-17009-XS2-1 | 149 | 50196 | 1562 (97.3) | 2168433 |
| **35013** | 12-14973-XS2-1 | 160 | 41070 | 1571 (97.9) | 2162718 |

* Number of alleles designated from the 1605 core genome MLST (cgMLST) v1.0 loci (217)

**Supplemental Table 2. ID and characteristics of cc5 *Nm*A isolated in previous studies.**

| pubMLST ID | Country | Year | Disease | rST | Strain designation | Reference |
|---|---|---|---|---|---|---|
| 34598 | Algeria | 2000 | Invasive (unspecified/other) | 6971 | A: P1.20,9: F3-1: ST-7 (cc5) | |
| 34654 | Bangladesh | 2003 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-4789 (cc5) | |
| 34655 | Bangladesh | 2006 | Invasive (unspecified/other) | 3173 | A: P1.20,9: F-ND: ST-8428 (cc5) | |
| 34572 | Brazil | 1975 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F2-1: ST-5 (cc5) | |
| 34573 | Brazil | 1975 | Invasive (unspecified/other) | ND | A: P1.20,9: F3-1: ST-5 (cc5) | |
| 84 | Brazil | 1976 | | 2434 | A: P1.20,9: F2-1: ST-5 (cc5) | Maiden, MC et al. 1998 |
| 34599 | Burkina Faso | 2001 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | |
| 34808 | Burkina Faso | 2006 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34809 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34810 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34812 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34817 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34818 | Burkina Faso | 2006 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34820 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34822 | Burkina Faso | 2006 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34824 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34834 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34838 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34841 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34842 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 34843 | Burkina Faso | 2006 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34847 | Burkina Faso | 2006 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34856 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34863 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34864 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34866 | Burkina Faso | 2006 | Carrier | 3195 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34872 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34876 | Burkina Faso | 2006 | Carrier | 3195 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34877 | Burkina Faso | 2006 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34883 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34888 | Burkina Faso | 2006 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34890 | Burkina Faso | 2006 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34892 | Burkina Faso | 2006 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34893 | Burkina Faso | 2006 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34894 | Burkina Faso | 2006 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34610 | Burkina Faso | 2007 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | |
| 34811 | Burkina Faso | 2007 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34819 | Burkina Faso | 2007 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34835 | Burkina Faso | 2007 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34854 | Burkina Faso | 2007 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34813 | Burkina Faso | 2008 | Carrier | 3068 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34882 | Burkina Faso | 2008 | Carrier | 3068 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 128 | Chad | 1988 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-5 (cc5) | Maiden et al. 1998 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 34578 | Chad | 1988 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-5 (cc5) | |
| 299 | China | 1963 | Carrier | 2511 | A: P1.5-2,10: F1-5: ST-5 (cc5) | Maiden et al. 1998 |
| 238 | China | 1966 | Invasive (unspecified/other) | 2468 | A: P1.20,9: F3-1: ST-5 (cc5) | Maiden et al. 1998 |
| 239 | China | 1966 | Invasive (unspecified/other) | 2503 | A: P1.20,9: F3-1: ST-6 (cc5) | Maiden et al. 1998 |
| 82 | China | 1984 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-8: ST-5 (cc5) | Maiden et al. 1998 |
| 597 | China | 1992 | Invasive (unspecified/other) | 2501 | A: P1.20,9: F3-1: ST-7 (cc5) | Maiden et al. 1998 |
| 30466 | China | 2006 | Meningitis | 2434 | A: P1.20,ND: F3-1: ST-7 (cc5) | Zhang, Y et al. 2014 |
| 24 | Denmark | 1974 | Invasive (unspecified/other) | 2434 | A: P1.5-1,9: F3-1: ST-5 (cc5) | Maiden et al. 1998 |
| 7 | Finland | 1975 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-5 (cc5) | Maiden et al. 1998 |
| 31215 | France | 2006 | Meningitis and septicemia | 2434 | A: P1.20,9: F3-1: ST-4789 (cc5) | |
| 19260 | Germany | 1991 | Meningitis | 2434 | A: P1.20,9: F1-21: ST-5 (cc5) | Schoen, C et al. 2011 |
| 34836 | Ghana | 2001 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34829 | Ghana | 2002 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34840 | Ghana | 2002 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34844 | Ghana | 2002 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34859 | Ghana | 2002 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34861 | Ghana | 2002 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34869 | Ghana | 2002 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34875 | Ghana | 2002 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34880 | Ghana | 2002 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34900 | Ghana | 2002 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34902 | Ghana | 2002 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34827 | Ghana | 2003 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |

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|---|---|---|---|---|---|---|
| 34850 | Ghana | 2003 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34852 | Ghana | 2003 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34855 | Ghana | 2003 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34858 | Ghana | 2003 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34860 | Ghana | 2003 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34871 | Ghana | 2003 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34878 | Ghana | 2003 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34881 | Ghana | 2003 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34884 | Ghana | 2003 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34887 | Ghana | 2003 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34825 | Ghana | 2004 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34826 | Ghana | 2004 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34828 | Ghana | 2004 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34837 | Ghana | 2004 | Invasive (unspecified/other) | 2974 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34845 | Ghana | 2004 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34848 | Ghana | 2004 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34849 | Ghana | 2004 | Carrier | 2974 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34853 | Ghana | 2004 | Invasive (unspecified/other) | 2974 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34862 | Ghana | 2004 | Carrier | 2974 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34865 | Ghana | 2004 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34867 | Ghana | 2004 | Carrier | 2974 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34868 | Ghana | 2004 | Invasive (unspecified/other) | 2974 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34873 | Ghana | 2004 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |

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|---|---|---|---|---|---|---|
| 34879 | Ghana | 2004 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34886 | Ghana | 2004 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34891 | Ghana | 2004 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34895 | Ghana | 2004 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34896 | Ghana | 2004 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34898 | Ghana | 2004 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34899 | Ghana | 2004 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34901 | Ghana | 2004 | Carrier | 2974 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 35095 | Ghana | 2004 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34870 | Ghana | 2005 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34874 | Ghana | 2005 | Invasive (unspecified/other) | 3025 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34885 | Ghana | 2005 | Carrier | 3025 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34889 | Ghana | 2005 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34897 | Ghana | 2005 | Carrier | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | Lamelas, A et al. 2014 |
| 34830 | Ghana | 2007 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34805 | Ghana | 2008 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34814 | Ghana | 2008 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34815 | Ghana | 2008 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34816 | Ghana | 2008 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34821 | Ghana | 2008 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34823 | Ghana | 2008 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34831 | Ghana | 2008 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34832 | Ghana | 2008 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |

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|---|---|---|---|---|---|---|
| 34833 | Ghana | 2008 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34839 | Ghana | 2008 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34846 | Ghana | 2008 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34851 | Ghana | 2008 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 35094 | Ghana | 2008 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34806 | Ghana | 2009 | Carrier | 2434 | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34807 | Ghana | 2009 | Carrier | ND | A: P1.20,9: F3-1: ST-2859 (cc5) | Lamelas, A et al. 2014 |
| 34589 | Mali | 1997 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-580 (cc5) | |
| 34590 | Mali | 1997 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-580 (cc5) | |
| 34583 | Niger | 1996 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-5 (cc5) | |
| 34584 | Niger | 1996 | Invasive (unspecified/other) | 3016 | A: P1.20,9: F3-1: ST-5 (cc5) | |
| 34587 | Niger | 1997 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-5 (cc5) | |
| 34594 | Niger | 1998 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-5 (cc5) | |
| 34597 | Niger | 2000 | Invasive (unspecified/other) | 6967 | A: P1.20,9: F3-1: ST-7 (cc5) | |
| 34600 | Niger | 2002 | Invasive (unspecified/other) | ND | A: P1.20,9: F3-1: ST-7 (cc5) | |
| 34604 | Niger | 2003 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | |
| 34606 | Niger | 2004 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | |
| 34607 | Niger | 2004 | Invasive (unspecified/other) | 3028 | A: P1.20,9: F3-1: ST-7 (cc5) | |
| 451 | Russia | 1970 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-5 (cc5) | Maiden et al. 1998 |
| 34857 | Russia | | | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | |
| 120 | Saudi Arabia | 1987 | Carrier | 2434 | A: P1.20,9: F3-1: ST-5 (cc5) | Maiden et al. 1998 |
| 29291 | South Africa | 2004 | Meningitis | 34706 | A: P1.20,9: F5-70: ST-7 (cc5) | |
| 29434 | South Africa | 2005 | Meningitis | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | |

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|---|---|---|---|---|---|---|
| 29304 | South Africa | 2010 | Meningitis | 2434 | A: P1.20,9: F3-1: ST-7 (cc5) | |
| 210 | UK | 1987 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-5 (cc5) | Maiden et al. 1998 |
| 30269 | UK | 1999 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-5 (cc5) | |
| 20338 | UK | 2011 | Invasive (unspecified/other) | 2434 | A: P1.20,9: F3-1: ST-4789 (cc5) | Hill, DM et al. 2015 |
| 34663 | USA | 2000 | Invasive (unspecified/other) | ND | A: P1.20-1,9: F3-1: ST-7 (cc5) | |
| 34665 | USA | 2001 | Invasive (unspecified/other) | 2985 | A: P1.20,9: F3-1: ST-7 (cc5) | |

## Comparison between Velvet/VelvetOptimiser and Spades assemblies

### Supplemental Table 3. Velvet/VelvetOptimiser and Spades assembly statistics

| | Velvet | Spades | Velvet | Spades | Velvet | Spades | Velvet | Spades |
|---|---|---|---|---|---|---|---|---|
| **Isolate ID** | **Number of Contigs** | | **Genome length** | | **N50** | | **Number of alleles designated (cgMLST v1.0 1605 loci) (%)** | |
| Tchad54/11 | 125 | 222 | 2160120 | 2152402 | 51921 | 36616 | 1574 (98.1) | 1590 (99.1) |
| Tchad78/11 | 171 | 275 | 2163900 | 2174251 | 40301 | 35212 | 1575 (98.1) | 1584 (98.7) |
| Tchad95/11 | 175 | 417 | 2159198 | 2233641 | 37578 | 33960 | 1574 (98.1) | 1588 (98.9) |
| Tchad106/11* | 185 | 3054 | 2174025 | 3362286 | 35661 | 1708 | 1561 (97.3) | 948 (59.1) |
| 8-2011 | 130 | 202 | 2161554 | 2155485 | 43934 | 32587 | 1573 (98) | 1588 (98.9) |
| 10-2011 | 113 | 216 | 2159817 | 2154902 | 51921 | 34753 | 1577 (98.3) | 1586 (98.8) |
| 39-2011 | 162 | 187 | 2166409 | 2146453 | 41190 | 33684 | 1560 (97.2) | 1589 (99) |
| 59-2011 | 126 | 212 | 2165858 | 2154741 | 51915 | 36616 | 1573 (98) | 1587 (98.9) |
| 63-2011 | 125 | 192 | 2165886 | 2149039 | 52444 | 34041 | 1573 (98) | 1588 (98.9) |
| 75-2011 | 134 | 263 | 2162502 | 2170834 | 40895 | 37875 | 1571 (97.9) | 1589 (99) |
| 76-2011 | 148 | 198 | 2163115 | 2149691 | 48158 | 33410 | 1575 (98.1) | 1587 (98.9) |
| 120-2011 | 156 | 225 | 2155465 | 2153417 | 38996 | 35995 | 1558 (97.1) | 1584 (98.7) |
| 403-2011 | 243 | 222 | 2173410 | 2160712 | 28533 | 40345 | 1539 (95.9) | 1587 (98.9) |
| 12-15398-XS2-1 | 135 | 195 | 2165054 | 2149651 | 52853 | 34752 | 1567 (97.6) | 1589 (99) |
| 12-13952-XS2-1 | 193 | 224 | 2163657 | 2152579 | 29845 | 35305 | 1564 (97.4) | 1585 (98.8) |
| 12-15317-XS2-1 | 173 | 262 | 2166457 | 2168661 | 39334 | 36616 | 1562 (97.3) | 1588 (98.9) |
| 12-15047-XS2-1 | 167 | 211 | 2166917 | 2153162 | 41374 | 34753 | 1572 (97.9) | 1589 (99) |
| 12-15661-XS2-1 | 134 | 261 | 2163800 | 2164291 | 44112 | 32587 | 1574 (98.1) | 1588 (98.9) |
| 12-15657-XS2-1 | 164 | 196 | 2165755 | 2152400 | 41379 | 32587 | 1567 (97.6) | 1586 (98.8) |
| 12-17186-XS2-1 | 145 | 197 | 2161231 | 2142409 | 45919 | 33410 | 1568 (97.7) | 1587 (98.9) |
| 12-17194-XS2-1 | 132 | 199 | 2164552 | 2152840 | 48170 | 34753 | 1570 (97.8) | 1587 (98.9) |
| 12-17009-XS2-1 | 149 | 227 | 2168433 | 2160729 | 50196 | 35212 | 1562 (97.3) | 1591 (99.1) |
| 12-14973-XS2-1 | 160 | 229 | 2162718 | 2160948 | 41070 | 40209 | 1571 (97.9) | 1584 (98.7) |
| **Average (excl. Tchad106/11)** | **152.7** | **228.7** | **2163900** | **2159693** | **43729** | **35240** | **1568.1 (97.7)** | **1587.3 (98.9)** |

***Method, Results and Discussion***

For comparison, the 23 isolates were assembled using Spades (v3.9.1) using the read error correction option ('--careful') and k-mers sampled from 21bp to 99bp.

Supplemental table 3 shows the assembly statistics for the Velvet/VelvetOptimiser and Spades assembly methods for all 23 genomes. Both methods were set for a minimum contig size of 200bp. One genome (Tchad106/11) did not assemble well by Spades, resulting in more than 3,000 contigs and was excluded from the calculation of averages. In general, Velvet assembled genomes with a smaller number of contigs (average of 152.7 for Velvet compared with 228.7 for Spades), and a larger N50 contig size (average

of 43,729 for Velvet compared with 35,240 for Spades). To measure the number of complete loci that were recovered by each assembly, the number of allele designations was calculated for the core genome MLST *N. meningitidis* scheme (v1.0) containing 1605 loci generally found in at least 95% of meningococci (217). Both Velvet/VelvetOptimiser and Spades methods consistently assembled more than 97% of the cgMLST loci to give known allelic variants, with Velvet averaging 97.7% and Spades averaging 98.9%. These values indicate that both methods are producing high quality genome assemblies.

Closer inspection of the allele designations for the 7 locus MLST genes (*abcZ, adk, aroE, fumC, gdh, pdhC, pgm)*, identified a different *fumC* allele in nine of the 23 Spades assemblies compared with the corresponding Velvet assembly. For example, isolate 8-2011 had *fumC* allele 1 in the Velvet assembly (resulting in ST-7) and *fumC* allele 843 in the Spades assembly. There were two bases different between these two alleles: T262 and C273 in allele 1 are G262 and T273 in allele 843. For both positions Spades was calling the minority base and was therefore less accurate in this case. In order to enable comparisons with previously published studies stored in the PubMLST *Neisseria* database, we chose to continue our analysis using Velvet/VelvetOptimiser assemblies.

| Cluster specific SNPs | Cluster 1 | | | | | Cluster 2 | Cluster 3 |
|---|---|---|---|---|---|---|---|
| | All Cluster 1 | Carried isolates of Cluster 1 | Carried isolates + 34992 and 34994 | 34991 and 35003 | 35007 | | |
| SNP LocusNum in Supplemental table 4 | 1500; 1667; 1895 | 1052 | 58; 178; 265; 463; 686; 1468; 1705; 1809; 1889 | 0; 719; 1382 | 26; 551; 695; 793; 828; 986; 1056; 1142; 1491; 1521; 1680; 1841; 1844 | 156; 572; 644; 914; 1790; 1870 | 47; 118; 174; 182; 291; 315; 320; 333; 404; 438; 522; 687; 769; 813; 833; 876; 878; 1161; 1239; 1385; 1430; 1431; 1504; 1556; 1765; 1793 |

**Supplemental Table 4. SNPs in the non-coding region or not found in the reference genome (WUE 2594)**

| Locus# | Context | Allele | Position Strand | ID | AnnotationType |
|---|---|---|---|---|---|
| 0 | AAAAAAAAAA.AAACTTACCT | T | 105910 R | 19260_WUE_2594 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 34995_8_2011 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 34996_10_2011 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 34997_39_2011 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 34998_59_2011 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 34999_63_2011 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 35000_75_2011 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 35001_76_2011 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 35002_120_2011 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | A | x | 35003_403_2011 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |

| | | | | | |
|---|---|---|---|---|---|
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 0 | AAAAAAAAAA.AAACTTACCT | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 11 | AAAAAGAAAG.GCAAACCATG | A | 1277332 F | 19260_WUE_2594 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 34995_8_2011 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 34996_10_2011 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 34997_39_2011 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 34998_59_2011 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 34999_63_2011 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35000_75_2011 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35001_76_2011 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35002_120_2011 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35003_403_2011 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 11 | AAAAAGAAAG.GCAAACCATG | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 34995_8_2011 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 34996_10_2011 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 34997_39_2011 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 34998_59_2011 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 34999_63_2011 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 35000_75_2011 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 35001_76_2011 | NotInAnnotatedGenome |

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|---|---|---|---|---|---|
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 35002_120_2011 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 35003_403_2011 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | C | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 26 | AAAACGCCAA.CGCGCCTATT | A | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 28 | AAAACGGCCG.TATGTTTCTA | A | 510399 F | 19260_WUE_2594 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 34995_8_2011 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 34996_10_2011 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 34997_39_2011 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 34998_59_2011 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 34999_63_2011 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35000_75_2011 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35001_76_2011 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35002_120_2011 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35003_403_2011 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 28 | AAAACGGCCG.TATGTTTCTA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 47 | AAAATTACCT.ACTAAATTCA | T | 2195329 F | 19260_WUE_2594 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | G | x | 34995_8_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 47 | AAAATTACCT.ACTAAATTCA | G | x | 34996_10_2011 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 34997_39_2011 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 34998_59_2011 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 34999_63_2011 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35000_75_2011 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35001_76_2011 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35002_120_2011 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35003_403_2011 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 47 | AAAATTACCT.ACTAAATTCA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 48 | AAAATTAGAC.TATTGTCCAT | G | 1121345 R | 19260_WUE_2594 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 34995_8_2011 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 34996_10_2011 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 34997_39_2011 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 34998_59_2011 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 34999_63_2011 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35000_75_2011 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35001_76_2011 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35002_120_2011 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35003_403_2011 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 48 | AAAATTAGAC.TATTGTCCAT | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
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| 55 | AAACAGGCAA.AAAACCAATC | C | 1106942 R | 19260_WUE_2594 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 34995_8_2011 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 34996_10_2011 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 34997_39_2011 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 34998_59_2011 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 34999_63_2011 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35000_75_2011 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35001_76_2011 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35002_120_2011 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35003_403_2011 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 55 | AAACAGGCAA.AAAACCAATC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 58 | AAACATTTCA.ACGGCCTGAA | G | 2161039 R | 19260_WUE_2594 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 34995_8_2011 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 34996_10_2011 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 34997_39_2011 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 34998_59_2011 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 34999_63_2011 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 35000_75_2011 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 35001_76_2011 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 35002_120_2011 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 35003_403_2011 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 58 | AAACATTTCA.ACGGCCTGAA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 66 | AAACCTATCT.GCCGCATTCC | C | 1436075 F | 19260_WUE_2594 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 34995_8_2011 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 34996_10_2011 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 34997_39_2011 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 34998_59_2011 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 34999_63_2011 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35000_75_2011 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35001_76_2011 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35002_120_2011 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35003_403_2011 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 66 | AAACCTATCT.GCCGCATTCC | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 77 | AAAGCAAAAC.CCGCCCCATC | A | 858300 F | 19260_WUE_2594 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 34995_8_2011 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 34996_10_2011 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 34997_39_2011 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 34998_59_2011 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 34999_63_2011 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35000_75_2011 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35001_76_2011 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35002_120_2011 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35003_403_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 77 | AAAGCAAAAC.CCGCCCCATC | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 81 | AAAGCGAAGA.TAGGGAAACA | G | 1731001 R | 19260_WUE_2594 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 34995_8_2011 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 34996_10_2011 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 34997_39_2011 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 34998_59_2011 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 34999_63_2011 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 35000_75_2011 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 35001_76_2011 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 35002_120_2011 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 35003_403_2011 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 81 | AAAGCGAAGA.TAGGGAAACA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 86 | AAAGGTTACA.TGAAAATTGT | G | 1741250 R | 19260_WUE_2594 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 34995_8_2011 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 34996_10_2011 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 34997_39_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 34998_59_2011 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 34999_63_2011 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35000_75_2011 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35001_76_2011 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35002_120_2011 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35003_403_2011 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 86 | AAAGGTTACA.TGAAAATTGT | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 87 | AAAGGTTGGG.GAGGGTTGGC | G | 1962065 R | 19260_WUE_2594 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 34995_8_2011 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 34996_10_2011 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 34997_39_2011 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 34998_59_2011 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 34999_63_2011 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35000_75_2011 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35001_76_2011 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35002_120_2011 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35003_403_2011 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 87 | AAAGGTTGGG.GAGGGTTGGC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 103 | AAATCGGGAA.ATGCCGTCTG | C | 740510 F | 19260_WUE_2594 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 34990_Tchad54_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 34995_8_2011 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 34996_10_2011 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 34997_39_2011 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 34998_59_2011 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 34999_63_2011 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35000_75_2011 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35001_76_2011 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35002_120_2011 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35003_403_2011 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 103 | AAATCGGGAA.ATGCCGTCTG | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 118 | AAATTCAAGC.GTTCAATGTG | A | 866155 R | 19260_WUE_2594 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | G | x | 34995_8_2011 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | G | x | 34996_10_2011 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 34997_39_2011 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 34998_59_2011 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 34999_63_2011 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35000_75_2011 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35001_76_2011 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35002_120_2011 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35003_403_2011 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 118 | AAATTCAAGC.GTTCAATGTG | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 120 | AAATTTCCCG.CAAAATTGAC | T | 1619707 F | 19260_WUE_2594 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 34995_8_2011 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 34996_10_2011 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 34997_39_2011 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 34998_59_2011 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 34999_63_2011 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35000_75_2011 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35001_76_2011 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35002_120_2011 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35003_403_2011 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 120 | AAATTTCCCG.CAAAATTGAC | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 122 | AAATTTGCGG.ATCCGCCGCA | A | 2037522 R | 19260_WUE_2594 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 34995_8_2011 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 34996_10_2011 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 34997_39_2011 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 34998_59_2011 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 34999_63_2011 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35000_75_2011 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35001_76_2011 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35002_120_2011 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35003_403_2011 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 122 | AAATTTGCGG.ATCCGCCGCA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 128 | AACACATTCC.GATTCGTATT | A | 856497 F | 19260_WUE_2594 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 34995_8_2011 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 34996_10_2011 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 34997_39_2011 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 34998_59_2011 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 34999_63_2011 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35000_75_2011 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35001_76_2011 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35002_120_2011 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35003_403_2011 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 128 | AACACATTCC.GATTCGTATT | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 139 | AACATTTGTT.CAGACGGCAT | T | 1119784 R | 19260_WUE_2594 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 34995_8_2011 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 34996_10_2011 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 34997_39_2011 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 34998_59_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 34999_63_2011 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35000_75_2011 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35001_76_2011 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35002_120_2011 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35003_403_2011 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 139 | AACATTTGTT.CAGACGGCAT | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 151 | AACCGATTTT.TTGCCTTAAA | A | 739707 R | 19260_WUE_2594 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 34995_8_2011 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 34996_10_2011 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 34997_39_2011 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 34998_59_2011 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 34999_63_2011 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35000_75_2011 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35001_76_2011 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35002_120_2011 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35003_403_2011 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 151 | AACCGATTTT.TTGCCTTAAA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 156 | AACCTGAGCC.TTTGTAACAC | C | 2160902 R | 19260_WUE_2594 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 34991_Tchad78_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 156 | AACCTGAGCC.TTTGTAACAC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | C | x | 34995_8_2011 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | C | x | 34996_10_2011 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 34997_39_2011 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 34998_59_2011 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 34999_63_2011 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 35000_75_2011 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 35001_76_2011 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 35002_120_2011 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 35003_403_2011 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 156 | AACCTGAGCC.TTTGTAACAC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 157 | AACCTGCACG.TTCGGCGTTC | A | 2073237 F | 19260_WUE_2594 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 34995_8_2011 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 34996_10_2011 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 34997_39_2011 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 34998_59_2011 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 34999_63_2011 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35000_75_2011 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35001_76_2011 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35002_120_2011 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35003_403_2011 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 157 | AACCTGCACG.TTCGGCGTTC | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 159 | AACCTGTGTT.GGGTTTCGGA | T | 460329 R | 19260_WUE_2594 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 34995_8_2011 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 34996_10_2011 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 34997_39_2011 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 34998_59_2011 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 34999_63_2011 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35000_75_2011 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35001_76_2011 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35002_120_2011 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35003_403_2011 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 159 | AACCTGTGTT.GGGTTTCGGA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 174 | AACGGTCAAT.CTTTTCTGAA | A | 154821 R | 19260_WUE_2594 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | A | x | 34995_8_2011 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | A | x | 34996_10_2011 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 34997_39_2011 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 34998_59_2011 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 34999_63_2011 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35000_75_2011 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35001_76_2011 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35002_120_2011 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35003_403_2011 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 174 | AACGGTCAAT.CTTTTCTGAA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 178 | AACTATTACA.AAAAAACAAA | T | 2162363 R | 19260_WUE_2594 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 34995_8_2011 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 34996_10_2011 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 34997_39_2011 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 34998_59_2011 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 34999_63_2011 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 35000_75_2011 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 35001_76_2011 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 35002_120_2011 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 35003_403_2011 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 178 | AACTATTACA.AAAAAACAAA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | 2079946 R | 19260_WUE_2594 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | G | x | 34995_8_2011 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | G | x | 34996_10_2011 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 34997_39_2011 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 34998_59_2011 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 34999_63_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35000_75_2011 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35001_76_2011 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35002_120_2011 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35003_403_2011 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 182 | AACTCCTTCG.ATGTTGCCGC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 215 | AAGCAGAAAT.TCAAAACAAT | G | 19607 R | 19260_WUE_2594 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 34995_8_2011 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 34996_10_2011 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 34997_39_2011 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 34998_59_2011 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 34999_63_2011 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35000_75_2011 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35001_76_2011 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35002_120_2011 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35003_403_2011 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 215 | AAGCAGAAAT.TCAAAACAAT | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 222 | AAGCCCCTCC.GCCCTTCAGA | T | 1147159 F | 19260_WUE_2594 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 34992_Tchad95_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 34995_8_2011 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 34996_10_2011 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 34997_39_2011 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 34998_59_2011 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 34999_63_2011 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35000_75_2011 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35001_76_2011 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35002_120_2011 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35003_403_2011 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 222 | AAGCCCCTCC.GCCCTTCAGA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | 2037439 R | 19260_WUE_2594 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 34995_8_2011 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 34996_10_2011 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 34997_39_2011 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 34998_59_2011 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 34999_63_2011 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 35000_75_2011 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 35001_76_2011 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 35002_120_2011 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 35003_403_2011 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 232 | AAGCGGCGTG.CAAAACGGGG | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 246 | AAGGGCAGGG.GTCAGCGTTG | G | 856769 F | 19260_WUE_2594 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 34995_8_2011 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 34996_10_2011 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 34997_39_2011 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 34998_59_2011 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 34999_63_2011 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35000_75_2011 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35001_76_2011 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35002_120_2011 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35003_403_2011 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 246 | AAGGGCAGGG.GTCAGCGTTG | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 261 | AATAACATTA.CCGACCGCAA | T | 1303309 R | 19260_WUE_2594 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 34995_8_2011 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 34996_10_2011 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 34997_39_2011 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 34998_59_2011 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 34999_63_2011 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35000_75_2011 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35001_76_2011 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35002_120_2011 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35003_403_2011 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 261 | AATAACATTA.CCGACCGCAA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | A | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 34995_8_2011 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 34996_10_2011 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 34997_39_2011 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 34998_59_2011 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 34999_63_2011 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 35000_75_2011 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 35001_76_2011 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 35002_120_2011 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 35003_403_2011 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | A | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | A | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | A | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | G | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 265 | AATACGGCAA.TTTTTTATTG | A | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 271 | AATAGAGTGG.AAATATGCAT | A | 160916 F | 19260_WUE_2594 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 34995_8_2011 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 34996_10_2011 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 34997_39_2011 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 34998_59_2011 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 34999_63_2011 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35000_75_2011 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35001_76_2011 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35002_120_2011 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35003_403_2011 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 271 | AATAGAGTGG.AAATATGCAT | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 274 | AATATCAACT.TCTGTTTTAA | G | 1139535 F | 19260_WUE_2594 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 34995_8_2011 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 34996_10_2011 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 34997_39_2011 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 34998_59_2011 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 34999_63_2011 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35000_75_2011 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35001_76_2011 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35002_120_2011 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35003_403_2011 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 274 | AATATCAACT.TCTGTTTTAA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 275 | AATATCCGGA.GCACAAAACA | C | 1333345 R | 19260_WUE_2594 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 34995_8_2011 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 34996_10_2011 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 34997_39_2011 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 34998_59_2011 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 34999_63_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35000_75_2011 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35001_76_2011 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35002_120_2011 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35003_403_2011 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 275 | AATATCCGGA.GCACAAAACA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 276 | AATATGTCGG.ATTTCCCGTA | C | 1147044 F | 19260_WUE_2594 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 34995_8_2011 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 34996_10_2011 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 34997_39_2011 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 34998_59_2011 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 34999_63_2011 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35000_75_2011 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35001_76_2011 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35002_120_2011 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35003_403_2011 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 276 | AATATGTCGG.ATTTCCCGTA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 280 | AATCCCGCAA.ATTTTTAGCT | A | 1303843 F | 19260_WUE_2594 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 34992_Tchad95_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 34995_8_2011 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 34996_10_2011 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 34997_39_2011 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 34998_59_2011 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 34999_63_2011 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35000_75_2011 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35001_76_2011 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35002_120_2011 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35003_403_2011 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 280 | AATCCCGCAA.ATTTTTAGCT | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | 390673 F | 19260_WUE_2594 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | A | x | 34995_8_2011 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | A | x | 34996_10_2011 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 34997_39_2011 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 34998_59_2011 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 34999_63_2011 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35000_75_2011 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35001_76_2011 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35002_120_2011 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35003_403_2011 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 291 | AATCGGGCGT.CGCCGCAGGT | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 300 | AATGACGACT.CTTCACCAGC | T | 1487308 R | 19260_WUE_2594 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 34995_8_2011 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 34996_10_2011 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 34997_39_2011 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 34998_59_2011 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 34999_63_2011 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35000_75_2011 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35001_76_2011 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35002_120_2011 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35003_403_2011 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 300 | AATGACGACT.CTTCACCAGC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 315 | AATTATATTA.CCGCGCCTCA | G | 258281 F | 19260_WUE_2594 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | A | x | 34995_8_2011 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | A | x | 34996_10_2011 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 34997_39_2011 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 34998_59_2011 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 34999_63_2011 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35000_75_2011 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35001_76_2011 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35002_120_2011 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35003_403_2011 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 315 | AATTATATTA.CCGCGCCTCA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 318 | AATTCTCTGC.TTTGCTTGAA | T | 508264 F | 19260_WUE_2594 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 34995_8_2011 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 34996_10_2011 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 34997_39_2011 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 34998_59_2011 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 34999_63_2011 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35000_75_2011 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35001_76_2011 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35002_120_2011 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35003_403_2011 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 318 | AATTCTCTGC.TTTGCTTGAA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | T | x | 34995_8_2011 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | T | x | 34996_10_2011 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 34997_39_2011 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 34998_59_2011 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 34999_63_2011 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35000_75_2011 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35001_76_2011 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35002_120_2011 | NotInAnnotatedGenome |

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|---|---|---|---|---|---|
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35003_403_2011 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 320 | AATTGAATGC.GAGTGTCATG | C | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | T | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 34995_8_2011 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 34996_10_2011 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 34997_39_2011 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 34998_59_2011 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 34999_63_2011 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35000_75_2011 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35001_76_2011 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35002_120_2011 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35003_403_2011 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 324 | AATTGGCGGT.GGGATAGATG | C | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 333 | ACAAAAGGAA.CCGATATGCG | G | 1331834 R | 19260_WUE_2594 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | A | x | 34995_8_2011 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | A | x | 34996_10_2011 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 34997_39_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 34998_59_2011 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 34999_63_2011 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35000_75_2011 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35001_76_2011 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35002_120_2011 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35003_403_2011 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 333 | ACAAAAGGAA.CCGATATGCG | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 387 | ACATTAAAAT.ACTGATGAGG | A | 1270322 F | 19260_WUE_2594 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 34995_8_2011 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 34996_10_2011 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 34997_39_2011 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 34998_59_2011 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 34999_63_2011 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35000_75_2011 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35001_76_2011 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35002_120_2011 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35003_403_2011 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 387 | ACATTAAAAT.ACTGATGAGG | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 404 | ACCATTGAGC.ACACCCGCAT | T | 2129775 F | 19260_WUE_2594 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 34990_Tchad54_11 | NotProteinCoding |

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|---|---|---|---|---|---|
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 34991_Tchad78_11 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 34992_Tchad95_11 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 34994_Tchad106_11 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | T | x | 34995_8_2011 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | T | x | 34996_10_2011 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 34997_39_2011 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 34998_59_2011 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 34999_63_2011 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35000_75_2011 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35001_76_2011 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35002_120_2011 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35003_403_2011 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35004_12_15398_XS2_1 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35005_12_13952_XS2_1 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35006_12_15317_XS2_1 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35007_12_15047_XS2_1 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35008_12_15661_XS2_1 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35009_12_15657_XS2_1 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35010_12_17186_XS2_1 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35011_12_17194_XS2_1 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35012_12_17009_XS2_1 | NotProteinCoding |
| 404 | ACCATTGAGC.ACACCCGCAT | C | x | 35013_12_14973_XS2_1 | NotProteinCoding |
| | | | | | |
| 428 | ACCGTTAAGG.ACAGGGTTAA | A | 1303265 F | 19260_WUE_2594 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 34995_8_2011 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 34996_10_2011 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 34997_39_2011 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 34998_59_2011 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 34999_63_2011 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35000_75_2011 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35001_76_2011 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35002_120_2011 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35003_403_2011 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 428 | ACCGTTAAGG.ACAGGGTTAA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 438 | ACCTTTGCTC.ATCAAACATC | C | 1937775 F | 19260_WUE_2594 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | C | x | 34995_8_2011 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | C | x | 34996_10_2011 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 34997_39_2011 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 34998_59_2011 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 34999_63_2011 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35000_75_2011 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35001_76_2011 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35002_120_2011 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35003_403_2011 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 438 | ACCTTTGCTC.ATCAAACATC | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 463 | ACGATGCAAA.GCAATGATGC | G | 2162420 F | 19260_WUE_2594 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 34995_8_2011 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 34996_10_2011 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 34997_39_2011 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 34998_59_2011 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 34999_63_2011 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 35000_75_2011 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 35001_76_2011 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 35002_120_2011 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 35003_403_2011 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 463 | ACGATGCAAA.GCAATGATGC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 489 | ACGGCATCGG.TGTTTATTTG | G | 1118268 F | 19260_WUE_2594 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 34995_8_2011 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 34996_10_2011 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 34997_39_2011 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 34998_59_2011 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 34999_63_2011 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35000_75_2011 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35001_76_2011 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35002_120_2011 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35003_403_2011 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 489 | ACGGCATCGG.TGTTTATTTG | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 497 | ACGGCGGGAA.GGAAAGGGGC | A | 1214778 R | 19260_WUE_2594 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 34995_8_2011 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 34996_10_2011 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 34997_39_2011 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 34998_59_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 34999_63_2011 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35000_75_2011 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35001_76_2011 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35002_120_2011 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35003_403_2011 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 497 | ACGGCGGGAA.GGAAAGGGGC | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 521 | ACTATGGATG.GACTATACGC | C | 2034527 R | 19260_WUE_2594 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 34995_8_2011 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 34996_10_2011 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 34997_39_2011 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 34998_59_2011 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 34999_63_2011 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35000_75_2011 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35001_76_2011 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35002_120_2011 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35003_403_2011 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 521 | ACTATGGATG.GACTATACGC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 522 | ACTCAATTTA.CAAAACAACC | A | 1950992 F | 19260_WUE_2594 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 34992_Tchad95_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | G | x | 34995_8_2011 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | G | x | 34996_10_2011 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 34997_39_2011 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 34998_59_2011 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 34999_63_2011 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35000_75_2011 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35001_76_2011 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35002_120_2011 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35003_403_2011 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 522 | ACTCAATTTA.CAAAACAACC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 551 | AGAATAAGGC.TCAGACGGCA | C | 1731044 R | 19260_WUE_2594 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 34995_8_2011 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 34996_10_2011 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 34997_39_2011 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 34998_59_2011 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 34999_63_2011 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 35000_75_2011 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 35001_76_2011 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 35002_120_2011 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 35003_403_2011 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 551 | AGAATAAGGC.TCAGACGGCA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | A | 1144637 R | 19260_WUE_2594 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 34995_8_2011 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 34996_10_2011 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 34997_39_2011 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 34998_59_2011 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 34999_63_2011 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35000_75_2011 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35001_76_2011 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35002_120_2011 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35003_403_2011 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 554 | AGACAGGAAA.ACACACACTG | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | C | 2072539 F | 19260_WUE_2594 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 34995_8_2011 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 34996_10_2011 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 34997_39_2011 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 34998_59_2011 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 34999_63_2011 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35000_75_2011 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35001_76_2011 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35002_120_2011 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35003_403_2011 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 557 | AGACGGCATC.CCAATCCGCC | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 558 | AGACGGCATC.GGGAGGCGCG | G | 1146379 F | 19260_WUE_2594 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 34995_8_2011 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 34996_10_2011 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 34997_39_2011 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 34998_59_2011 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 34999_63_2011 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35000_75_2011 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35001_76_2011 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35002_120_2011 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35003_403_2011 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 558 | AGACGGCATC.GGGAGGCGCG | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 559 | AGACGGCATC.GGTTCGGCAT | G | 1118237 R | 19260_WUE_2594 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 34995_8_2011 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 34996_10_2011 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 34997_39_2011 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 34998_59_2011 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 34999_63_2011 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35000_75_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35001_76_2011 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35002_120_2011 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35003_403_2011 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 559 | AGACGGCATC.GGTTCGGCAT | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 560 | AGACGGCATT.TGGCTCAGGG | T | 1621314 R | 19260_WUE_2594 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 34995_8_2011 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 34996_10_2011 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 34997_39_2011 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 34998_59_2011 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 34999_63_2011 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35000_75_2011 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35001_76_2011 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35002_120_2011 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35003_403_2011 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 560 | AGACGGCATT.TGGCTCAGGG | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 565 | AGAGGCGGTT.ATAATCAGCG | G | 856365 R | 19260_WUE_2594 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 34994_Tchad106_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 34995_8_2011 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 34996_10_2011 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 34997_39_2011 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 34998_59_2011 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 34999_63_2011 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35000_75_2011 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35001_76_2011 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35002_120_2011 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35003_403_2011 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 565 | AGAGGCGGTT.ATAATCAGCG | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 572 | AGATGATGCC.GGAAACATCA | A | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | G | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | G | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | G | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | G | x | 34995_8_2011 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | G | x | 34996_10_2011 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | A | x | 34997_39_2011 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | A | x | 34998_59_2011 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | A | x | 34999_63_2011 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | A | x | 35000_75_2011 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | A | x | 35001_76_2011 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | A | x | 35002_120_2011 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | G | x | 35003_403_2011 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | A | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | A | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | A | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | G | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | G | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | G | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | A | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | A | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | A | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 572 | AGATGATGCC.GGAAACATCA | G | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |

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|---|---|---|---|---|---|
| 589 | AGCCCTTCCA.AGTACATAGA | T | 460182 F | 19260_WUE_2594 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 34995_8_2011 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 34996_10_2011 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 34997_39_2011 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 34998_59_2011 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 34999_63_2011 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35000_75_2011 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35001_76_2011 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35002_120_2011 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35003_403_2011 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 589 | AGCCCTTCCA.AGTACATAGA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 600 | AGCCTGAAAC.GTGTGGGCAT | T | 1303649 F | 19260_WUE_2594 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 34995_8_2011 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 34996_10_2011 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 34997_39_2011 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 34998_59_2011 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 34999_63_2011 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35000_75_2011 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35001_76_2011 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35002_120_2011 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35003_403_2011 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 600 | AGCCTGAAAC.GTGTGGGCAT | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | 1108539 R | 19260_WUE_2594 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 34995_8_2011 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 34996_10_2011 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 34997_39_2011 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 34998_59_2011 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 34999_63_2011 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35000_75_2011 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35001_76_2011 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35002_120_2011 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35003_403_2011 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 613 | AGCGGTTCAG.CGGCATTTCC | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 644 | AGGGAACAAA.ACGCCTGATA | T | 504969 R | 19260_WUE_2594 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | T | x | 34995_8_2011 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | T | x | 34996_10_2011 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | G | x | 34997_39_2011 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | G | x | 34998_59_2011 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | G | x | 34999_63_2011 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | G | x | 35000_75_2011 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | G | x | 35001_76_2011 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | G | x | 35002_120_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 644 | AGGGAACAAA.ACGCCTGATA | T | x | 35003_403_2011 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 644 | AGGGAACAAA.ACGCCTGATA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 652 | AGGTATAATC.CCCGCATTGC | A | 1186388 F | 19260_WUE_2594 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 34995_8_2011 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 34996_10_2011 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 34997_39_2011 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 34998_59_2011 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 34999_63_2011 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35000_75_2011 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35001_76_2011 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35002_120_2011 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35003_403_2011 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 652 | AGGTATAATC.CCCGCATTGC | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 662 | AGTACAAAAC.TTAAAAAATA | C | 1303786 F | 19260_WUE_2594 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 34995_8_2011 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 34996_10_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 34997_39_2011 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 34998_59_2011 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 34999_63_2011 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35000_75_2011 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35001_76_2011 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35002_120_2011 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35003_403_2011 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 662 | AGTACAAAAC.TTAAAAAATA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 672 | AGTCTGTCTT.GAGATAAACC | C | 265479 F | 19260_WUE_2594 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 34995_8_2011 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 34996_10_2011 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 34997_39_2011 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 34998_59_2011 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 34999_63_2011 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35000_75_2011 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35001_76_2011 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35002_120_2011 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35003_403_2011 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 672 | AGTCTGTCTT.GAGATAAACC | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 686 | ATAAAAGGAA.TATAACTTTA | C | 1694283 F | 19260_WUE_2594 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 34995_8_2011 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 34996_10_2011 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 34997_39_2011 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 34998_59_2011 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 34999_63_2011 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 35000_75_2011 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 35001_76_2011 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 35002_120_2011 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 35003_403_2011 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 686 | ATAAAAGGAA.TATAACTTTA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 687 | ATAAACAACA.ACAGATGCCG | G | 110903 F | 19260_WUE_2594 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | A | x | 34995_8_2011 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | A | x | 34996_10_2011 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 34997_39_2011 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 34998_59_2011 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 34999_63_2011 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35000_75_2011 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35001_76_2011 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35002_120_2011 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35003_403_2011 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 687 | ATAAACAACA.ACAGATGCCG | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 695 | ATAAGCACGG.TGCCGAACAA | T | 1731068 R | 19260_WUE_2594 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 34995_8_2011 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 34996_10_2011 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 34997_39_2011 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 34998_59_2011 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 34999_63_2011 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 35000_75_2011 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 35001_76_2011 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 35002_120_2011 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 35003_403_2011 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 695 | ATAAGCACGG.TGCCGAACAA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 696 | ATAAGCGGGG.GGGTGTCCGA | C | 1270203 R | 19260_WUE_2594 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 34995_8_2011 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 34996_10_2011 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 34997_39_2011 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 34998_59_2011 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 34999_63_2011 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35000_75_2011 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35001_76_2011 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35002_120_2011 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35003_403_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 696 | ATAAGCGGGG.GGGTGTCCGA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
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| 708 | ATAGTTTTAA.TAATTTATAT | A | 860835 F | 19260_WUE_2594 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 34995_8_2011 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 34996_10_2011 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 34997_39_2011 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 34998_59_2011 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 34999_63_2011 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35000_75_2011 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35001_76_2011 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35002_120_2011 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35003_403_2011 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 708 | ATAGTTTTAA.TAATTTATAT | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 709 | ATATCGCCCC.GTATGTCCCG | C | 1959692 F | 19260_WUE_2594 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 34995_8_2011 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 34996_10_2011 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 34997_39_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 34998_59_2011 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 34999_63_2011 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35000_75_2011 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35001_76_2011 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35002_120_2011 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35003_403_2011 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 709 | ATATCGCCCC.GTATGTCCCG | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
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| 719 | ATCAAATTTT.AATAGATAAA | T | 72397 R | 19260_WUE_2594 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 34995_8_2011 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 34996_10_2011 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 34997_39_2011 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 34998_59_2011 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 34999_63_2011 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 35000_75_2011 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 35001_76_2011 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 35002_120_2011 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | C | x | 35003_403_2011 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 719 | ATCAAATTTT.AATAGATAAA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 729 | ATCCGATAAA.ACGGATACAA | T | 255448 F | 19260_WUE_2594 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 34990_Tchad54_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 34995_8_2011 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 34996_10_2011 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 34997_39_2011 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 34998_59_2011 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 34999_63_2011 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35000_75_2011 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35001_76_2011 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35002_120_2011 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35003_403_2011 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 729 | ATCCGATAAA.ACGGATACAA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 740 | ATCGGTTTTT.CGAATCTGCG | G | 741993 R | 19260_WUE_2594 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 34995_8_2011 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 34996_10_2011 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 34997_39_2011 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 34998_59_2011 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 34999_63_2011 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35000_75_2011 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35001_76_2011 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35002_120_2011 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35003_403_2011 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 740 | ATCGGTTTTT.CGAATCTGCG | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 741 | ATCGTCGCTG.GGCTTTGGGG | T | 1253301 R | 19260_WUE_2594 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 34995_8_2011 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 34996_10_2011 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 34997_39_2011 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 34998_59_2011 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 34999_63_2011 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35000_75_2011 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35001_76_2011 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35002_120_2011 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35003_403_2011 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 741 | ATCGTCGCTG.GGCTTTGGGG | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 750 | ATGAAAAGAA.ACCCTATTCC | G | 230324 R | 19260_WUE_2594 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 34995_8_2011 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 34996_10_2011 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 34997_39_2011 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 34998_59_2011 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 34999_63_2011 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35000_75_2011 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35001_76_2011 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35002_120_2011 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35003_403_2011 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 750 | ATGAAAAGAA.ACCCTATTCC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 751 | ATGAAAATCC.TTTTCACAAT | A | 229113 R | 19260_WUE_2594 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 34995_8_2011 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 34996_10_2011 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 34997_39_2011 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 34998_59_2011 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 34999_63_2011 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35000_75_2011 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35001_76_2011 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35002_120_2011 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35003_403_2011 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 751 | ATGAAAATCC.TTTTCACAAT | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 752 | ATGAATGAAG.ACCTTCGAAT | A | 2170025 F | 19260_WUE_2594 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 34995_8_2011 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 34996_10_2011 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 34997_39_2011 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 34998_59_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 34999_63_2011 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35000_75_2011 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35001_76_2011 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35002_120_2011 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35003_403_2011 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 752 | ATGAATGAAG.ACCTTCGAAT | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 762 | ATGCCCTGAC.CCCTGTTTTA | A | 1119068 R | 19260_WUE_2594 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 34995_8_2011 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 34996_10_2011 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 34997_39_2011 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 34998_59_2011 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 34999_63_2011 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35000_75_2011 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35001_76_2011 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35002_120_2011 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35003_403_2011 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 762 | ATGCCCTGAC.CCCTGTTTTA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | 1478583 F | 19260_WUE_2594 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 34991_Tchad78_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | C | x | 34995_8_2011 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | C | x | 34996_10_2011 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 34997_39_2011 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 34998_59_2011 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 34999_63_2011 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35000_75_2011 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35001_76_2011 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35002_120_2011 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35003_403_2011 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 769 | ATGCCGTCTG.CCCCCTTCGG | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 790 | ATGTGTCGTG.ACCGCTTTTC | C | 1144614 F | 19260_WUE_2594 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 34995_8_2011 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 34996_10_2011 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 34997_39_2011 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 34998_59_2011 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 34999_63_2011 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35000_75_2011 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35001_76_2011 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35002_120_2011 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35003_403_2011 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 790 | ATGTGTCGTG.ACCGCTTTTC | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 34995_8_2011 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 34996_10_2011 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 34997_39_2011 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 34998_59_2011 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 34999_63_2011 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 35000_75_2011 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 35001_76_2011 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 35002_120_2011 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 35003_403_2011 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | G | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 793 | ATGTTGTTTG.TTTCATTCTC | A | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 797 | ATTATATCAG.AAAAGCAAAC | G | 1599590 F | 19260_WUE_2594 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 34995_8_2011 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 34996_10_2011 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 34997_39_2011 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 34998_59_2011 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 34999_63_2011 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35000_75_2011 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35001_76_2011 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35002_120_2011 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35003_403_2011 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |

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| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 797 | ATTATATCAG.AAAAGCAAAC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
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| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | G | x | 34995_8_2011 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | G | x | 34996_10_2011 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 34997_39_2011 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 34998_59_2011 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 34999_63_2011 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35000_75_2011 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35001_76_2011 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35002_120_2011 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35003_403_2011 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 813 | ATTGCCAAAG.ATTTTACAGC | A | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
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| 817 | ATTGTTTTGC.GGTTTACGGC | T | 24705 F | 19260_WUE_2594 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 34995_8_2011 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 34996_10_2011 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 34997_39_2011 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 34998_59_2011 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 34999_63_2011 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35000_75_2011 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35001_76_2011 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35002_120_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35003_403_2011 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 817 | ATTGTTTTGC.GGTTTACGGC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 818 | ATTTAATATT.TTATAAGCAA | A | 2034475 R | 19260_WUE_2594 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 34995_8_2011 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 34996_10_2011 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 34997_39_2011 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 34998_59_2011 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 34999_63_2011 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35000_75_2011 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35001_76_2011 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35002_120_2011 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35003_403_2011 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 818 | ATTTAATATT.TTATAAGCAA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 819 | ATTTACAATA.CGGCCGATTC | T | 858333 F | 19260_WUE_2594 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 34995_8_2011 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 34996_10_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 34997_39_2011 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 34998_59_2011 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 34999_63_2011 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35000_75_2011 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35001_76_2011 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35002_120_2011 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35003_403_2011 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 819 | ATTTACAATA.CGGCCGATTC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 820 | ATTTATTATA.AAATGAGAAA | T | 1143474 F | 19260_WUE_2594 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 34995_8_2011 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 34996_10_2011 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 34997_39_2011 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 34998_59_2011 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 34999_63_2011 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35000_75_2011 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35001_76_2011 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35002_120_2011 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35003_403_2011 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 820 | ATTTATTATA.AAATGAGAAA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
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| 828 | ATTTGGATGA.TCCTGTTTGA | T | 2037563 R | 19260_WUE_2594 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 34995_8_2011 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 34996_10_2011 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 34997_39_2011 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 34998_59_2011 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 34999_63_2011 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 35000_75_2011 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 35001_76_2011 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 35002_120_2011 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 35003_403_2011 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 828 | ATTTGGATGA.TCCTGTTTGA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 832 | ATTTTGTAAG.ACCGGTTCAA | A | 858357 R | 19260_WUE_2594 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 34995_8_2011 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 34996_10_2011 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 34997_39_2011 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 34998_59_2011 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 34999_63_2011 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35000_75_2011 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35001_76_2011 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35002_120_2011 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35003_403_2011 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 832 | ATTTTGTAAG.ACCGGTTCAA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | 1158286 R | 19260_WUE_2594 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | T | x | 34995_8_2011 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | T | x | 34996_10_2011 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 34997_39_2011 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 34998_59_2011 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 34999_63_2011 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35000_75_2011 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35001_76_2011 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35002_120_2011 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35003_403_2011 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 833 | ATTTTTGCAT.CTTTTATGGG | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 847 | CAAACGACGC.CTTTGTGGGG | A | 1062756 R | 19260_WUE_2594 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 34995_8_2011 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 34996_10_2011 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 34997_39_2011 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 34998_59_2011 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 34999_63_2011 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35000_75_2011 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35001_76_2011 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35002_120_2011 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35003_403_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 847 | CAAACGACGC.CTTTGTGGGG | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 862 | CAACAGAGCA.GGTTTGAAAC | T | 1843525 R | 19260_WUE_2594 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 34995_8_2011 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 34996_10_2011 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 34997_39_2011 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 34998_59_2011 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 34999_63_2011 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35000_75_2011 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35001_76_2011 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35002_120_2011 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35003_403_2011 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 862 | CAACAGAGCA.GGTTTGAAAC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | 114074 R | 19260_WUE_2594 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | C | x | 34995_8_2011 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | C | x | 34996_10_2011 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 34997_39_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 34998_59_2011 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 34999_63_2011 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35000_75_2011 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35001_76_2011 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35002_120_2011 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35003_403_2011 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 876 | CAAGCGGGCA.TCTAATCGCA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 878 | CAATAATGTA.AGAAAATAAA | G | 2194506 R | 19260_WUE_2594 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | A | x | 34995_8_2011 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | A | x | 34996_10_2011 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 34997_39_2011 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 34998_59_2011 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 34999_63_2011 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35000_75_2011 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35001_76_2011 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35002_120_2011 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35003_403_2011 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 878 | CAATAATGTA.AGAAAATAAA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 882 | CAATCCGCCT.CCTTGTCGTC | A | 2072551 F | 19260_WUE_2594 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 34991_Tchad78_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 34995_8_2011 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 34996_10_2011 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 34997_39_2011 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 34998_59_2011 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 34999_63_2011 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35000_75_2011 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35001_76_2011 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35002_120_2011 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35003_403_2011 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 882 | CAATCCGCCT.CCTTGTCGTC | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 886 | CAATGCGGCA.TTTGAATGCG | G | 1619651 R | 19260_WUE_2594 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 34995_8_2011 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 34996_10_2011 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 34997_39_2011 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 34998_59_2011 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 34999_63_2011 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35000_75_2011 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35001_76_2011 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35002_120_2011 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35003_403_2011 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 886 | CAATGCGGCA.TTTGAATGCG | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 895 | CACAAGCGCA.GAAAGCATTA | C | 1214837 F | 19260_WUE_2594 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 34995_8_2011 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 34996_10_2011 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 34997_39_2011 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 34998_59_2011 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 34999_63_2011 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35000_75_2011 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35001_76_2011 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35002_120_2011 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35003_403_2011 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 895 | CACAAGCGCA.GAAAGCATTA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 914 | CACTTTCAGA.AACTTACAGC | T | 2103713 F | 19260_WUE_2594 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | T | x | 34995_8_2011 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | T | x | 34996_10_2011 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | C | x | 34997_39_2011 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | C | x | 34998_59_2011 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | C | x | 34999_63_2011 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | C | x | 35000_75_2011 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | C | x | 35001_76_2011 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | C | x | 35002_120_2011 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | T | x | 35003_403_2011 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 914 | CACTTTCAGA.AACTTACAGC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 914 | CACTTTCAGA.AACTTACAGC | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 919 | CAGAATGGCT.GGATGGGGCG | C | 858312 R | 19260_WUE_2594 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 34995_8_2011 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 34996_10_2011 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 34997_39_2011 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 34998_59_2011 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 34999_63_2011 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35000_75_2011 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35001_76_2011 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35002_120_2011 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35003_403_2011 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 919 | CAGAATGGCT.GGATGGGGCG | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 923 | CAGACGGCAT.TGTTTACCAA | C | 1099202 F | 19260_WUE_2594 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 34995_8_2011 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 34996_10_2011 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 34997_39_2011 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 34998_59_2011 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 34999_63_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35000_75_2011 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35001_76_2011 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35002_120_2011 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35003_403_2011 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 923 | CAGACGGCAT.TGTTTACCAA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 937 | CAGGTCATCC.CCCCGCAAAA | A | 701580 R | 19260_WUE_2594 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| | | | | | |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 34995_8_2011 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 34996_10_2011 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 34997_39_2011 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 34998_59_2011 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 34999_63_2011 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35000_75_2011 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35001_76_2011 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35002_120_2011 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35003_403_2011 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 937 | CAGGTCATCC.CCCCGCAAAA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 946 | CATAGCAGGC.GATAATGGAG | A | 675652 R | 19260_WUE_2594 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 34991_Tchad78_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 34995_8_2011 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 34996_10_2011 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 34997_39_2011 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 34998_59_2011 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 34999_63_2011 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35000_75_2011 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35001_76_2011 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35002_120_2011 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35003_403_2011 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 946 | CATAGCAGGC.GATAATGGAG | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 958 | CATCGCCTTG.CAATCGGCGC | G | 1146818 F | 19260_WUE_2594 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 34995_8_2011 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 34996_10_2011 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 34997_39_2011 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 34998_59_2011 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 34999_63_2011 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35000_75_2011 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35001_76_2011 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35002_120_2011 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35003_403_2011 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 958 | CATCGCCTTG.CAATCGGCGC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 965 | CATGATTTGT.TGCTTTGTAA | A | 1619810 R | 19260_WUE_2594 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 34995_8_2011 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 34996_10_2011 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 34997_39_2011 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 34998_59_2011 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 34999_63_2011 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35000_75_2011 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35001_76_2011 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35002_120_2011 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35003_403_2011 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 965 | CATGATTTGT.TGCTTTGTAA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 968 | CATTTATCCT.TCTAAAGCCG | C | 192652 R | 19260_WUE_2594 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 34995_8_2011 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 34996_10_2011 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 34997_39_2011 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 34998_59_2011 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 34999_63_2011 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35000_75_2011 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35001_76_2011 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35002_120_2011 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35003_403_2011 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 968 | CATTTATCCT.TCTAAAGCCG | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
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| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 34995_8_2011 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 34996_10_2011 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 34997_39_2011 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 34998_59_2011 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 34999_63_2011 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 35000_75_2011 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 35001_76_2011 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 35002_120_2011 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 35003_403_2011 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | T | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 986 | CCAACCGCTT.CTCTCCGATC | C | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | 1533356 R | 19260_WUE_2594 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 34995_8_2011 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 34996_10_2011 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 34997_39_2011 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 34998_59_2011 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 34999_63_2011 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 35000_75_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 35001_76_2011 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 35002_120_2011 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 35003_403_2011 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1052 | CCCTTTGTGG.GGCAGGAACA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1056 | CCGAACAATC.AGAATAAGGC | A | 1731055 R | 19260_WUE_2594 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 34995_8_2011 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 34996_10_2011 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 34997_39_2011 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 34998_59_2011 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 34999_63_2011 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 35000_75_2011 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 35001_76_2011 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 35002_120_2011 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 35003_403_2011 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1056 | CCGAACAATC.AGAATAAGGC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1078 | CCGCAAAATC.CGACACACTC | A | 1270184 F | 19260_WUE_2594 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 34994_Tchad106_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 34995_8_2011 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 34996_10_2011 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 34997_39_2011 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 34998_59_2011 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 34999_63_2011 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35000_75_2011 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35001_76_2011 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35002_120_2011 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35003_403_2011 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1078 | CCGCAAAATC.CGACACACTC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | G | 1139601 F | 19260_WUE_2594 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 34995_8_2011 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 34996_10_2011 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 34997_39_2011 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 34998_59_2011 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 34999_63_2011 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35000_75_2011 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35001_76_2011 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35002_120_2011 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35003_403_2011 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1119 | CCGTCTGAAC.TCTGTCTGCG | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 34995_8_2011 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 34996_10_2011 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 34997_39_2011 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 34998_59_2011 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 34999_63_2011 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 35000_75_2011 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 35001_76_2011 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 35002_120_2011 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 35003_403_2011 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | G | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 1142 | CCTGCCGGTC.TAAGAGAGGC | A | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 1153 | CCTTTTATTC.ATACACCCGA | A | 507224 R | 19260_WUE_2594 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 34995_8_2011 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 34996_10_2011 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 34997_39_2011 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 34998_59_2011 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 34999_63_2011 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35000_75_2011 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35001_76_2011 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35002_120_2011 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35003_403_2011 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1153 | CCTTTTATTC.ATACACCCGA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1155 | CGAAAATCAA.AACCGATTGC | G | 2034458 F | 19260_WUE_2594 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 34995_8_2011 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 34996_10_2011 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 34997_39_2011 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 34998_59_2011 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 34999_63_2011 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35000_75_2011 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35001_76_2011 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35002_120_2011 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35003_403_2011 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1155 | CGAAAATCAA.AACCGATTGC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | A | x | 34995_8_2011 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | A | x | 34996_10_2011 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 34997_39_2011 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 34998_59_2011 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 34999_63_2011 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35000_75_2011 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35001_76_2011 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35002_120_2011 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35003_403_2011 | NotInAnnotatedGenome |

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|---|---|---|---|---|---|
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 1161 | CGAACAAGCC.AAAACCTGCG | G | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
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| 1188 | CGATAAAATA.CCGATTTAAC | T | 255491 F | 19260_WUE_2594 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 34995_8_2011 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 34996_10_2011 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 34997_39_2011 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 34998_59_2011 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 34999_63_2011 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35000_75_2011 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35001_76_2011 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35002_120_2011 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35003_403_2011 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1188 | CGATAAAATA.CCGATTTAAC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1232 | CGCCATATCC.AACCTGACCG | G | 1147124 F | 19260_WUE_2594 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 34995_8_2011 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 34996_10_2011 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 34997_39_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 34998_59_2011 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 34999_63_2011 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35000_75_2011 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35001_76_2011 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35002_120_2011 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35003_403_2011 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1232 | CGCCATATCC.AACCTGACCG | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | 2080463 F | 19260_WUE_2594 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | T | x | 34995_8_2011 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | T | x | 34996_10_2011 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 34997_39_2011 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 34998_59_2011 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 34999_63_2011 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35000_75_2011 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35001_76_2011 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35002_120_2011 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35003_403_2011 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1239 | CGCCCGCTGA.CCTTTCAGAC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1240 | CGCCCGGACT.AATCGGTTTA | G | 739919 R | 19260_WUE_2594 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 34990_Tchad54_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 34995_8_2011 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 34996_10_2011 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 34997_39_2011 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 34998_59_2011 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 34999_63_2011 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35000_75_2011 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35001_76_2011 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35002_120_2011 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35003_403_2011 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1240 | CGCCCGGACT.AATCGGTTTA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 34995_8_2011 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 34996_10_2011 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 34997_39_2011 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | A | x | 34998_59_2011 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 34999_63_2011 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35000_75_2011 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35001_76_2011 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35002_120_2011 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35003_403_2011 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |

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|---|---|---|---|---|---|
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 1242 | CGCCCGTGCC.GCGATGTACC | G | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 1243 | CGCCCGTTTC.CAAAAAACGC | C | 1139577 R | 19260_WUE_2594 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 34995_8_2011 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 34996_10_2011 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 34997_39_2011 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 34998_59_2011 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 34999_63_2011 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35000_75_2011 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35001_76_2011 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35002_120_2011 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35003_403_2011 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1243 | CGCCCGTTTC.CAAAAAACGC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1259 | CGCCTCAAGG.TTCAGACGGC | G | 19586 F | 19260_WUE_2594 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 34995_8_2011 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 34996_10_2011 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 34997_39_2011 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 34998_59_2011 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 34999_63_2011 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35000_75_2011 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35001_76_2011 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35002_120_2011 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35003_403_2011 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1259 | CGCCTCAAGG.TTCAGACGGC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1287 | CGCTTCCCGA.ATGATAGGCA | T | 856308 F | 19260_WUE_2594 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 34995_8_2011 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 34996_10_2011 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 34997_39_2011 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 34998_59_2011 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 34999_63_2011 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35000_75_2011 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35001_76_2011 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35002_120_2011 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35003_403_2011 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1287 | CGCTTCCCGA.ATGATAGGCA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1292 | CGCTTTGAAG.CAGGCAATGC | A | 915990 R | 19260_WUE_2594 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 34995_8_2011 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 34996_10_2011 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 34997_39_2011 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 34998_59_2011 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 34999_63_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35000_75_2011 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35001_76_2011 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35002_120_2011 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35003_403_2011 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1292 | CGCTTTGAAG.CAGGCAATGC | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1303 | CGGATTGCCG.CGGGACTTGC | T | 1144672 F | 19260_WUE_2594 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 34995_8_2011 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 34996_10_2011 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 34997_39_2011 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 34998_59_2011 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 34999_63_2011 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35000_75_2011 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35001_76_2011 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35002_120_2011 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35003_403_2011 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1303 | CGGATTGCCG.CGGGACTTGC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | C | 510484 R | 19260_WUE_2594 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 34992_Tchad95_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 34995_8_2011 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 34996_10_2011 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 34997_39_2011 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 34998_59_2011 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 34999_63_2011 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35000_75_2011 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35001_76_2011 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35002_120_2011 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35003_403_2011 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1330 | CGGCTTCAAA.ACAAAAGGAA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | C | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 34995_8_2011 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 34996_10_2011 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 34997_39_2011 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 34998_59_2011 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 34999_63_2011 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 35000_75_2011 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 35001_76_2011 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 35002_120_2011 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 35003_403_2011 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 1362 | CGTCAAAAAA.CCGTTACCTC | A | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | 211542 R | 19260_WUE_2594 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 34992_Tchad95_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 34995_8_2011 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 34996_10_2011 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 34997_39_2011 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 34998_59_2011 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 34999_63_2011 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 35000_75_2011 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 35001_76_2011 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 35002_120_2011 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | T | x | 35003_403_2011 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1382 | CGTTATAATC.GGGGTTGTGC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1385 | CGTTGATACT.GGATTAAGAC | C | 1785322 F | 19260_WUE_2594 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | T | x | 34995_8_2011 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | T | x | 34996_10_2011 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 34997_39_2011 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 34998_59_2011 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 34999_63_2011 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35000_75_2011 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35001_76_2011 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35002_120_2011 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35003_403_2011 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1385 | CGTTGATACT.GGATTAAGAC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | 1010178 F | 19260_WUE_2594 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 34995_8_2011 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 34996_10_2011 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 34997_39_2011 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 34998_59_2011 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 34999_63_2011 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 35000_75_2011 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 35001_76_2011 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 35002_120_2011 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 35003_403_2011 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1400 | CTATGCCCCG.CAATCCTGCC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1412 | CTGATTGCCG.TGAAGCAATA | G | 234757 F | 19260_WUE_2594 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 34995_8_2011 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 34996_10_2011 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 34997_39_2011 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 34998_59_2011 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 34999_63_2011 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35000_75_2011 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35001_76_2011 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35002_120_2011 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35003_403_2011 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1412 | CTGATTGCCG.TGAAGCAATA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1422 | CTGCTCTACC.ACTGAGCTAA | G | 9266 F | 19260_WUE_2594 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 34990_Tchad54_11 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 34991_Tchad78_11 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 34992_Tchad95_11 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 34994_Tchad106_11 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 34995_8_2011 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 34996_10_2011 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 34997_39_2011 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 34998_59_2011 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 34999_63_2011 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35000_75_2011 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35001_76_2011 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35002_120_2011 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35003_403_2011 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35004_12_15398_XS2_1 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35005_12_13952_XS2_1 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35006_12_15317_XS2_1 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35007_12_15047_XS2_1 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35008_12_15661_XS2_1 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35009_12_15657_XS2_1 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35010_12_17186_XS2_1 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35011_12_17194_XS2_1 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35012_12_17009_XS2_1 | NotProteinCoding |
| 1422 | CTGCTCTACC.ACTGAGCTAA | A | x | 35013_12_14973_XS2_1 | NotProteinCoding |
| | | | | | |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | 1331900 F | 19260_WUE_2594 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | C | x | 34995_8_2011 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | C | x | 34996_10_2011 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 34997_39_2011 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 34998_59_2011 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 34999_63_2011 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35000_75_2011 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35001_76_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35002_120_2011 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35003_403_2011 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1430 | CTTCAATTAT.CCCCCCCCCC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | G | x | 34995_8_2011 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | G | x | 34996_10_2011 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 34997_39_2011 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 34998_59_2011 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 34999_63_2011 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35000_75_2011 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35001_76_2011 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35002_120_2011 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35003_403_2011 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 1431 | CTTCAGGACG.CTTACGTCGC | A | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | 1284627 R | 19260_WUE_2594 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 34995_8_2011 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 34996_10_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 34997_39_2011 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 34998_59_2011 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 34999_63_2011 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 35000_75_2011 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 35001_76_2011 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 35003_403_2011 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1448 | CTTGGATGCG.GAATGTCGGC | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1452 | CTTGTCAGGT.TCGACCCAAC | T | 1995480 F | 19260_WUE_2594 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 34995_8_2011 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 34996_10_2011 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 34997_39_2011 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 34998_59_2011 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 34999_63_2011 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35000_75_2011 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35001_76_2011 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35002_120_2011 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35003_403_2011 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1452 | CTTGTCAGGT.TCGACCCAAC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | G | 1134555 R | 19260_WUE_2594 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 34990_Tchad54_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 34995_8_2011 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 34996_10_2011 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 34997_39_2011 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 34998_59_2011 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 34999_63_2011 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35000_75_2011 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35001_76_2011 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35002_120_2011 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35003_403_2011 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1463 | CTTTTAAAAT.CCGTCTGAAA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1468 | GAAACACACT.CATCCGGAAC | A | 2159141 R | 19260_WUE_2594 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 34995_8_2011 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 34996_10_2011 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 34997_39_2011 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 34998_59_2011 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 34999_63_2011 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 35000_75_2011 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 35001_76_2011 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 35002_120_2011 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 35003_403_2011 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1468 | GAAACACACT.CATCCGGAAC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1468 | GAAACACACT.CATCCGGAAC | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1470 | GAAACCCTTT.AGACGGCATC | C | 1142200 F | 19260_WUE_2594 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 34995_8_2011 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 34996_10_2011 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 34997_39_2011 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 34998_59_2011 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 34999_63_2011 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35000_75_2011 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35001_76_2011 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35002_120_2011 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35003_403_2011 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1470 | GAAACCCTTT.AGACGGCATC | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 34995_8_2011 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 34996_10_2011 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 34997_39_2011 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 34998_59_2011 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 34999_63_2011 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 35000_75_2011 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 35001_76_2011 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 35002_120_2011 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 35003_403_2011 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |

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|---|---|---|---|---|---|
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | G | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 1490 | GAATGCAGCA.CATCCTGACC | T | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 34995_8_2011 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 34996_10_2011 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 34997_39_2011 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 34998_59_2011 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 34999_63_2011 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 35000_75_2011 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 35001_76_2011 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 35002_120_2011 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 35003_403_2011 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | A | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 1491 | GAATTACGAA.CGTGTAAAGC | G | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 1494 | GACCGTTAAC.CCGAAACAAA | A | 509050 R | 19260_WUE_2594 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 34995_8_2011 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 34996_10_2011 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 34997_39_2011 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 34998_59_2011 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 34999_63_2011 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35000_75_2011 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35001_76_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35002_120_2011 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35003_403_2011 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1494 | GACCGTTAAC.CCGAAACAAA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | A | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | A | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | A | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 34995_8_2011 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 34996_10_2011 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 34997_39_2011 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 34998_59_2011 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 34999_63_2011 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 35000_75_2011 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 35001_76_2011 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 35002_120_2011 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | A | x | 35003_403_2011 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | A | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | A | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | A | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | G | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 1500 | GACGGGTCGC.GGAACAATAA | A | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | 692112 F | 19260_WUE_2594 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | A | x | 34995_8_2011 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | A | x | 34996_10_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 34997_39_2011 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 34998_59_2011 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 34999_63_2011 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35000_75_2011 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35001_76_2011 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35002_120_2011 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35003_403_2011 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1504 | GAGAAGGGAA.ATTAACAAAA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1514 | GATGCAGTAA.GTGGGTTATA | C | 867252 F | 19260_WUE_2594 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 34995_8_2011 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 34996_10_2011 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 34997_39_2011 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 34998_59_2011 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 34999_63_2011 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35000_75_2011 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35001_76_2011 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35002_120_2011 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35003_403_2011 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1514 | GATGCAGTAA.GTGGGTTATA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1519 | GATGTTGTGG.GGTTTCAAAC | C | 253859 R | 19260_WUE_2594 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 34995_8_2011 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 34996_10_2011 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 34997_39_2011 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 34998_59_2011 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 34999_63_2011 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35000_75_2011 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35001_76_2011 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35002_120_2011 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35003_403_2011 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1519 | GATGTTGTGG.GGTTTCAAAC | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 34995_8_2011 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 34996_10_2011 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 34997_39_2011 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 34998_59_2011 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 34999_63_2011 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 35000_75_2011 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 35001_76_2011 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 35002_120_2011 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 35003_403_2011 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | A | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |

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|---|---|---|---|---|---|
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 1521 | GATTATTATT.TCAAAACGCC | T | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 1554 | GCATAAACAG.GAATTTATGA | G | 1141633 R | 19260_WUE_2594 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 34995_8_2011 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 34996_10_2011 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 34997_39_2011 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 34998_59_2011 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 34999_63_2011 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35000_75_2011 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35001_76_2011 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35002_120_2011 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35003_403_2011 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1554 | GCATAAACAG.GAATTTATGA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1556 | GCATAACCGC.GGTTGGAACA | C | 1085026 F | 19260_WUE_2594 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | C | x | 34995_8_2011 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | C | x | 34996_10_2011 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 34997_39_2011 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 34998_59_2011 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 34999_63_2011 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35000_75_2011 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35001_76_2011 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35002_120_2011 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35003_403_2011 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1556 | GCATAACCGC.GGTTGGAACA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1557 | GCATACCGGC.ATGCCGATAC | A | 1147062 R | 19260_WUE_2594 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 34995_8_2011 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 34996_10_2011 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 34997_39_2011 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 34998_59_2011 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 34999_63_2011 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35000_75_2011 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35001_76_2011 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35002_120_2011 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35003_403_2011 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1557 | GCATACCGGC.ATGCCGATAC | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1560 | GCATATGCGC.CCTACCAGCC | T | 2109393 F | 19260_WUE_2594 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 34995_8_2011 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 34996_10_2011 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 34997_39_2011 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 34998_59_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 34999_63_2011 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35000_75_2011 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35001_76_2011 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35002_120_2011 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35003_403_2011 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1560 | GCATATGCGC.CCTACCAGCC | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1577 | GCCCCATGCC.TTTTTTTACA | A | 956185 R | 19260_WUE_2594 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 34995_8_2011 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 34996_10_2011 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 34997_39_2011 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 34998_59_2011 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 34999_63_2011 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35000_75_2011 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35001_76_2011 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35002_120_2011 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35003_403_2011 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1577 | GCCCCATGCC.TTTTTTTACA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1640 | GCGGTTCGGC.TTCAAATGCC | G | 2073262 R | 19260_WUE_2594 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 34991_Tchad78_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 34995_8_2011 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 34996_10_2011 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 34997_39_2011 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 34998_59_2011 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 34999_63_2011 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35000_75_2011 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35001_76_2011 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35002_120_2011 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35003_403_2011 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1640 | GCGGTTCGGC.TTCAAATGCC | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | A | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | A | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | A | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 34995_8_2011 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 34996_10_2011 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 34997_39_2011 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 34998_59_2011 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 34999_63_2011 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 35000_75_2011 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 35001_76_2011 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 35002_120_2011 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | A | x | 35003_403_2011 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | A | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | A | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | A | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 1667 | GCTTCTTCCT.GCGCGAAGCC | G | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |

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|---|---|---|---|---|---|
| 1667 | GCTTCTTCCT.GCGCGAAGCC | A | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | 1731033 F | 19260_WUE_2594 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 34995_8_2011 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 34996_10_2011 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 34997_39_2011 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 34998_59_2011 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 34999_63_2011 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 35000_75_2011 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 35001_76_2011 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 35002_120_2011 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 35003_403_2011 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1680 | GGAAGGAGCG.TGCCGTCTGA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | 2159169 F | 19260_WUE_2594 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 34995_8_2011 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 34996_10_2011 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 34997_39_2011 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 34998_59_2011 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 34999_63_2011 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 35000_75_2011 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 35001_76_2011 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 35002_120_2011 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 35003_403_2011 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1705 | GGCGTTATCC.CCGAGTGTCA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1705 | GGCGTTATCC.CCGAGTGTCA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1728 | GGTGCATAGG.GGGAAGATAA | C | 1695155 R | 19260_WUE_2594 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 34995_8_2011 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 34996_10_2011 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 34997_39_2011 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 34998_59_2011 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 34999_63_2011 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35000_75_2011 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35001_76_2011 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35002_120_2011 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35003_403_2011 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1728 | GGTGCATAGG.GGGAAGATAA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | A | 1215599 R | 19260_WUE_2594 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 34995_8_2011 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 34996_10_2011 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 34997_39_2011 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 34998_59_2011 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 34999_63_2011 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35000_75_2011 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35001_76_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35002_120_2011 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35003_403_2011 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1738 | GTAAGCAAAC.TGCTTCAGAC | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1753 | GTCTAACGGA.GCGCCGGAGA | T | 851310 R | 19260_WUE_2594 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 34995_8_2011 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 34996_10_2011 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 34997_39_2011 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 34998_59_2011 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 34999_63_2011 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35000_75_2011 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35001_76_2011 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35002_120_2011 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35003_403_2011 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1753 | GTCTAACGGA.GCGCCGGAGA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1754 | GTCTGAAAAC.GGATGGGAAA | A | 742054 F | 19260_WUE_2594 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 34995_8_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 34996_10_2011 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 34997_39_2011 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 34998_59_2011 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 34999_63_2011 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35000_75_2011 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35001_76_2011 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35002_120_2011 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35003_403_2011 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1754 | GTCTGAAAAC.GGATGGGAAA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1764 | GTTATTATAT.GCAAACGGCA | A | 856189 F | 19260_WUE_2594 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 34995_8_2011 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 34996_10_2011 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 34997_39_2011 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 34998_59_2011 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 34999_63_2011 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35000_75_2011 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35001_76_2011 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35002_120_2011 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35003_403_2011 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1764 | GTTATTATAT.GCAAACGGCA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | 2172965 F | 19260_WUE_2594 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | G | x | 34995_8_2011 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | G | x | 34996_10_2011 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 34997_39_2011 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 34998_59_2011 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 34999_63_2011 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35000_75_2011 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35001_76_2011 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35002_120_2011 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35003_403_2011 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1765 | GTTCTACAAA.TAAAGTGGTA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1771 | GTTTCCATTG.GCAAATGAAA | G | 1256139 R | 19260_WUE_2594 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 34995_8_2011 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 34996_10_2011 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 34997_39_2011 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 34998_59_2011 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 34999_63_2011 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35000_75_2011 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35001_76_2011 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35002_120_2011 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35003_403_2011 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1771 | GTTTCCATTG.GCAAATGAAA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1786 | TAAATTAATG.AATAATGCAA | T | 1124059 F | 19260_WUE_2594 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 34995_8_2011 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 34996_10_2011 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 34997_39_2011 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 34998_59_2011 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 34999_63_2011 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35000_75_2011 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35001_76_2011 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35002_120_2011 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35003_403_2011 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1786 | TAAATTAATG.AATAATGCAA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1790 | TAATCCTGTT.CTTATGGAAA | G | 529244 R | 19260_WUE_2594 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | G | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | G | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | G | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | G | x | 34995_8_2011 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | G | x | 34996_10_2011 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | A | x | 34997_39_2011 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | A | x | 34998_59_2011 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | A | x | 34999_63_2011 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | A | x | 35000_75_2011 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | A | x | 35001_76_2011 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | A | x | 35002_120_2011 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1790 | TAATCCTGTT.CTTATGGAAA | G | x | 35003_403_2011 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | G | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | G | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1790 | TAATCCTGTT.CTTATGGAAA | G | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1793 | TACCAATACC.AACAGACAAA | A | 2037386 F | 19260_WUE_2594 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | A | x | 34995_8_2011 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | A | x | 34996_10_2011 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | C | x | 34997_39_2011 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | C | x | 34998_59_2011 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | C | x | 34999_63_2011 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | C | x | 35000_75_2011 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | C | x | 35001_76_2011 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | C | x | 35002_120_2011 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1793 | TACCAATACC.AACAGACAAA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1803 | TATAAAAAAT.TTTTTCTTAA | C | 1398299 R | 19260_WUE_2594 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 34995_8_2011 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 34996_10_2011 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 34997_39_2011 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 34998_59_2011 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 34999_63_2011 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35000_75_2011 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35001_76_2011 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35002_120_2011 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35003_403_2011 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1803 | TATAAAAAAT.TTTTTCTTAA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | 2160757 R | 19260_WUE_2594 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 34995_8_2011 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 34996_10_2011 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 34997_39_2011 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 34998_59_2011 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 34999_63_2011 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 35000_75_2011 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 35001_76_2011 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 35002_120_2011 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 35003_403_2011 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1809 | TATCGCCGCC.ATATGCCGCA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 34990_Tchad54_11 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 34991_Tchad78_11 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 34992_Tchad95_11 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 34994_Tchad106_11 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 34995_8_2011 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 34996_10_2011 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 34997_39_2011 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 34998_59_2011 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 34999_63_2011 | NotInAnnotatedGenome |

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|---|---|---|---|---|---|
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 35000_75_2011 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 35001_76_2011 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 35002_120_2011 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 35003_403_2011 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 35004_12_15398_XS2_1 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 35005_12_13952_XS2_1 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 35006_12_15317_XS2_1 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | T | x | 35007_12_15047_XS2_1 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 35008_12_15661_XS2_1 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 35009_12_15657_XS2_1 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 35010_12_17186_XS2_1 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 35011_12_17194_XS2_1 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 35012_12_17009_XS2_1 | NotInAnnotatedGenome |
| 1841 | TCCTCACCCT.CGGGCCGAAA | G | x | 35013_12_14973_XS2_1 | NotInAnnotatedGenome |
| | | | | | |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | C | 1253393 F | 19260_WUE_2594 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 34995_8_2011 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 34996_10_2011 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 34997_39_2011 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 34998_59_2011 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 34999_63_2011 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35000_75_2011 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35001_76_2011 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35002_120_2011 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35003_403_2011 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1843 | TCCTGCCGCA.ACGCCGCAGA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | 1731019 R | 19260_WUE_2594 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 34992_Tchad95_11 | UnannotatedRegion |

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|---|---|---|---|---|---|
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 34995_8_2011 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 34996_10_2011 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 34997_39_2011 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 34998_59_2011 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 34999_63_2011 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 35000_75_2011 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 35001_76_2011 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 35002_120_2011 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 35003_403_2011 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | G | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1844 | TCCTTCCGAT.CCGTCTGAAA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1854 | TCGCGGCGGC.GCACCGAGCA | T | 856443 R | 19260_WUE_2594 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 34995_8_2011 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 34996_10_2011 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 34997_39_2011 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 34998_59_2011 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 34999_63_2011 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35000_75_2011 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35001_76_2011 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35002_120_2011 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35003_403_2011 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |

| | | | | | |
|---|---|---|---|---|---|
| 1854 | TCGCGGCGGC.GCACCGAGCA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1870 | TCGTTCATAT.GCTTCCTTAA | C | 2063679 R | 19260_WUE_2594 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | C | x | 34995_8_2011 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | C | x | 34996_10_2011 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | T | x | 34997_39_2011 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | T | x | 34998_59_2011 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | T | x | 34999_63_2011 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | T | x | 35000_75_2011 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | T | x | 35001_76_2011 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | T | x | 35002_120_2011 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | C | x | 35003_403_2011 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1870 | TCGTTCATAT.GCTTCCTTAA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1872 | TCTGAAACAG.AGATGTTTCA | T | 1254523 R | 19260_WUE_2594 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 34995_8_2011 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 34996_10_2011 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 34997_39_2011 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 34998_59_2011 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 34999_63_2011 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35000_75_2011 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35001_76_2011 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35002_120_2011 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35003_403_2011 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |

| | | | | | |
|---|---|---|---|---|---|
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1872 | TCTGAAACAG.AGATGTTTCA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1880 | TGAATTGGGT.TATATGAACA | T | 1733175 R | 19260_WUE_2594 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 34995_8_2011 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 34996_10_2011 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 34997_39_2011 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 34998_59_2011 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 34999_63_2011 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35000_75_2011 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35001_76_2011 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35002_120_2011 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35003_403_2011 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1880 | TGAATTGGGT.TATATGAACA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | 2160743 R | 19260_WUE_2594 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | C | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | C | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 34995_8_2011 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 34996_10_2011 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 34997_39_2011 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 34998_59_2011 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 34999_63_2011 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 35000_75_2011 | UnannotatedRegion |

| | | | | | |
|---|---|---|---|---|---|
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 35001_76_2011 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 35002_120_2011 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 35003_403_2011 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | C | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | C | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | C | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1889 | TGCCGCAGCA.CCGTCTTCCA | C | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | 2037462 F | 19260_WUE_2594 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | A | x | 34994_Tchad106_11 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 34995_8_2011 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 34996_10_2011 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 34997_39_2011 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 34998_59_2011 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 34999_63_2011 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 35000_75_2011 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 35001_76_2011 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 35002_120_2011 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | A | x | 35003_403_2011 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | G | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1895 | TGGAAAGAAG.CGAACCGAAA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1910 | TTAATTACAC.CCACTACAAA | G | 2051759 F | 19260_WUE_2594 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 34995_8_2011 | UnannotatedRegion |

| | | | | | |
|---|---|---|---|---|---|
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 34996_10_2011 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 34997_39_2011 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 34998_59_2011 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 34999_63_2011 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35000_75_2011 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35001_76_2011 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35002_120_2011 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35003_403_2011 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1910 | TTAATTACAC.CCACTACAAA | A | x | 35013_12_14973_XS2_1 | UnannotatedRegion |
| | | | | | |
| 1912 | TTATTAGAAT.TATTTGCAAA | C | 1270275 F | 19260_WUE_2594 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 34990_Tchad54_11 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 34991_Tchad78_11 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 34992_Tchad95_11 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 34995_8_2011 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 34996_10_2011 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 34997_39_2011 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 34998_59_2011 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 34999_63_2011 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35000_75_2011 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35001_76_2011 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35002_120_2011 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35003_403_2011 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35004_12_15398_XS2_1 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35005_12_13952_XS2_1 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35006_12_15317_XS2_1 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35007_12_15047_XS2_1 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35008_12_15661_XS2_1 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35009_12_15657_XS2_1 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35010_12_17186_XS2_1 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35011_12_17194_XS2_1 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35012_12_17009_XS2_1 | UnannotatedRegion |
| 1912 | TTATTAGAAT.TATTTGCAAA | T | x | 35013_12_14973_XS2_1 | UnannotatedRegion |

# Appendix 3: Supplemental material for Chapter 5

## Supplemental Tables

### Supplemental Table 1: cgMLST list of genes and function

| Locus | Full name/Product | sequence status |
|---|---|---|
| **NEIS0001** | UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase (EC 3.5.1.-) | Complete |
| **NEIS0004** | peptidyl-prolyl cis-trans isomerase | Complete |
| **NEIS0006** | glycerate dehydrogenase | Complete |
| **NEIS0008** | glucosamine--fructose-6-phosphate aminotransferase | Complete |
| **NEIS0010** | outer membrane lipoprotein Gna33 | Complete |
| **NEIS0011** | hypothetical protein | Complete |
| **NEIS0012** | hypothetical protein | Complete |
| **NEIS0013** | hypothetical protein | Complete |
| **NEIS0014** | putative phosphonoacetate hydrolase | Complete |
| **NEIS0015** | UDP-N-acetylglucosamine pyrophosphorylase | Complete |
| **NEIS0017** | putative solute-binding periplasmic protein | Complete |
| **NEIS0018** | putative inner membrane protein | Complete |
| **NEIS0019** | hypothetical protein | Complete |
| **NEIS0020** | peptide methionine sulfoxide reductase MsrA/MsrB | Incomplete |
| **NEIS0021** | probable signal recognition particle protein  cell division protein | Incomplete |
| **NEIS0034** | putative inner membrane protein | Incomplete |
| **NEIS0035** | PilT-like protein | Complete |
| **NEIS0036** | type IV pilus retraction ATPase PilT | Complete |
| **NEIS0037** | hypothetical protein | Incomplete |
| **NEIS0038** | putative lipoprotein | Complete |
| **NEIS0039** | pyrroline-5-carboxylate reductase | Incomplete |
| **NEIS0040** | DnaK suppressor protein | Complete |
| **NEIS0043** | chaperone protein DnaJ | Complete |
| **NEIS0045** | dTDP-4-dehydrorhamnose 3,5-epimerase | Incomplete |
| **NEIS0048** | UDP-glucose epimerase | Incomplete |
| **NEIS0059** | putative transcriptional accessory protein | Incomplete |
| **NEIS0069** | sodium/glutamate symport carrier protein | Complete |
| **NEIS0071** | putative lipoprotein | Complete |
| **NEIS0073** | outer membrane transport protein | Complete |
| **NEIS0074** | pyruvate kinase (EC 2.7.1.40) | Complete |
| **NEIS0092** | putative inner membrane protein | Complete |
| **NEIS0097** | hypothetical protein | Incomplete |
| **NEIS0098** | aspartate carbamoyltransferase catalytic subunit | Complete |
| **NEIS0099** | pyrI | Complete |
| **NEIS0100** | hypothetical protein | Complete |

| | | |
|---|---|---|
| **NEIS0101** | hypothetical protein | Complete |
| **NEIS0102** | peptide deformylase | Complete |
| **NEIS0103** | methionyl-tRNA formyltransferase | Complete |
| **NEIS0104** | SUN-family protein | Incomplete |
| **NEIS0105** | hypothetical protein | Incomplete |
| **NEIS0106** | putative two-component sensor kinase | Incomplete |
| **NEIS0107** | putative two-component trancriptional regulator | Complete |
| **NEIS0108** | SMF-family protein | Complete |
| **NEIS0109** | SMG-family protein | Complete |
| **NEIS0110** | DNA topoisomerase I | Complete |
| **NEIS0113** | hypothetical protein | Complete |
| **NEIS0114** | hypothetical protein | Complete |
| **NEIS0115** | putative ferredoxin | Complete |
| **NEIS0118** | transcription antitermination protein | Complete |
| **NEIS0119** | 50S ribosomal protein L11 | Complete |
| **NEIS0120** | 50S ribosomal protein L1 | Complete |
| **NEIS0121** | 50S ribosomal protein L10 | Complete |
| **NEIS0122** | 50S ribosomal protein L7/L12 | Complete |
| **NEIS0123** | DNA-directed RNA polymerase subunit beta | Incomplete |
| **NEIS0124** | DNA-directed RNA polymerase subunit beta' | Incomplete |
| **NEIS0125** | 30S ribosomal protein S12 | Complete |
| **NEIS0126** | 30S ribosomal protein S7 | Complete |
| **NEIS0127** | elongation factor G | Complete |
| **NEIS0129** | 30S ribosomal protein S10 | Complete |
| **NEIS0132** | 50S ribosomal protein L3 | Complete |
| **NEIS0133** | 50S ribosomal protein L4 | Complete |
| **NEIS0134** | 50S ribosomal protein L23 | Complete |
| **NEIS0135** | 50S ribosomal protein L2 | Complete |
| **NEIS0136** | 30S ribosomal protein S19 | Complete |
| **NEIS0137** | 50S ribosomal protein L22 | Complete |
| **NEIS0138** | 30S ribosomal protein S3 | Complete |
| **NEIS0140** | 50S ribosomal protein L29 | Complete |
| **NEIS0141** | 30S ribosomal protein S17 | Complete |
| **NEIS0143** | 50S ribosomal protein L24 | Complete |
| **NEIS0144** | 50S ribosomal protein L5 | Complete |
| **NEIS0145** | 30S ribosomal protein S14 | Complete |
| **NEIS0146** | 30S ribosomal protein S8 | Complete |
| **NEIS0147** | 50S ribosomal protein L6 | Complete |
| **NEIS0149** | 30S ribosomal protein S5 | Complete |
| **NEIS0150** | 50S ribosomal protein L30 | Complete |
| **NEIS0152** | preprotein translocase subunit SecY | Complete |
| **NEIS0155** | 30S ribosomal protein S13 | Complete |
| **NEIS0157** | 30S ribosomal protein S4 | Complete |

| | | |
|---|---|---|
| **NEIS0158** | DNA-directed RNA polymerase subunit alpha | Complete |
| **NEIS0159** | 50S ribosomal protein L17 | Complete |
| **NEIS0160** | septum formation inhibitor | Complete |
| **NEIS0161** | septum site-determining protein | Complete |
| **NEIS0162** | cell division topological specificity factor MinE | Complete |
| **NEIS0163** | putative hydrogen peroxide-inducible genes activator | Incomplete |
| **NEIS0164** | valyl-tRNA synthetase | Incomplete |
| **NEIS0168** | UDP-N-acetylglucosamine acyltransferase | Complete |
| **NEIS0170** | (3R)-hydroxymyristoyl-ACP dehydratase | Complete |
| **NEIS0172** | putative outer membrane protein | Complete |
| **NEIS0173** | outer membrane protein OMP85 | Complete |
| **NEIS0174** | putative inner membrane protease | Incomplete |
| **NEIS0175** | 1-deoxy-D-xylulose 5-phosphate reductoisomerase | Complete |
| **NEIS0176** | phosphatidate cytidylyltransferase | Incomplete |
| **NEIS0177** | putative undecaprenyl diphosphate synthase | Complete |
| **NEIS0178** | ribosome recycling factor | Complete |
| **NEIS0179** | putative inner membrane protein | Incomplete |
| **NEIS0180** | hypothetical protein | Incomplete |
| **NEIS0181** | 16S rRNA methyltransferase GidB | Complete |
| **NEIS0182** | hypothetical protein | Complete |
| **NEIS0183** | ribonuclease HII | Complete |
| **NEIS0184** | tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA | Incomplete |
| **NEIS0185** | putative inner membrane amino-acid transport protein | Complete |
| **NEIS0186** | 4-hydroxythreonine-4-phosphate dehydrogenase | Incomplete |
| **NEIS0187** | ribonuclease E | Incomplete |
| **NEIS0190** | ribosomal large subunit pseudouridine synthase C | Complete |
| **NEIS0191** | lipid-A-disaccharide synthase (EC 2.4.1.182) | Incomplete |
| **NEIS0195** | dihydrodipicolinate reductase | Complete |
| **NEIS0196** | putative outer membrane lipoprotein | Complete |
| **NEIS0197** | ferric uptake regulation protein | Incomplete |
| **NEIS0198** | leucyl/phenylalanyl-tRNA--protein transferase | Complete |
| **NEIS0199** | glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) | Complete |
| **NEIS0200** | putative ferredoxin | Incomplete |
| **NEIS0201** | putative inner membrane transport protein | Complete |
| **NEIS0204** | DNA gyrase subunit B | Complete |
| **NEIS0205** | putative inner membrane protein | Incomplete |
| **NEIS0206** | oligopeptidase A | Complete |
| **NEIS0207** | conserved hypothetical protein | Complete |
| **NEIS0211** | catalase (KatA) | Incomplete |
| **NEIS0216** | 3-oxoacyl-(acyl carrier protein) synthase II | Complete |
| **NEIS0217** | acyl carrier protein | Complete |
| **NEIS0218** | dihydroorotate dehydrogenase 2 | Complete |
| **NEIS0222** | hypothetical protein | Complete |

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|---|---|---|
| **NEIS0224** | bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase | Incomplete |
| **NEIS0230** | DNA helicase II | Incomplete |
| **NEIS0237** | NADH dehydrogenase I chain A | Complete |
| **NEIS0238** | nuoB; NADH dehydrogenase subunit B | Incomplete |
| **NEIS0239** | NADH dehydrogenase subunit C | Incomplete |
| **NEIS0240** | NADH dehydrogenase subunit D | Complete |
| **NEIS0241** | NADH dehydrogenase subunit E | Complete |
| **NEIS0242** | NADH dehydrogenase I chain F | Complete |
| **NEIS0244** | NADH dehydrogenase subunit G | Complete |
| **NEIS0245** | NADH dehydrogenase I chain H | Complete |
| **NEIS0246** | NADH dehydrogenase subunit I | Complete |
| **NEIS0247** | NADH dehydrogenase I chain J | Complete |
| **NEIS0248** | NADH dehydrogenase subunit K | Complete |
| **NEIS0251** | NADH dehydrogenase subunit L | Complete |
| **NEIS0252** | NADH dehydrogenase subunit M | Complete |
| **NEIS0253** | NADH dehydrogenase subunit N | Incomplete |
| **NEIS0254** | inner membrane protein | Complete |
| **NEIS0255** | geranyltranstransferase | Complete |
| **NEIS0256** | exodeoxyribonuclease VII small subunit | Complete |
| **NEIS0257** | ribosome-associated GTPase | Complete |
| **NEIS0258** | putative ABC transporter | Complete |
| **NEIS0259** | Holliday junction DNA helicase RuvA | Complete |
| **NEIS0260** | hypothetical protein | Complete |
| **NEIS0261** | putative periplasmic protein | Complete |
| **NEIS0262** | putative tRNA/rRNA methyltransferase | Complete |
| **NEIS0263** | hypothetical protein | Complete |
| **NEIS0264** | hydrolase | Complete |
| **NEIS0265** | hypothetical protein | Complete |
| **NEIS0269** | ATP-dependent DNA helicase | Incomplete |
| **NEIS0270** | indole-3-glycerol-phosphate synthase | Incomplete |
| **NEIS0271** | hypothetical protein | Complete |
| **NEIS0272** | putative inner membrane protein | Complete |
| **NEIS0273** | thiol:disulphide interchange protein encodes DsbA1; oxidoreductase | Complete |
| **NEIS0274** | hypothetical protein | Complete |
| **NEIS0275** | putative outer membrane solvent tolerance protein | Complete |
| **NEIS0276** | putative rotamase | Complete |
| **NEIS0288** | hypothetical protein | Incomplete |
| **NEIS0289** | hypothetical protein | Complete |
| **NEIS0290** | adenylosuccinate lyase | Complete |
| **NEIS0292** | conserved hypothetical protein | Complete |
| **NEIS0293** | ATP-dependent DNA helicase DinG | Complete |
| **NEIS0302** | 3-ketoacyl-(acyl-carrier-protein) reductase | Complete |
| **NEIS0303** | GMP synthase | Incomplete |

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|---|---|---|
| **NEIS0304** | Lipid A export ATP-binding/permease protein (IM) | Complete |
| **NEIS0305** | putative malonyl CoA-acyl carrier protein transacylase | Complete |
| **NEIS0307** | 3-oxoacyl-(acyl carrier protein) synthase III | Complete |
| **NEIS0310** | putative glycerol-3-phosphate acyltransferase PlsX | Complete |
| **NEIS0311** | hypothetical protein | Complete |
| **NEIS0312** | 50S ribosomal protein L32 | Complete |
| **NEIS0313** | hypothetical protein | Complete |
| **NEIS0314** | Maf-like protein | Incomplete |
| **NEIS0315** | hypothetical protein | Complete |
| **NEIS0316** | putative inner membrane protein translocase component YidC | Complete |
| **NEIS0317** | hypothetical protein | Complete |
| **NEIS0318** | ribonuclease P | Complete |
| **NEIS0319** | 50S ribosomal protein L34 | Complete |
| **NEIS0320** | chromosomal replication initiation protein | Incomplete |
| **NEIS0321** | DNA polymerase III subunit beta | Complete |
| **NEIS0323** | polyphosphate kinase | Incomplete |
| **NEIS0324** | putative periplasmic protein | Complete |
| **NEIS0325** | lipoprotein | Complete |
| **NEIS0326** | leucyl-tRNA synthetase | Complete |
| **NEIS0331** | DNA binding protein | Complete |
| **NEIS0333** | preprotein translocase subunit SecG | Complete |
| **NEIS0334** | triosephosphate isomerase | Complete |
| **NEIS0335** | hypothetical protein | Complete |
| **NEIS0336** | protein-L-isoaspartate O-methyltransferase | Incomplete |
| **NEIS0337** | hypothetical protein | Complete |
| **NEIS0342** | putative prolyl endopeptidase | Incomplete |
| **NEIS0343** | N-acetylglutamate synthase | Incomplete |
| **NEIS0344** | hypothetical protein | Incomplete |
| **NEIS0345** | orotate phosphoribosyltransferase | Complete |
| **NEIS0346** | hypothetical protein | Complete |
| **NEIS0347** | putative acetyltransferase | Complete |
| **NEIS0348** | hypothetical protein | Complete |
| **NEIS0350** | fructose-1,6-bisphosphate aldolase (EC 4.1.2.13) | Complete |
| **NEIS0351** | putative integrase/recombinase | Complete |
| **NEIS0352** | 1-deoxy-D-xylulose-5-phosphate synthase | Incomplete |
| **NEIS0353** | (dimethylallyl)adenosine tRNA methylthiotransferase | Complete |
| **NEIS0354** | glutamate-1-semialdehyde aminotransferase | Complete |
| **NEIS0355** | oligoribonuclease | Complete |
| **NEIS0356** | ribosomal protein L11 methyltransferase | Complete |
| **NEIS0357** | putative acetyl-CoA carboxylase biotin carboxylase component | Complete |
| **NEIS0358** | acetyl-CoA carboxylase biotin carboxyl carrier protein subunit | Incomplete |
| **NEIS0360** | S-adenosylmethionine:tRNA ribosyltransferase-isomerase | Complete |
| **NEIS0363** | carbamoyl phosphate synthase large subunit (EC 6.3.5.5) | Incomplete |

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|---|---|---|
| **NEIS0370** | carbamoyl phosphate synthase small subunit | Complete |
| **NEIS0371** | type IV pilus associated protein | Incomplete |
| **NEIS0372** | hypothetical protein | Complete |
| **NEIS0373** | putative periplasmic thioredoxin | Complete |
| **NEIS0374** | marR family transcriptional regulator | Complete |
| **NEIS0375** | putative NADH:FMN oxidoreductase | Complete |
| **NEIS0376** | putative sugar-phosphate nucleotidyl transferase | Complete |
| **NEIS0377** | putative integral membrane protein | Complete |
| **NEIS0378** | formate--tetrahydrofolate ligase | Complete |
| **NEIS0379** | conserved hypothetical protein | Complete |
| **NEIS0381** | tyrosyl-tRNA synthetase | Complete |
| **NEIS0382** | bifunctional riboflavin kinase/FMN adenylyltransferase | Complete |
| **NEIS0383** | isoleucyl-tRNA synthetase | Incomplete |
| **NEIS0384** | lipoprotein signal peptidase | Complete |
| **NEIS0385** | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase | Complete |
| **NEIS0386** | phosphatase | Incomplete |
| **NEIS0389** | DNA polymerase III, alpha subunit | Incomplete |
| **NEIS0390** | hypothetical protein | Complete |
| **NEIS0392** | hypothetical protein | Complete |
| **NEIS0394** | hypothetical protein | Incomplete |
| **NEIS0395** | valine--pyruvate transaminase | Incomplete |
| **NEIS0396** | pilin glycosylation protein | Complete |
| **NEIS0397** | pilin glycosylation protein | Complete |
| **NEIS0402** | putative lipopolysaccharide biosynthesis translocase | Incomplete |
| **NEIS0403** | putative diaminohydroxyphosphoribosylaminopyrimidine deaminase/phosphoribosylamino)uracil reductase | Complete |
| **NEIS0404** | transcriptional regulator NrdR | Complete |
| **NEIS0405** | hypothetical protein | Complete |
| **NEIS0406** | 3-dehydroquinate synthase | Complete |
| **NEIS0407** | shikimate kinase | Complete |
| **NEIS0408** | type IV secretin protein | Incomplete |
| **NEIS0409** | type IV biogenesis protein | Complete |
| **NEIS0410** | type IV biogenesis protein | Complete |
| **NEIS0411** | type IV biogenesis protein | Complete |
| **NEIS0412** | type IV biogenesis protein | Complete |
| **NEIS0414** | penicillin-binding protein 1 | Complete |
| **NEIS0415** | ribosome biogenesis GTP-binding protein YsxC | Complete |
| **NEIS0416** | putative cytochrome C | Incomplete |
| **NEIS0417** | hypothetical protein | Incomplete |
| **NEIS0418** | hypothetical protein | Complete |
| **NEIS0419** | DNA-binding/iron metalloprotein/AP endonuclease | Incomplete |
| **NEIS0421** | lipid A biosynthesis lauroyl transferase | Complete |
| **NEIS0422** | S-adenosylmethionine synthetase | Complete |

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|---|---|---|
| **NEIS0425** | putative peptidase | Complete |
| **NEIS0426** | putative oxidoreductase | Complete |
| **NEIS0429** | two-component system sensor kinase | Complete |
| **NEIS0430** | hypothetical protein | Complete |
| **NEIS0431** | putative glutaredoxin | Complete |
| **NEIS0432** | preprotein translocase subunit SecB | Complete |
| **NEIS0433** | ATP-dependent DNA helicase RecG | Incomplete |
| **NEIS0434** | N-acetyl-gamma-glutamyl-phosphate reductase | Incomplete |
| **NEIS0462** | ribonuclease BN/unknown domain fusion protein | Complete |
| **NEIS0464** | hypothetical protein | Complete |
| **NEIS0465** | hypothetical protein | Complete |
| **NEIS0466** | hypothetical protein | Complete |
| **NEIS0467** | hypothetical protein | Complete |
| **NEIS0468** | hypothetical protein | Complete |
| **NEIS0469** | beta-hexosaminidase | Complete |
| **NEIS0470** | putative integral membrane protein | Complete |
| **NEIS0471** | putative periplasmic serine protease | Complete |
| **NEIS0472** | endonuclease III | Complete |
| **NEIS0473** | hypothetical protein | Complete |
| **NEIS0474** | transmembrane hexose transporter | Incomplete |
| **NEIS0475** | putative transmembrane transport protein | Incomplete |
| **NEIS0476** | hypothetical protein | Complete |
| **NEIS0477** | hypothetical protein | Complete |
| **NEIS0478** | porphobilinogen deaminase | Complete |
| **NEIS0479** | aromatic amino acid aminotransferase | Complete |
| **NEIS0480** | hypothetical protein | Complete |
| **NEIS0481** | hypothetical protein | Complete |
| **NEIS0482** | putative transmembrane transport protein | Complete |
| **NEIS0483** | UDP-2,3-diacylglucosamine hydrolase | Complete |
| **NEIS0484** | hypothetical protein | Complete |
| **NEIS0486** | alcohol dehydrogenase | Complete |
| **NEIS0487** | minor pilin | Complete |
| **NEIS0488** | putative periplasmic protein; macrolide-specific effux protein | Complete |
| **NEIS0489** | putative ABC transporter ATP-binding protein; macrolide export ATP-binding/permease protein | Complete |
| **NEIS0490** | putative thiol:disulphide interchange protein | Incomplete |
| **NEIS0491** | primosome assembly protein PriA | Incomplete |
| **NEIS0493** | hypothetical protein | Incomplete |
| **NEIS0495** | molecular chaperone DnaK | Complete |
| **NEIS0496** | hypothetical protein | Complete |
| **NEIS0497** | putative transcriptional regulator | Complete |
| **NEIS0498** | iron-sulfur cluster insertion protein ErpA | Complete |
| **NEIS0500** | putative ubiquinone biosynthesis protein UbiB | Complete |

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|---|---|---|
| **NEIS0501** | serine acetyltransferase | Complete |
| **NEIS0502** | heat shock protein GrpE | Incomplete |
| **NEIS0503** | putative periplasmic protein | Complete |
| **NEIS0504** | putative thiamine biosynthesis protein | Complete |
| **NEIS0505** | Na(+)-translocating NADH-quinone reductase subunit F | Complete |
| **NEIS0506** | Na(+)-translocating NADH-quinone reductase subunit E | Complete |
| **NEIS0507** | Na(+)-translocating NADH-quinone reductase subunit D | Complete |
| **NEIS0508** | Na(+)-translocating NADH-quinone reductase subunit C | Complete |
| **NEIS0509** | Na(+)-translocating NADH-quinone reductase subunit B | Complete |
| **NEIS0510** | Na(+)-translocating NADH-quinone reductase subunit A | Complete |
| **NEIS0512** | hypothetical protein | Complete |
| **NEIS0513** | hypothetical protein | Complete |
| **NEIS0515** | AsnC family transcriptional regulator | Complete |
| **NEIS0516** | glycine cleavage system aminomethyltransferase T | Complete |
| **NEIS0517** | glycine cleavage system protein H | Complete |
| **NEIS0518** | glutamyl-tRNA reductase | Complete |
| **NEIS0521** | ABC transporter ATP-binding protein | Complete |
| **NEIS0522** | lipoprotein | Complete |
| **NEIS0523** | electron transfer flavoprotein-ubiquinone oxidoreductase | Complete |
| **NEIS0528** | putative periplasmic binding protein | Complete |
| **NEIS0529** | putative ABC-transporter membrane protein | Incomplete |
| **NEIS0530** | ABC transporter ATP-binding protein | Complete |
| **NEIS0531** | 50S ribosomal protein L19 | Complete |
| **NEIS0532** | tRNA (guanine-N(1)-)-methyltransferase | Incomplete |
| **NEIS0533** | 16S rRNA-processing protein RimM | Complete |
| **NEIS0534** | 30S ribosomal protein S16 | Complete |
| **NEIS0536** | putative two-component system sensor kinase | Complete |
| **NEIS0537** | putative two-component system regulator | Complete |
| **NEIS0539** | integral membrane protein | Complete |
| **NEIS0540** | hypothetical protein | Complete |
| **NEIS0541** | Maf-like protein | Complete |
| **NEIS0542** | putative sec-independent protein translocase component | Complete |
| **NEIS0543** | putative sec-independent protein translocase component | Complete |
| **NEIS0545** | putative nucleotide-binding protein | Complete |
| **NEIS0546** | phosphoribosyl-ATP pyrophosphatase | Complete |
| **NEIS0547** | putative zinc-binding alcohol dehydrogenase | Complete |
| **NEIS0548** | hypothetical protein | Complete |
| **NEIS0549** | hypothetical protein | Complete |
| **NEIS0550** | preprotein translocase subunit SecD | Complete |
| **NEIS0551** | preprotein translocase subunit SecF | Complete |
| **NEIS0552** | 30S ribosomal protein S15 | Complete |
| **NEIS0553** | putative polyamine permease ATP-binding protein | Complete |
| **NEIS0554** | polyamine permease inner membrane protein | Complete |

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|---|---|---|
| **NEIS0555** | putative polyamine permease inner membrane protein | Complete |
| **NEIS0556** | putative oxidoreductase | Complete |
| **NEIS0560** | transcription termination factor Rho | Complete |
| **NEIS0561** | phosphoenolpyruvate synthase | Complete |
| **NEIS0562** | hypothetical protein | Complete |
| **NEIS0563** | putative phosphatase | Incomplete |
| **NEIS0565** | hypothetical protein | Complete |
| **NEIS0566** | outer membrane lipoprotein LolB | Complete |
| **NEIS0569** | hypothetical protein | Complete |
| **NEIS0570** | peptide chain release factor 3 | Complete |
| **NEIS0571** | phosphoribosyl-AMP cyclohydrolase | Complete |
| **NEIS0572** | imidazole glycerol phosphate synthase subunit HisF | Complete |
| **NEIS0573** | 1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase | Complete |
| **NEIS0574** | imidazole glycerol phosphate synthase subunit HisH | Complete |
| **NEIS0575** | putative phosphate acyltransferase | Complete |
| **NEIS0576** | putative iron-uptake permease ATP-binding protein | Complete |
| **NEIS0577** | putative iron-uptake permease inner membrane protein | Complete |
| **NEIS0578** | major ferric iron binding protein | Complete |
| **NEIS0579** | hypothetical protein | Complete |
| **NEIS0580** | argininosuccinate lyase | Complete |
| **NEIS0581** | glucose 1-phosphate uridylyltransferase | Complete |
| **NEIS0582** | putative deoxyribonucleotide triphosphate pyrophosphatase | Complete |
| **NEIS0583** | hypothetical protein | Complete |
| **NEIS0584** | inorganic pyrophosphatase | Complete |
| **NEIS0585** | dATP pyrophosphohydrolase | Complete |
| **NEIS0609** | transmembrane potassium transporter | Incomplete |
| **NEIS0610** | diadenosine tetraphosphatase | Complete |
| **NEIS0611** | hypothetical protein | Complete |
| **NEIS0612** | outer membrane protein | Complete |
| **NEIS0613** | coproporphyrinogen III oxidase | Complete |
| **NEIS0614** | DNA ligase | Incomplete |
| **NEIS0615** | hypothetical protein | Complete |
| **NEIS0617** | N-acetyl-anhydromuranmyl-L-alanine amidase | Complete |
| **NEIS0618** | putative periplasmic protein | Complete |
| **NEIS0619** | thymidylate kinase | Complete |
| **NEIS0620** | malate oxidoreductase (EC 1.1.1.38) | Incomplete |
| **NEIS0621** | tetraacyldisaccharide 4'-kinase (EC 2.7.1.130) | Complete |
| **NEIS0622** | putative periplasmic protein | Incomplete |
| **NEIS0623** | hypothetical protein | Complete |
| **NEIS0624** | 3-deoxy-manno-octulosonate cytidylyltransferase | Complete |
| **NEIS0625** | hypothetical protein | Complete |
| **NEIS0628** | tryptophan synthase subunit alpha | Complete |

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|---|---|---|
| **NEIS0629** | acetyl-CoA carboxylase subunit beta | Complete |
| **NEIS0630** | putative periplasmic protein | Complete |
| **NEIS0631** | hypothetical protein | Complete |
| **NEIS0632** | lipoprotein | Incomplete |
| **NEIS0633** | dihydroorotase | Incomplete |
| **NEIS0634** | transcription antitermination protein NusB | Complete |
| **NEIS0635** | 6,7-dimethyl-8-ribityllumazine synthase | Incomplete |
| **NEIS0636** | hypothetical protein | Complete |
| **NEIS0637** | ribonuclease III | Incomplete |
| **NEIS0638** | GTP-binding protein Era | Complete |
| **NEIS0639** | N-(5'-phosphoribosyl)anthranilate isomerase | Complete |
| **NEIS0640** | transcription elongation factor GreB | Complete |
| **NEIS0641** | amidophosphoribosyltransferase | Complete |
| **NEIS0642** | hypothetical protein | Complete |
| **NEIS0643** | putative tetrapac protein | Complete |
| **NEIS0644** | bifunctional folylpolyglutamate synthase/dihydrofolate synthase | Complete |
| **NEIS0645** | putative transcriptional regulator | Complete |
| **NEIS0646** | hypothetical protein | Complete |
| **NEIS0647** | putative amino acid permease ATP-binding protein | Complete |
| **NEIS0648** | dimethyladenosine transferase | Complete |
| **NEIS0649** | hypothetical protein | Incomplete |
| **NEIS0650** | tryptophan synthase subunit beta | Complete |
| **NEIS0652** | competence protein | Incomplete |
| **NEIS0653** | competence lipoprotein | Complete |
| **NEIS0654** | ribosomal large subunit pseudouridine synthase D | Incomplete |
| **NEIS0655** | transmembrane transport protein | Complete |
| **NEIS0656** | hypothetical protein | Incomplete |
| **NEIS0657** | LPS-assembly lipoprotein | Incomplete |
| **NEIS0658** | DNA polymerase III subunit delta | Complete |
| **NEIS0659** | hypothetical protein | Complete |
| **NEIS0660** | hypothetical protein | Incomplete |
| **NEIS0661** | hypothetical protein | Complete |
| **NEIS0663** | RNA polymerase factor sigma-32 | Complete |
| **NEIS0664** | apolipoprotein N-acyltransferase | Incomplete |
| **NEIS0668** | cytochrome C | Incomplete |
| **NEIS0669** | ferrochelatase | Complete |
| **NEIS0671** | queuine tRNA-ribosyltransferase | Incomplete |
| **NEIS0672** | threonyl-tRNA synthetase | Incomplete |
| **NEIS0673** | translation initiation factor IF-3 | Incomplete |
| **NEIS0674** | 50S ribosomal protein L35 | Complete |
| **NEIS0675** | 50S ribosomal protein L20 | Complete |
| **NEIS0676** | phenylalanyl-tRNA synthetase subunit alpha | Incomplete |
| **NEIS0681** | phenylalanyl-tRNA synthetase subunit beta | Complete |

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|---|---|---|
| **NEIS0682** | integration host factor subunit alpha | Complete |
| **NEIS0683** | hypothetical protein | Complete |
| **NEIS0684** | FxsA | Complete |
| **NEIS0685** | adenosylmethionine-8-amino-7-oxononanoate aminotransferase | Complete |
| **NEIS0686** | dithiobiotin synthetase | Complete |
| **NEIS0687** | hypothetical protein | Complete |
| **NEIS0688** | 4-hydroxybenzoate octaprenyltransferase | Incomplete |
| **NEIS0689** | putative regulatory protein | Complete |
| **NEIS0690** | HPr kinase/phosphorylase | Incomplete |
| **NEIS0691** | hypothetical protein | Complete |
| **NEIS0692** | ribosomal biogenesis GTPase | Complete |
| **NEIS0693** | hypothetical protein | Complete |
| **NEIS0694** | putative DNA repair protein | Complete |
| **NEIS0695** | hypothetical protein | Incomplete |
| **NEIS0696** | hypothetical protein | Incomplete |
| **NEIS0697** | ubiquinone/menaquinone biosynthesis methyltransferase | Incomplete |
| **NEIS0698** | hypothetical protein | Complete |
| **NEIS0699** | putative 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine-pyrophosphokinase | Complete |
| **NEIS0700** | putative regulator | Complete |
| **NEIS0701** | hypothetical protein | Incomplete |
| **NEIS0702** | putative regulator | Complete |
| **NEIS0703** | putative D-alanyl-D-alanine-endopeptidase | Incomplete |
| **NEIS0704** | hypothetical protein | Complete |
| **NEIS0705** | putative integrase/recombinase | Complete |
| **NEIS0706** | ferredoxin | Complete |
| **NEIS0707** | putative thioredoxin | Complete |
| **NEIS0708** | putative dTDP-4-dehydrorhamnose reductase | Complete |
| **NEIS0709** | phosphoribosylaminoimidazole-succinocarboxamide synthase | Complete |
| **NEIS0710** | polynucleotide phosphorylase/polyadenylase | Complete |
| **NEIS0711** | hypothetical protein | Complete |
| **NEIS0712** | putative lipoprotein | Complete |
| **NEIS0713** | diaminopimelate epimerase | Incomplete |
| **NEIS0714** | hypothetical protein | Incomplete |
| **NEIS0715** | cysteine synthase | Incomplete |
| **NEIS0717** | hypothetical protein | Incomplete |
| **NEIS0718** | signal peptidase I | Complete |
| **NEIS0719** | GTP-binding protein LepA | Complete |
| **NEIS0720** | putative 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase | Complete |
| **NEIS0721** | pilT_like protein | Complete |
| **NEIS0722** | DNA polymerase III subunit delta' | Complete |
| **NEIS0723** | type IV pilus assembly protein | Complete |
| **NEIS0724** | hypothetical protein | Complete |

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|---|---|---|
| **NEIS0726** | hypothetical protein | Complete |
| **NEIS0727** | uracil phosphoribosyltransferase | Complete |
| **NEIS0728** | hypothetical protein | Complete |
| **NEIS0729** | putative secreted protein | Complete |
| **NEIS0730** | uroporphyrinogen-III synthase | Complete |
| **NEIS0731** | hypothetical protein | Complete |
| **NEIS0732** | hypothetical protein | Complete |
| **NEIS0733** | uroporphyrinogen decarboxylase | Complete |
| **NEIS0734** | DNA repair protein RadA | Complete |
| **NEIS0735** | hypothetical protein | Complete |
| **NEIS0736** | putative periplasmic protein | Complete |
| **NEIS0737** | putative exodeoxyribonuclease V beta chain | Complete |
| **NEIS0738** | hypothetical protein | Complete |
| **NEIS0739** | putative amino acid permease substrate-binding protein | Complete |
| **NEIS0741** | putative amino acid permease integral membrane protein | Complete |
| **NEIS0742** | putative amino acid permease ATP-binding protein | Complete |
| **NEIS0743** | Phosphoglucomutase (EC 5.4.2.2) | Complete |
| **NEIS0744** | putative peptidyl-prolyl cis-trans isomerase B | Complete |
| **NEIS0745** | putative transmembrane transport protein | Incomplete |
| **NEIS0746** | hypothetical protein | Complete |
| **NEIS0747** | peptidyl-tRNA hydrolase | Complete |
| **NEIS0748** | hypothetical protein | Complete |
| **NEIS0749** | hypothetical protein | Complete |
| **NEIS0750** | putative ATP-dependent zinc metallopeptidase | Complete |
| **NEIS0751** | putative cell division protein | Complete |
| **NEIS0752** | hypothetical protein | Complete |
| **NEIS0753** | delta-aminolevulinic acid dehydratase | Incomplete |
| **NEIS0754** | putative carbon-sulphur lyase | Incomplete |
| **NEIS0755** | putative GTP cyclohydrolase | Complete |
| **NEIS0756** | putative NAD(P)H-flavin oxidoreductase | Complete |
| **NEIS0757** | putative RNA-binding protein | Complete |
| **NEIS0758** | inorganic polyphosphate/ATP-NAD kinase | Complete |
| **NEIS0759** | hypothetical protein | Complete |
| **NEIS0760** | hypothetical protein | Incomplete |
| **NEIS0761** | TetR family transcriptional regulator | Complete |
| **NEIS0762** | UDP-N-acetylenolpyruvoylglucosamine reductase | Complete |
| **NEIS0763** | multidrug efflux protein | Complete |
| **NEIS0764** | ATP phosphoribosyltransferase regulatory subunit | Complete |
| **NEIS0765** | adenylosuccinate synthetase | Complete |
| **NEIS0766** | heat shock protein HtpX | Complete |
| **NEIS0767** | adenylate kinase | Complete |
| **NEIS0768** | orotidine 5'-phosphate decarboxylase | Complete |
| **NEIS0769** | D-beta-D-heptose-7-phosphate kinase | Complete |

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|---|---|---|
| **NEIS0773** | ADP-D-beta-D heptose epimerase | Complete |
| **NEIS0774** | putative ATP-dependent protease ATP-binding protein | Complete |
| **NEIS0775** | ATP-dependent Clp protease adaptor protein ClpS | Complete |
| **NEIS0776** | putative transcriptional regulator | Complete |
| **NEIS0777** | hypothetical protein | Complete |
| **NEIS0778** | hypothetical protein | Complete |
| **NEIS0779** | hypothetical protein | Complete |
| **NEIS0780** | putative single-stranded-DNA-specific exonuclease | Complete |
| **NEIS0781** | putative poly(A) polymerase | Complete |
| **NEIS0784** | hypothetical protein | Complete |
| **NEIS0788** | putative periplasmic protein | Complete |
| **NEIS0789** | deoxycytidine triphosphate deaminase | Complete |
| **NEIS0790** | hypothetical protein | Incomplete |
| **NEIS0791** | recombination associated protein | Incomplete |
| **NEIS0792** | GTP-binding protein EngA | Incomplete |
| **NEIS0793** | hypothetical protein | Complete |
| **NEIS0794** | histidyl-tRNA synthetase | Complete |
| **NEIS0808** | hypothetical protein | Incomplete |
| **NEIS0809** | hypothetical protein | Complete |
| **NEIS0810** | spermidine synthase | Complete |
| **NEIS0811** | 3-methyl-2-oxobutanoate hydroxymethyltransferase | Incomplete |
| **NEIS0812** | pantoate--beta-alanine ligase | Complete |
| **NEIS0813** | putative periplasmic protein | Complete |
| **NEIS0814** | outer membrane lipoprotein LolB | Complete |
| **NEIS0815** | 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase | Complete |
| **NEIS0816** | ribose-phosphate pyrophosphokinase | Complete |
| **NEIS0817** | 50S ribosomal protein L25 | Complete |
| **NEIS0818** | putative D-alanyl-D-alanine carboxypeptidase | Complete |
| **NEIS0819** | threonine dehydratase | Complete |
| **NEIS0823** | hypothetical protein | Complete |
| **NEIS0825** | superoxide dismutase | Complete |
| **NEIS0826** | replicative DNA helicase | Incomplete |
| **NEIS0827** | type IV biogenesis protein | Complete |
| **NEIS0828** | type IV biogenesis protein | Complete |
| **NEIS0829** | type IV biogenesis protein | Complete |
| **NEIS0830** | type IV biogenesis protein | Complete |
| **NEIS0831** | minor pilin | Complete |
| **NEIS0833** | deoxyuridine 5'-triphosphate nucleotidohydrolase | Complete |
| **NEIS0834** | succinyldiaminopimelate transaminase | Complete |
| **NEIS0835** | hypothetical protein | Complete |
| **NEIS0897** | isocitrate dehydrogenase (NADP+) (EC 1.1.1.42) | Complete |
| **NEIS0899** | alpha-2,3-sialyltransferase | Complete |
| **NEIS0900** | putative C-type cytochrome | Complete |

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|---|---|---|
| **NEIS0901** | putative oxidoreductase | Complete |
| **NEIS0902** | putative acyl-CoA hydrolase | Complete |
| **NEIS0905** | proline iminopeptidase | Complete |
| **NEIS0906** | putative lipoprotein | Incomplete |
| **NEIS0907** | dihydrodipicolinate synthase | Complete |
| **NEIS0908** | transmembrane transport protein | Complete |
| **NEIS0909** | RNA methylase | Incomplete |
| **NEIS0910** | hypothetical protein | Incomplete |
| **NEIS0911** | putative cytosine deaminase | Complete |
| **NEIS0912** | tRNA delta(2)-isopentenylpyrophosphate transferase | Incomplete |
| **NEIS0913** | hypothetical protein | Complete |
| **NEIS0915** | elongation factor P | Complete |
| **NEIS0917** | hypothetical protein | Complete |
| **NEIS0918** | homoserine O-acetyltransferase | Complete |
| **NEIS0919** | 50S ribosomal protein L36 | Complete |
| **NEIS0920** | 50S ribosomal protein L31 type B | Complete |
| **NEIS0921** | 5,10-methylenetetrahydrofolate reductase | Complete |
| **NEIS0922** | 5-methyltetrahydropteroyltriglutamate-- homocysteine S-methyltransferase | Incomplete |
| **NEIS0923** | putative redoxin | Complete |
| **NEIS0924** | dihydrolipoamide dehydrogenase (EC 1.8.1.4) | Complete |
| **NEIS0925** | succinate dehydrogenase cytochrome B subunit (EC 1.3.99.1) | Complete |
| **NEIS0926** | succinate dehydrogenase hydrophobic membrane anchor protein (EC 1.3.99.1) | Complete |
| **NEIS0927** | succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1) | Complete |
| **NEIS0928** | succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1) | Complete |
| **NEIS0929** | hypothetical protein | Complete |
| **NEIS0930** | citrate synthase (EC 2.3.3.1) | Complete |
| **NEIS0931** | 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) | Complete |
| **NEIS0932** | dihydrolipoamide succinyltransferase E2 component (EC 2.3.1.61) | Incomplete |
| **NEIS0933** | dihydrolipoamide dehydrogenase | Complete |
| **NEIS0934** | hypothetical protein | Incomplete |
| **NEIS0935** | succinyl-CoA synthetase subunit beta (EC 6.2.1.5) | Complete |
| **NEIS0936** | succinyl-CoA synthetase subunit alpha (EC 6.2.1.5) | Complete |
| **NEIS0941** | excinuclease ABC subunit A | Incomplete |
| **NEIS0942** | phosphatidylserine decarboxylase | Complete |
| **NEIS0944** | putative outer-membrane receptor protein | Incomplete |
| **NEIS0947** | anthranilate synthase component II | Complete |
| **NEIS0948** | anthranilate phosphoribosyltransferase | Incomplete |
| **NEIS0958** | pyridine nucleotide transhydrogenase | Incomplete |
| **NEIS0959** | hypothetical protein | Complete |
| **NEIS0960** | NAD(P) transhydrogenase subunit alpha | Incomplete |
| **NEIS0961** | phosphoserine phosphatase | Complete |
| **NEIS0963** | bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase | Complete |

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|---|---|---|
| **NEIS0980** | rubredoxin | Complete |
| **NEIS0981** | putative acyl-CoA dehydrogenase | Incomplete |
| **NEIS0982** | Hypothetical protein | Complete |
| **NEIS0983** | hypothetical protein | Incomplete |
| **NEIS0984** | D-lactate dehydrogenase | Complete |
| **NEIS0985** | putative oxidoreductase | Complete |
| **NEIS0986** | hypothetical protein | Incomplete |
| **NEIS1007** | hypothetical protein | Incomplete |
| **NEIS1009** | sulfate-binding protein | Incomplete |
| **NEIS1010** | hypothetical protein | Complete |
| **NEIS1011** | phosphoribosylaminoimidazole carboxylase ATPase subunit | Complete |
| **NEIS1013** | anthranilate synthase component I | Complete |
| **NEIS1015** | ABC transporter ATP-binding protein | Incomplete |
| **NEIS1016** | DedA protein ortholog | Incomplete |
| **NEIS1017** | serine hydroxymethyltransferase | Complete |
| **NEIS1021** | hypothetical protein | Complete |
| **NEIS1022** | fructose-1,6-bisphosphatase (EC 3.1.3.11) | Complete |
| **NEIS1024** | hypothetical protein | Complete |
| **NEIS1026** | putative integral membrane protein | Complete |
| **NEIS1027** | dihydroneopterin aldolase | Complete |
| **NEIS1028** | hypothetical protein | Complete |
| **NEIS1029** | camphor resistance protein CrcB | Complete |
| **NEIS1030** | putative integral membrane protein | Complete |
| **NEIS1031** | putative cell-division protein | Complete |
| **NEIS1032** | gamma-glutamyl phosphate reductase | Incomplete |
| **NEIS1033** | gamma-glutamyl kinase | Incomplete |
| **NEIS1034** | 2-isopropylmalate synthase | Complete |
| **NEIS1035** | hypothetical protein | Complete |
| **NEIS1036** | prolipoprotein diacylglyceryl transferase | Complete |
| **NEIS1037** | hypothetical protein | Complete |
| **NEIS1038** | acetylglutamate kinase | Complete |
| **NEIS1039** | hypothetical protein | Complete |
| **NEIS1040** | DnaA regulatory inactivator Hda | Complete |
| **NEIS1063** | putative periplasmic protein | Complete |
| **NEIS1065** | hypothetical protein | Complete |
| **NEIS1066** | putative periplasmic protein | Complete |
| **NEIS1067** | short chain dehydrogenase | Complete |
| **NEIS1068** | putative oxidoreductase | Incomplete |
| **NEIS1069** | putative poly-isoprenyl transferase | Incomplete |
| **NEIS1070** | chaperone protein HscA | Complete |
| **NEIS1072** | hypothetical protein | Complete |
| **NEIS1073** | putative ferredoxin | Complete |
| **NEIS1074** | hypothetical protein | Complete |

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|---|---|---|
| **NEIS1076** | hypothetical protein | Complete |
| **NEIS1077** | hypothetical protein | Complete |
| **NEIS1078** | acetyl-CoA carboxylase carboxyltransferase subunit alpha | Incomplete |
| **NEIS1080** | hypothetical protein | Complete |
| **NEIS1081** | RNA methyltransferase | Complete |
| **NEIS1082** | lipoprotein | Complete |
| **NEIS1084** | putative periplasmic protein | Complete |
| **NEIS1085** | putative UDP-N-acetylmuramate: L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase | Incomplete |
| **NEIS1087** | putative biotin synthase | Incomplete |
| **NEIS1090** | dihydroxy-acid dehydratase | Complete |
| **NEIS1097** | hypothetical protein | Complete |
| **NEIS1098** | hypothetical protein | Complete |
| **NEIS1099** | putative GTP-binding protein | Complete |
| **NEIS1102** | putative ribonuclease | Complete |
| **NEIS1103** | inosine 5'-monophosphate dehydrogenase | Incomplete |
| **NEIS1104** | putative [protein-PII] uridylyltransferase | Incomplete |
| **NEIS1106** | transcriptional regulator | Complete |
| **NEIS1107** | bacterioferritin B | Complete |
| **NEIS1108** | bacterioferritin A | Complete |
| **NEIS1110** | lipoyl synthase | Incomplete |
| **NEIS1111** | lipoate-protein ligase B | Complete |
| **NEIS1112** | hypothetical protein | Complete |
| **NEIS1113** | putative integral membrane protein | Complete |
| **NEIS1114** | putative periplasmic protein | Complete |
| **NEIS1115** | hypothetical protein | Complete |
| **NEIS1116** | uracil-DNA glycosylase | Incomplete |
| **NEIS1125** | putative periplasmic protein | Incomplete |
| **NEIS1126** | ABC transporter ATP-binding protein | Complete |
| **NEIS1127** | hypothetical protein | Complete |
| **NEIS1128** | homoserine dehydrogenase | Complete |
| **NEIS1129** | hypothetical protein | Complete |
| **NEIS1130** | putative DNA-binding protein | Complete |
| **NEIS1131** | putative ATP-dependent protease | Complete |
| **NEIS1132** | hypothetical protein | Incomplete |
| **NEIS1133** | exodeoxyribonuclease V alpha subunit | Complete |
| **NEIS1134** | putative ABC-transporter ATP-binding protein | Complete |
| **NEIS1135** | putative integral membrane protein | Complete |
| **NEIS1136** | hypothetical protein | Complete |
| **NEIS1137** | recombination protein RecR | Complete |
| **NEIS1138** | putative peptidyl-prolyl cis-trans isomerase | Complete |
| **NEIS1139** | hypothetical protein | Complete |
| **NEIS1140** | putative ABC-transporter ATP-binding protein | Complete |

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|---|---|---|
| **NEIS1142** | multifunctional tRNA nucleotidyl transferase/ 2'3'-cyclic phosphodiesterase/ 2'nucleotidase/ phosphatase | Incomplete |
| **NEIS1143** | hypothetical protein | Complete |
| **NEIS1144** | Holliday junction DNA helicase RuvB | Complete |
| **NEIS1145** | ribulose-phosphate 3-epimerase | Incomplete |
| **NEIS1146** | hypothetical protein | Incomplete |
| **NEIS1147** | hypothetical protein | Incomplete |
| **NEIS1148** | riboflavin synthase subunit alpha | Incomplete |
| **NEIS1149** | molybdopterin-guanine dinucleotide biosynthesis protein A | Complete |
| **NEIS1150** | putative two-component system sensor kinase | Complete |
| **NEIS1151** | putative two-component system response regulator | Incomplete |
| **NEIS1152** | phosphoribosylaminoimidazole synthetase | Complete |
| **NEIS1154** | hypothetical protein | Complete |
| **NEIS1155** | GTP cyclohydrolase II | Complete |
| **NEIS1157** | bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II-like protein | Complete |
| **NEIS1159** | recombination factor protein RarA | Complete |
| **NEIS1164** | putative lipoprotein | Complete |
| **NEIS1165** | threonine synthase | Complete |
| **NEIS1166** | hypothetical protein | Complete |
| **NEIS1168** | ferredoxin--NADP reductase | Complete |
| **NEIS1170** | putative P-type cation-transporting ATPase | Complete |
| **NEIS1171** | hypothetical protein | Complete |
| **NEIS1172** | putative periplasmic protein | Incomplete |
| **NEIS1173** | hypothetical protein | Complete |
| **NEIS1174** | DNA repair protein RadC | Complete |
| **NEIS1175** | glutamate--cysteine ligase | Complete |
| **NEIS1176** | isopropylmalate isomerase large subunit | Incomplete |
| **NEIS1179** | isopropylmalate isomerase small subunit | Complete |
| **NEIS1182** | 3-isopropylmalate dehydrogenase | Complete |
| **NEIS1183** | putative periplasmic protein | Incomplete |
| **NEIS1185** | aspartate ammonia-lyase | Complete |
| **NEIS1186** | putative integral membrane protein | Complete |
| **NEIS1188** | putative dnaJ-family protein | Incomplete |
| **NEIS1189** | hypothetical protein | Complete |
| **NEIS1190** | hypothetical protein | Incomplete |
| **NEIS1191** | hypothetical protein | Incomplete |
| **NEIS1192** | C32 tRNA thiolase | Complete |
| **NEIS1196** | hypothetical protein | Complete |
| **NEIS1197** | putative cation uptake regulator | Complete |
| **NEIS1198** | putative protein-tyrosine-phosphatase | Complete |
| **NEIS1200** | hypothetical protein | Complete |
| **NEIS1201** | hypothetical protein | Complete |
| **NEIS1202** | mercuric ion binding protein | Complete |

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|---|---|---|
| **NEIS1203** | putative polysaccharide modification protein | Complete |
| **NEIS1205** | putative periplasmic protein | Incomplete |
| **NEIS1207** | long-chain-fatty-acid--CoA ligase | Complete |
| **NEIS1208** | putative transmembrane transport protein | Complete |
| **NEIS1210** | site-specific recombinase | Complete |
| **NEIS1212** | murein hydrolase | Incomplete |
| **NEIS1213** | putative oxidoreductase | Incomplete |
| **NEIS1214** | transcription-repair coupling factor | Incomplete |
| **NEIS1216** | aspartate alpha-decarboxylase | Complete |
| **NEIS1219** | hypothetical protein | Complete |
| **NEIS1220** | phosphopyruvate hydratase (EC 4.2.1.11) | Incomplete |
| **NEIS1221** | hypothetical protein | Complete |
| **NEIS1223** | ribonucleotide-diphosphate reductase subunit beta | Complete |
| **NEIS1226** | ribonucleotide-diphosphate reductase subunit alpha | Complete |
| **NEIS1229** | hypothetical protein | Complete |
| **NEIS1231** | 1-acyl-sn-glycerol-3-phosphate acyltransferase | Complete |
| **NEIS1232** | formamidopyrimidine-DNA glycosylase | Complete |
| **NEIS1233** | hypothetical protein | Incomplete |
| **NEIS1234** | putative membrane bound murein transglycosylase | Complete |
| **NEIS1235** | putative ribosomal small subunit pseudouridine synthase | Complete |
| **NEIS1236** | pseudo | Complete |
| **NEIS1237** | cytidylate kinase | Complete |
| **NEIS1238** | 30S ribosomal protein S1 | Complete |
| **NEIS1239** | integration host factor subunit beta | Incomplete |
| **NEIS1240** | putative transcriptional regulator | Complete |
| **NEIS1241** | alcohol dehydrogenase | Complete |
| **NEIS1242** | esterase D | Complete |
| **NEIS1243** | putative nucleotide-binding protein | Incomplete |
| **NEIS1244** | nucleoside diphosphate kinase | Complete |
| **NEIS1245** | hypothetical protein | Complete |
| **NEIS1246** | type IV biogenesis protein | Complete |
| **NEIS1247** | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase | Complete |
| **NEIS1248** | ATP-dependent Clp protease proteolytic subunit | Complete |
| **NEIS1250** | trigger factor | Complete |
| **NEIS1251** | ftsK-like cell division/stress response protein | Complete |
| **NEIS1252** | uracil permease | Complete |
| **NEIS1253** | hypothetical protein | Complete |
| **NEIS1255** | phosphatidylserine synthase | Incomplete |
| **NEIS1256** | hypothetical protein | Complete |
| **NEIS1257** | 50S ribosomal protein L9 | Complete |
| **NEIS1258** | 30S ribosomal protein S18 | Complete |
| **NEIS1260** | 30S ribosomal protein S6 | Complete |
| **NEIS1261** | thioredoxin reductase | Incomplete |

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|---|---|---|
| **NEIS1262** | putative cation-transporting ATPase | Complete |
| **NEIS1263** | excinuclease ABC subunit C | Incomplete |
| **NEIS1265** | hypothetical protein | Complete |
| **NEIS1267** | tRNA (guanine-N(7)-)-methyltransferase | Complete |
| **NEIS1269** | excinuclease ABC subunit B | Complete |
| **NEIS1270** | putative carboxy-terminal processing protease | Incomplete |
| **NEIS1271** | hypothetical protein | Complete |
| **NEIS1274** | hypothetical protein | Incomplete |
| **NEIS1275** | Holliday junction resolvase-like protein | Complete |
| **NEIS1276** | putative hydrolase | Incomplete |
| **NEIS1277** | prolyl-tRNA synthetase | Complete |
| **NEIS1278** | pyruvate dehydrogenase (EC 1.2.4.1) | Complete |
| **NEIS1279** | dihydrolipoamide acetyltransferase (EC 2.3.1.12) | Incomplete |
| **NEIS1280** | dihydrolipoamide dehydrogenase (EC 1.8.1.4) | Incomplete |
| **NEIS1281** | hypothetical protein | Complete |
| **NEIS1283** | inositol monophosphate family protein | Complete |
| **NEIS1284** | SpoU methylase family protein | Incomplete |
| **NEIS1285** | hypothetical protein | Complete |
| **NEIS1286** | SUN-family protein | Complete |
| **NEIS1287** | hypothetical protein | Complete |
| **NEIS1288** | putative aldehyde dehydrogenase | Incomplete |
| **NEIS1289** | hypothetical protein | Complete |
| **NEIS1290** | aspartyl/glutamyl-tRNA(Asp/Gln) amidotransferase subunit C | Complete |
| **NEIS1291** | aspartyl/glutamyl-tRNA amidotransferase subunit A | Complete |
| **NEIS1293** | aspartyl/glutamyl-tRNA amidotransferase subunit B | Complete |
| **NEIS1294** | iron/sulphur-binding oxidoreductase | Complete |
| **NEIS1295** | pyridoxamine 5'-phosphate oxidase | Complete |
| **NEIS1296** | pseudouridine synthase | Complete |
| **NEIS1297** | putative integral membrane transporter | Complete |
| **NEIS1298** | exodeoxyribonuclease VII large subunit | Incomplete |
| **NEIS1299** | NH(3)-dependent NAD synthetase | Incomplete |
| **NEIS1300** | hypothetical protein | Complete |
| **NEIS1301** | thioredoxin I | Complete |
| **NEIS1302** | hypothetical protein | Complete |
| **NEIS1303** | putative ATP-dependent RNA helicase | Complete |
| **NEIS1304** | putative membrane lipoprotein | Incomplete |
| **NEIS1305** | hypothetical protein | Complete |
| **NEIS1306** | bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein | Complete |
| **NEIS1307** | ATP-dependent protease ATP-binding subunit ClpX | Incomplete |
| **NEIS1308** | ribosome-binding factor A | Complete |
| **NEIS1309** | tRNA pseudouridine synthase B | Complete |
| **NEIS1312** | L-lactate dehydrogenase | Complete |

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|---|---|---|
| **NEIS1314** | DNA-binding protein | Complete |
| **NEIS1315** | cysteine desulfurase | Complete |
| **NEIS1317** | scaffold protein | Complete |
| **NEIS1318** | HesB-like protein | Complete |
| **NEIS1319** | chaperone protein | Complete |
| **NEIS1320** | DNA gyrase subunit A | Incomplete |
| **NEIS1326** | glucose-6-phosphate isomerase (EC 5.3.1.9) | Incomplete |
| **NEIS1328** | putative transcriptional regulator | Incomplete |
| **NEIS1329** | glucokinase | Incomplete |
| **NEIS1330** | 6-phosphogluconolactonase | Complete |
| **NEIS1331** | glucose-6-phosphate 1-dehydrogenase | Complete |
| **NEIS1332** | phosphogluconate dehydratase | Complete |
| **NEIS1333** | keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase | Incomplete |
| **NEIS1334** | L-threonine 3-dehydrogenase (pseudogene) | Complete |
| **NEIS1336** | adenine glycosylase | Incomplete |
| **NEIS1347** | aminopeptidase N | Complete |
| **NEIS1348** | hypothetical protein | Complete |
| **NEIS1351** | lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-) | Complete |
| **NEIS1352** | Holliday junction resolvase | Complete |
| **NEIS1353** | Fis family transcriptional regulator | Complete |
| **NEIS1354** | hypothetical protein | Incomplete |
| **NEIS1355** | putative ATP-dependent RNA helicase | Complete |
| **NEIS1361** | lysyl-tRNA synthetase | Complete |
| **NEIS1362** | putative integral membrane protein | Complete |
| **NEIS1363** | putative aminopeptidase | Incomplete |
| **NEIS1365** | transcription elongation factor GreA | Complete |
| **NEIS1366** | 3-phosphoshikimate 1-carboxyvinyltransferase | Complete |
| **NEIS1367** | putative lipoprotein | Complete |
| **NEIS1368** | phopholipase D-family protein | Incomplete |
| **NEIS1370** | putative integral membrane protein | Complete |
| **NEIS1371** | hypothetical protein | Complete |
| **NEIS1372** | hypothetical protein | Incomplete |
| **NEIS1373** | iron-sulphur protein | Complete |
| **NEIS1374** | phosphoribosylaminoimidazole carboxylase catalytic subunit | Complete |
| **NEIS1375** | putative periplasmic protein | Complete |
| **NEIS1376** | methyltransferase | Complete |
| **NEIS1378** | DNA mismatch repair protein | Incomplete |
| **NEIS1379** | DNA polymerase III subunits gamma and tau | Incomplete |
| **NEIS1380** | hypothetical protein | Complete |
| **NEIS1382** | recombinase A | Complete |
| **NEIS1383** | 3-dehydroquinate dehydratase | Complete |
| **NEIS1385** | ATP-dependent DNA helicase | Complete |
| **NEIS1386** | DNA polymerase IV | Complete |

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|---|---|---|
| **NEIS1389** | putative ferredoxin NADP+ reductase | Complete |
| **NEIS1391** | DNA polymerase III subunit | Complete |
| **NEIS1392** | hypothetical protein | Incomplete |
| **NEIS1393** | putative inner membrane protein | Complete |
| **NEIS1394** | putative ferredoxin | Complete |
| **NEIS1395** | transketolase | Complete |
| **NEIS1396** | fumarate hydratase class II (EC 4.2.1.2) | Incomplete |
| **NEIS1397** | hypothetical protein | Incomplete |
| **NEIS1398** | single-stranded binding protein | Incomplete |
| **NEIS1400** | putative integral membrane transporter | Incomplete |
| **NEIS1401** | putative transglycosylase | Complete |
| **NEIS1404** | hypothetical protein | Complete |
| **NEIS1405** | exopolyphosphatase | Complete |
| **NEIS1407** | hypothetical protein | Complete |
| **NEIS1408** | tryptophanyl-tRNA synthetase | Complete |
| **NEIS1409** | ClpB protein | Complete |
| **NEIS1410** | aminotransferase AlaT | Complete |
| **NEIS1411** | tautomerase | Complete |
| **NEIS1413** | putative glutamate dehydrogenase | Complete |
| **NEIS1414** | phosphoglycolate phosphatase | Complete |
| **NEIS1415** | recombination regulator RecX | Complete |
| **NEIS1417** | putative acyl-CoA hydrolase | Complete |
| **NEIS1418** | putative membrane peptidase | Complete |
| **NEIS1419** | stationary phase survival protein SurE | Complete |
| **NEIS1420** | hypothetical protein | Complete |
| **NEIS1422** | fimbrial assembly protein | Complete |
| **NEIS1423** | succinate semialdehyde dehydrogenase | Complete |
| **NEIS1425** | lipoprotein | Complete |
| **NEIS1426** | putative integral membrane protein (CstA-like) | Complete |
| **NEIS1429** | aspartate kinase | Incomplete |
| **NEIS1430** | ribonuclease PH | Complete |
| **NEIS1431** | hypothetical protein | Complete |
| **NEIS1432** | hypothetical protein | Complete |
| **NEIS1433** | hypothetical protein | Incomplete |
| **NEIS1435** | nicotinate phosphoribosyltransferase | Incomplete |
| **NEIS1436** | arginyl-tRNA synthetase | Incomplete |
| **NEIS1437** | hypothetical protein | Incomplete |
| **NEIS1438** | putative binding-protein-dependent transport systems inner membrane protein | Incomplete |
| **NEIS1439** | putative nuclease | Incomplete |
| **NEIS1440** | ribose-5-phosphate isomerase A | Incomplete |
| **NEIS1441** | 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase | Complete |
| **NEIS1442** | 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase | Incomplete |

| | | |
|---|---|---|
| **NEIS1443** | DNA polymerase III subunit epsilon | Complete |
| **NEIS1444** | putative integral membrane protein | Incomplete |
| **NEIS1445** | putative inner membrane protein | Complete |
| **NEIS1446** | hypothetical protein | Complete |
| **NEIS1447** | acetate kinase | Incomplete |
| **NEIS1448** | thiol:disulfide interchange protein precursor | Complete |
| **NEIS1449** | hypothetical protein | Complete |
| **NEIS1450** | putative transferase | Complete |
| **NEIS1451** | putative peptidyl-prolyl isomerase | Complete |
| **NEIS1453** | hypothetical protein | Complete |
| **NEIS1455** | SsrA-binding protein | Complete |
| **NEIS1456** | Heptosyltransferase II | Complete |
| **NEIS1457** | putative methylated-DNA-protein-cysteine methyltransferase | Complete |
| **NEIS1458** | hypothetical protein | Complete |
| **NEIS1459** | succinyl-diaminopimelate desuccinylase | Incomplete |
| **NEIS1460** | hypothetical protein | Complete |
| **NEIS1461** | hypothetical protein | Complete |
| **NEIS1462** | H.8 outer membrane protein | Complete |
| **NEIS1464** | preprotein translocase subunit SecA | Incomplete |
| **NEIS1465** | DNA primase | Complete |
| **NEIS1466** | RNA polymerase sigma factor RpoD | Incomplete |
| **NEIS1471** | CTP synthetase | Complete |
| **NEIS1472** | long-chain-fatty-acid--CoA-ligase | Complete |
| **NEIS1473** | tRNA-specific 2-thiouridylase MnmA | Complete |
| **NEIS1474** | hypothetical protein | Complete |
| **NEIS1475** | diacylglycerol kinase | Complete |
| **NEIS1477** | glutathione synthetase | Complete |
| **NEIS1478** | glutaminyl-tRNA synthetase | Complete |
| **NEIS1479** | glycerol 3-phosphate regulon repressor | Complete |
| **NEIS1480** | hypothetical protein | Complete |
| **NEIS1481** | GntR family transcriptional regulator | Incomplete |
| **NEIS1483** | hypothetical protein | Complete |
| **NEIS1485** | hypothetical protein | Complete |
| **NEIS1486** | phosphoribosylglycinamide transformylase | Incomplete |
| **NEIS1487** | peptidylprolyl isomerase (EC:5.2.1.8) | Complete |
| **NEIS1488** | DNA polymerase III chi subunit | Complete |
| **NEIS1489** | aminopeptidase A | Complete |
| **NEIS1490** | hypothetical protein | Complete |
| **NEIS1491** | hypothetical protein | Complete |
| **NEIS1492** | aconitate hydratase 2 (EC 4.2.1.3) | Complete |
| **NEIS1493** | ornithine carbamoyltransferase | Complete |
| **NEIS1494** | ketol-acid reductoisomerase | Complete |
| **NEIS1495** | hypothetical protein | Complete |

| | | |
|---|---|---|
| **NEIS1496** | acetolactate synthase 3 regulatory subunit | Complete |
| **NEIS1497** | acetolactate synthase isozyme III large subunit | Complete |
| **NEIS1498** | putative lipoprotein | Complete |
| **NEIS1499** | ATP phosphoribosyltransferase catalytic subunit | Complete |
| **NEIS1501** | histidinol dehydrogenase | Complete |
| **NEIS1502** | histidinol-phosphate aminotransferase | Complete |
| **NEIS1503** | imidazoleglycerol-phosphate dehydratase | Incomplete |
| **NEIS1504** | hypothetical protein | Complete |
| **NEIS1505** | transcriptional regulator | Complete |
| **NEIS1508** | putative periplasmic protease | Complete |
| **NEIS1509** | CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase | Complete |
| **NEIS1511** | hypothetical protein | Complete |
| **NEIS1512** | hypothetical protein | Complete |
| **NEIS1513** | AraC family transcription regulator | Complete |
| **NEIS1514** | hypothetical protein | Complete |
| **NEIS1515** | hypothetical protein | Complete |
| **NEIS1518** | alanyl-tRNA synthetase | Complete |
| **NEIS1524** | phosphoglycerate mutase (EC 5.4.2.1) | Complete |
| **NEIS1525** | DNA topoisomerase IV subunit A | Complete |
| **NEIS1526** | two component sensor kinase | Incomplete |
| **NEIS1528** | hypothetical protein | Complete |
| **NEIS1530** | O-succinylhomoserine sulfhydrolase | Incomplete |
| **NEIS1531** | hypothetical protein | Complete |
| **NEIS1532** | hypothetical protein | Complete |
| **NEIS1533** | histidine-binding periplasmic protein | Complete |
| **NEIS1534** | fumarate hydratase class I (EC 4.2.1.2) | Incomplete |
| **NEIS1535** | potassium transporter peripheral membrane component | Incomplete |
| **NEIS1538** | phosphomethylpyrimidine kinase | Complete |
| **NEIS1544** | ribonuclease H | Complete |
| **NEIS1545** | hypothetical protein | Complete |
| **NEIS1546** | hypothetical protein | Complete |
| **NEIS1548** | nitric oxide reductase | Incomplete |
| **NEIS1550** | hypothetical protein | Complete |
| **NEIS1552** | hypothetical protein | Complete |
| **NEIS1554** | phosphoserine aminotransferase | Complete |
| **NEIS1555** | hypothetical protein | Complete |
| **NEIS1556** | transcription elongation factor NusA | Complete |
| **NEIS1557** | translation initiation factor IF-2 | Incomplete |
| **NEIS1558** | putative integral membrane protein | Incomplete |
| **NEIS1559** | putative integral membrane protein | Complete |
| **NEIS1560** | hemolysin | Incomplete |
| **NEIS1562** | putative sodium:alanine symporter | Complete |
| **NEIS1563** | hypothetical protein | Complete |

| | | |
|---|---|---|
| **NEIS1564** | putative disulphide bond formation protein | Complete |
| **NEIS1566** | transcription regulator AsnC | Complete |
| **NEIS1567** | alanine racemase | Complete |
| **NEIS1568** | hypothetical protein | Incomplete |
| **NEIS1569** | hypothetical protein | Complete |
| **NEIS1570** | putative periplasmic protein | Complete |
| **NEIS1571** | N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase | Complete |
| **NEIS1576** | hypothetical protein | Complete |
| **NEIS1577** | guanosine-3',5'-bis(diphosphate) 3'-pyrophophohydrolase | Incomplete |
| **NEIS1578** | DNA-directed RNA polymerase omega chain | Complete |
| **NEIS1579** | guanylate kinase | Complete |
| **NEIS1580** | adenine phosphoribosyltransferase | Complete |
| **NEIS1581** | hypothetical protein | Complete |
| **NEIS1582** | protease | Incomplete |
| **NEIS1583** | hypothetical protein | Incomplete |
| **NEIS1587** | haem utilisation protein | Incomplete |
| **NEIS1588** | Putative paraquat-inducible protein A | Complete |
| **NEIS1589** | Putative paraquat-inducible protein B | Complete |
| **NEIS1590** | putative lipoprotein | Complete |
| **NEIS1591** | DNA-3-methyladenine glycosylase I | Complete |
| **NEIS1592** | putative lipase | Complete |
| **NEIS1594** | glycine dehydrogenase | Complete |
| **NEIS1595** | putative cytochrome | Complete |
| **NEIS1596** | aromatic amino acid aminotransferase | Complete |
| **NEIS1597** | tRNA (uracil-5-)-methyltransferase | Complete |
| **NEIS1598** | chorismate synthase | Complete |
| **NEIS1599** | hypothetical protein | Complete |
| **NEIS1600** | DNA topoisomerase IV subunit B | Complete |
| **NEIS1601** | dinucleoside polyphosphate hydrolase | Complete |
| **NEIS1602** | seryl-tRNA synthetase | Complete |
| **NEIS1603** | D-lactate dehydrogenase | Complete |
| **NEIS1604** | peptide chain release factor 1 | Complete |
| **NEIS1605** | hypothetical protein | Complete |
| **NEIS1606** | L-asparaginase | Complete |
| **NEIS1607** | DedA family integral membrane protein | Complete |
| **NEIS1608** | phosphoglucosamine mutase | Incomplete |
| **NEIS1609** | dihydropteroate synthase | Complete |
| **NEIS1610** | hypothetical protein | Incomplete |
| **NEIS1611** | 3-octaprenyl-4-hydroxybenzoate carboxy-lyase | Complete |
| **NEIS1613** | hypothetical protein | Complete |
| **NEIS1614** | hypothetical protein | Complete |
| **NEIS1617** | 3-oxoacyl-(acyl carrier protein) synthase II | Complete |
| **NEIS1622** | putative integral membrane ion transporter | Complete |

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|---|---|---|
| **NEIS1624** | thymidylate synthase | Complete |
| **NEIS1625** | glutamate dehydrogenase | Complete |
| **NEIS1629** | GntR family transcriptional regulator | Complete |
| **NEIS1632** | putative outer membrane lipoprotein | Complete |
| **NEIS1633** | drug efflux protein | Complete |
| **NEIS1634** | membrane fusion protein | Complete |
| **NEIS1635** | transcriptional regulator | Incomplete |
| **NEIS1638** | exodeoxyribonuclease V | Complete |
| **NEIS1639** | putative integral membrane protein | Incomplete |
| **NEIS1640** | Cytochrome c oxidase subunit III / Cbb3-type cytochrome c oxidase subunit | Incomplete |
| **NEIS1643** | cbb3-type cytochrome c oxidase subunit II | Complete |
| **NEIS1645** | cbb3-type cytochrome c oxidase subunit I | Complete |
| **NEIS1646** | glycyl aminopeptidase | Incomplete |
| **NEIS1647** | hypothetical protein | Complete |
| **NEIS1648** | biopolymer transport protein | Complete |
| **NEIS1649** | biopolymer transport protein | Complete |
| **NEIS1650** | TonB protein | Complete |
| **NEIS1651** | hypothetical protein | Complete |
| **NEIS1654** | glutaredoxin 2 | Complete |
| **NEIS1655** | GTP pyrophosphokinase | Complete |
| **NEIS1669** | hypothetical protein | Complete |
| **NEIS1670** | hypothetical protein | Incomplete |
| **NEIS1671** | hypothetical protein | Complete |
| **NEIS1673** | hypothetical protein | Complete |
| **NEIS1677** | hypothetical protein | Complete |
| **NEIS1679** | putative integral membrane transport protein | Complete |
| **NEIS1683** | hypothetical protein | Complete |
| **NEIS1684** | aspartyl-tRNA synthetase | Complete |
| **NEIS1686** | putative integral membrane protein | Complete |
| **NEIS1687** | outer membrane phospholipase A precursor (ec 3.1.1.32) | Incomplete |
| **NEIS1688** | 30S ribosomal protein S20 | Complete |
| **NEIS1689** | putative polyamine permease substrate-binding protein | Complete |
| **NEIS1692** | glutamate racemase | Complete |
| **NEIS1693** | hypothetical protein | Complete |
| **NEIS1694** | N-acetylmuramoyl-L-alanine amidase | Complete |
| **NEIS1697** | hypothetical protein | Complete |
| **NEIS1698** | putative secreted protein | Complete |
| **NEIS1699** | MutT-related protein | Complete |
| **NEIS1700** | 4'-phosphopantetheinyl transferase | Complete |
| **NEIS1703** | pyridoxine 5'-phosphate synthase | Complete |
| **NEIS1704** | DNA repair protein (recombination protein o) | Complete |
| **NEIS1705** | chorismate mutase | Complete |
| **NEIS1706** | integral membrane efflux protein | Complete |

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|---|---|---|
| **NEIS1708** | hypothetical protein | Complete |
| **NEIS1720** | hypothetical protein | Complete |
| **NEIS1721** | oxidoreductase | Complete |
| **NEIS1722** | hypothetical protein | Complete |
| **NEIS1724** | hypothetical protein | Complete |
| **NEIS1725** | hypothetical protein | Complete |
| **NEIS1726** | hypothetical protein | Complete |
| **NEIS1735** | putative permease | Incomplete |
| **NEIS1737** | cell division protein FtsZ | Complete |
| **NEIS1738** | cell division protein | Complete |
| **NEIS1739** | cell division protein | Complete |
| **NEIS1740** | D-alanine--D-alanine ligase | Complete |
| **NEIS1741** | UDP-N-acetylmuramate--L-alanine ligase | Complete |
| **NEIS1742** | undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase | Complete |
| **NEIS1743** | cell division protein | Incomplete |
| **NEIS1745** | UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase | Complete |
| **NEIS1747** | phospho-N-acetylmuramoyl-pentapeptide- transferase | Complete |
| **NEIS1748** | putative periplasmic protein | Complete |
| **NEIS1749** | UDP-MurNAc-pentapeptide synthetase | Complete |
| **NEIS1751** | UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase | Incomplete |
| **NEIS1753** | penicillin-binding protein 2 | Incomplete |
| **NEIS1754** | putative small periplasmic protein | Complete |
| **NEIS1755** | S-adenosyl-methyltransferase MraW | Complete |
| **NEIS1756** | cell division protein MraZ | Complete |
| **NEIS1757** | hypothetical protein | Incomplete |
| **NEIS1759** | undecaprenyl pyrophosphate phosphatase | Complete |
| **NEIS1760** | putative thiol:disulphide interchange protein DsbA3; oxidoreductase | Complete |
| **NEIS1762** | hypothetical protein | Complete |
| **NEIS1763** | putative chelatase | Complete |
| **NEIS1764** | hypothetical protein | Complete |
| **NEIS1765** | sodium/proline symporter | Complete |
| **NEIS1766** | bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase | Incomplete |
| **NEIS1768** | exodeoxyribonuclease III | Complete |
| **NEIS1769** | ArsR family transcriptional regulator | Complete |
| **NEIS1770** | nicotinate-nucleotide pyrophosphorylase | Complete |
| **NEIS1771** | putative cytoplasmic membrane protein | Complete |
| **NEIS1772** | quinolinate synthetase | Incomplete |
| **NEIS1773** | L-aspartate oxidase | Incomplete |
| **NEIS1776** | beta-phosphoglucomutase | Complete |
| **NEIS1777** | maltose phosphorylase | Incomplete |
| **NEIS1779** | integral membrane transport protein | Incomplete |
| **NEIS1780** | putative ABC transporter ATP-binding protein | Complete |

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|---|---|---|
| **NEIS1781** | phosphatidylglycerophosphatase A | Complete |
| **NEIS1782** | thiamine monophosphate kinase | Incomplete |
| **NEIS1783** | outer membrane protein class 4 | Complete |
| **NEIS1784** | transcriptional regulator CysB-like protein | Complete |
| **NEIS1785** | putative anaerobic transcriptional regulatory protein | Complete |
| **NEIS1786** | coproporphyrinogen III oxidase | Complete |
| **NEIS1787** | putative phosphate permease | Complete |
| **NEIS1788** | anhydro-N-acetylmuramic acid kinase | Incomplete |
| **NEIS1804** | hypothetical periplasmic protein | Complete |
| **NEIS1807** | hypothetical protein | Complete |
| **NEIS1808** | putative integral membrane signal transducer protein | Complete |
| **NEIS1809** | glutamine synthetase | Complete |
| **NEIS1810** | shikimate dehydrogenase | Complete |
| **NEIS1811** | monofunctional biosynthetic peptidoglycan transglycosylase | Complete |
| **NEIS1812** | lipopolysaccharide ABC transporter | Complete |
| **NEIS1813** | LPS-assembly protein LptD | Complete |
| **NEIS1814** | lipopolysaccharide export system protein (OM) | Complete |
| **NEIS1815** | 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase, KDO 8-P phosphatase (EC 3.1.3.45) | Complete |
| **NEIS1816** | arabinose-5-phosphate isomerase (EC 5.3.1.13) | Complete |
| **NEIS1818** | transaldolase | Complete |
| **NEIS1820** | glutamyl-Q tRNA(Asp) synthetase | Incomplete |
| **NEIS1822** | tRNA-dihydrouridine synthase A | Complete |
| **NEIS1823** | D-tyrosyl-tRNA(Tyr) deacylase | Complete |
| **NEIS1824** | hypothetical protein | Complete |
| **NEIS1825** | hypothetical protein | Complete |
| **NEIS1826** | hypothetical protein | Complete |
| **NEIS1827** | YciI-like protein | Complete |
| **NEIS1828** | intracellular septation protein A | Complete |
| **NEIS1830** | lactoylglutathione lyase | Incomplete |
| **NEIS1831** | tetratricopeptide repeat protein | Complete |
| **NEIS1832** | hypothetical protein | Complete |
| **NEIS1833** | branched-chain amino acid aminotransferase | Complete |
| **NEIS1834** | enoyl-(acyl carrier protein) reductase | Complete |
| **NEIS1835** | 2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase | Complete |
| **NEIS1837** | glucose-6-phosphate isomerase 2 (EC 5.3.1.9) | Complete |
| **NEIS1838** | type IV biogenesis protein | Complete |
| **NEIS1839** | type IV prepilin like protein leader peptide processing enzyme | Complete |
| **NEIS1841** | hypothetical protein | Complete |
| **NEIS1842** | hypothetical protein | Complete |
| **NEIS1844** | type IV biogenesis protein | Complete |
| **NEIS1845** | hypothetical protein | Incomplete |
| **NEIS1846** | octaprenyl-diphosphate synthase | Complete |

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|---|---|---|
| **NEIS1847** | 50S ribosomal protein L21 | Complete |
| **NEIS1848** | 50S ribosomal protein L27 | Complete |
| **NEIS1849** | hypothetical protein | Complete |
| **NEIS1850** | 50S ribosomal protein L33 | Complete |
| **NEIS1851** | 50S ribosomal protein L28 | Complete |
| **NEIS1852** | multidrug resistance translocase; fatty acid efflux system protein | Incomplete |
| **NEIS1853** | multidrug resistance translocase; fatty acid efflux system protein | Incomplete |
| **NEIS1854** | 7-cyano-7-deazaguanine reductase | Complete |
| **NEIS1855** | hypothetical protein | Complete |
| **NEIS1856** | hypothetical protein | Incomplete |
| **NEIS1857** | hypothetical protein | Complete |
| **NEIS1858** | hypothetical protein | Incomplete |
| **NEIS1870** | hypothetical protein | Complete |
| **NEIS1871** | hypothetical protein | Complete |
| **NEIS1872** | hypothetical protein | Complete |
| **NEIS1873** | dihydrofolate reductase | Complete |
| **NEIS1882** | hypothetical protein | Complete |
| **NEIS1883** | signal recognition particle protein | Complete |
| **NEIS1889** | hypothetical protein | Complete |
| **NEIS1890** | hypothetical protein | Complete |
| **NEIS1891** | LysR family transcriptional regulator | Complete |
| **NEIS1892** | deoxyribodopyrimidine photolyase | Incomplete |
| **NEIS1896** | hypothetical protein | Complete |
| **NEIS1898** | hypothetical protein | Complete |
| **NEIS1899** | 16S ribosomal RNA methyltransferase RsmE | Complete |
| **NEIS1900** | lacto-N-neotetraose biosynthesis glycosyl transferase | Incomplete |
| **NEIS1902** | lacto-N-neotetraose biosynthesis glycosyl transferase | Incomplete |
| **NEIS1903** | glycyl-tRNA synthetase subunit beta | Complete |
| **NEIS1904** | glycyl-tRNA synthetase subunit alpha | Complete |
| **NEIS1905** | F0F1 ATP synthase subunit epsilon | Incomplete |
| **NEIS1906** | F0F1 ATP synthase subunit beta | Complete |
| **NEIS1907** | F0F1 ATP synthase subunit gamma | Incomplete |
| **NEIS1908** | F0F1 ATP synthase subunit alpha | Incomplete |
| **NEIS1909** | F0F1 ATP synthase subunit delta | Complete |
| **NEIS1910** | F0F1 ATP synthase subunit B | Complete |
| **NEIS1911** | F0F1 ATP synthase subunit C | Complete |
| **NEIS1912** | F0F1 ATP synthase subunit A | Incomplete |
| **NEIS1913** | putative ATP synthase I | Complete |
| **NEIS1915** | putative chromosome segregation proteins | Complete |
| **NEIS1916** | aromatic acid decarboxylase | Complete |
| **NEIS1917** | putative lipoprotein | Incomplete |
| **NEIS1918** | inner membrane transport protein | Incomplete |
| **NEIS1919** | putative ABC transport ATP-binding subunit | Complete |

| | | |
|---|---|---|
| **NEIS1920** | putative transglycosylase | Incomplete |
| **NEIS1921** | 30S ribosomal protein S21 | Complete |
| **NEIS1922** | hypothetical protein | Complete |
| **NEIS1924** | ClpXP protease specificity-enhancing factor | Complete |
| **NEIS1925** | pilE expression regulator/putative sspA-like protein | Complete |
| **NEIS1926** | putative inner membrane protein | Incomplete |
| **NEIS1928** | 50S ribosomal protein L31 | Complete |
| **NEIS1929** | acetyltransferase | Complete |
| **NEIS1930** | putative periplasmic protein | Complete |
| **NEIS1931** | hypothetical protein | Incomplete |
| **NEIS1932** | hypothetical protein | Incomplete |
| **NEIS1933** | periplasmic/outer membrane protein | Incomplete |
| **NEIS1934** | hypothetical protein | Incomplete |
| **NEIS1935** | putative periplasmic transport protein | Incomplete |
| **NEIS1936** | putative outer membrane transport protein | Complete |
| **NEIS1937** | putative ABC transport inner membrane subunit | Complete |
| **NEIS1938** | putative ABC transport ATP-binding protein | Incomplete |
| **NEIS1942** | aldehyde dehydrogenase | Complete |
| **NEIS1944** | putative para-aminobenzoate synthase component I | Complete |
| **NEIS1945** | hypothetical protein | Incomplete |
| **NEIS1948** | chaperonin GroEL | Incomplete |
| **NEIS1949** | co-chaperonin GroES | Complete |
| **NEIS1951** | putative sodium-dependent inner membrane transport protein | Complete |
| **NEIS1952** | diaminopimelate decarboxylase | Complete |
| **NEIS1953** | putative lipoprotein | Complete |
| **NEIS1954** | frataxin-like protein | Complete |
| **NEIS1955** | hypothetical protein | Complete |
| **NEIS1956** | S-ribosylhomocysteinase | Complete |
| **NEIS1957** | DNA polymerase I | Incomplete |
| **NEIS1962** | tRNA modification GTPase TrmE | Complete |
| **NEIS1964** | putative membrane transport solute-binding protein | Complete |
| **NEIS1965** | putative inner membrane transport protein | Incomplete |
| **NEIS1966** | putative inner membrane transport protein | Incomplete |
| **NEIS1967** | hypothetical protein | Complete |
| **NEIS1968** | putative ABC transporter ATP-binding subunit | Complete |
| **NEIS1971** | nitrogen regulatory protein P-II 1 | Complete |
| **NEIS1972** | phosphoribosylformylglycinamidine synthase | Complete |
| **NEIS1973** | hydroxyacylglutathione hydrolase | Complete |
| **NEIS1976** | putative magnesium transporter | Complete |
| **NEIS1977** | Hsp33-like chaperonin | Complete |
| **NEIS1978** | hypothetical protein | Incomplete |
| **NEIS1979** | hypothetical protein | Complete |
| **NEIS1980** | hypothetical protein | Complete |

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|---|---|---|
| **NEIS1981** | hypothetical protein | Incomplete |
| **NEIS1982** | bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein | Incomplete |
| **NEIS1983** | hypothetical protein | Complete |
| **NEIS1984** | ATP-dependent DNA helicase | Complete |
| **NEIS1987** | putative DNA helicase | Incomplete |
| **NEIS1995** | minor pilin | Complete |
| **NEIS1997** | psedouridine synthase | Complete |
| **NEIS1998** | phosphopantetheine adenylyltransferase | Complete |
| **NEIS1999** | putative integral membrane protein | Complete |
| **NEIS2000** | hypothetical protein | Complete |
| **NEIS2001** | rRNA large subunit methyltransferase | Complete |
| **NEIS2002** | hypothetical protein | Complete |
| **NEIS2003** | Probable nicotinate-nucleotide adenylyltransferase EC=2.7.7.18 | Complete |
| **NEIS2004** | hypothetical protein | Complete |
| **NEIS2008** | homoserine kinase | Incomplete |
| **NEIS2009** | 3-demethylubiquinone-9 3-methyltransferase | Complete |
| **NEIS2010** | amino-acid transport protein | Complete |
| **NEIS2014** | D-alpha,beta,D-Heptose 1,7 bisphosphate phosphatase | Complete |
| **NEIS2015** | 1-acyl-SN-glycerol-3-phosphate acyltransferase | Complete |
| **NEIS2016** | hypothetical protein | Complete |
| **NEIS2017** | tRNA pseudouridine synthase A | Complete |
| **NEIS2020** | PorB, porin, major outer membrane protein | Complete |
| **NEIS2021** | thiamine biosynthesis protein ThiC | Complete |
| **NEIS2022** | hypothetical protein | Complete |
| **NEIS2023** | ABC-transport system ATP-binding protein | Complete |
| **NEIS2024** | phosphoenolpyruvate-protein phosphotransferase | Complete |
| **NEIS2025** | sugar transport PTS system phosphocarrier protein HPr | Complete |
| **NEIS2026** | sugar transport PTS system IIA component | Incomplete |
| **NEIS2027** | hypoxanthine-guanine phosphoribosyltransferase | Complete |
| **NEIS2028** | DNA ligase | Complete |
| **NEIS2029** | putative hydrolase | Complete |
| **NEIS2030** | putative periplasmic protein | Incomplete |
| **NEIS2032** | cytochrome C1 precursor | Complete |
| **NEIS2033** | cytochrome B | Complete |
| **NEIS2034** | ubiquinol-cytochrome c reductase iron-sulfur subunit | Complete |
| **NEIS2035** | hypothetical protein | Complete |
| **NEIS2036** | putative transcriptional activator protein METR | Complete |
| **NEIS2037** | 30S ribosomal protein S9 | Complete |
| **NEIS2038** | 50S ribosomal protein L13 | Complete |
| **NEIS2039** | hypothetical protein | Complete |
| **NEIS2040** | hypothetical protein | Complete |
| **NEIS2041** | NAD(P)H-dependent glycerol-3-phosphate dehydrogenase | Complete |
| **NEIS2042** | phosphoenolpyruvate carboxylase | Incomplete |

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|---|---|---|
| **NEIS2044** | hypothetical protein | Complete |
| **NEIS2045** | putative integral membrane protein | Complete |
| **NEIS2046** | hemk protein | Complete |
| **NEIS2047** | TLDD protein | Complete |
| **NEIS2049** | putative oxidoreductase | Complete |
| **NEIS2050** | thiamin-phosphate pyrophosphorylase | Complete |
| **NEIS2051** | hypothetical protein | Complete |
| **NEIS2052** | thiazole synthase | Complete |
| **NEIS2053** | putative periplasmic protein | Complete |
| **NEIS2054** | bifunctional biotin--[acetyl-CoA-carboxylase] ligase/pantothenate kinase | Incomplete |
| **NEIS2055** | D-beta-D-heptose-1-phosphate adenylyltransferase | Complete |
| **NEIS2056** | bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase | Complete |
| **NEIS2057** | putative integral membrane protein | Complete |
| **NEIS2058** | aspartate-semialdehyde dehydrogenase | Complete |
| **NEIS2059** | hypothetical protein | Complete |
| **NEIS2060** | hypothetical protein | Complete |
| **NEIS2061** | putative nuclease | Complete |
| **NEIS2062** | cysteinyl-tRNA synthetase | Incomplete |
| **NEIS2065** | GTPase ObgE | Incomplete |
| **NEIS2069** | hypothetical protein | Complete |
| **NEIS2070** | sedoheptulose-7-phosphate isomerase | Complete |
| **NEIS2071** | putative lipoprotein | Complete |
| **NEIS2072** | putative periplasmic protein | Incomplete |
| **NEIS2073** | methionine aminopeptidase | Complete |
| **NEIS2074** | hypothetical protein | Incomplete |
| **NEIS2075** | putative adhesin complex protein | Complete |
| **NEIS2076** | malate:quinone oxidoreductase | Incomplete |
| **NEIS2077** | hypothetical protein | Complete |
| **NEIS2078** | hypothetical protein | Complete |
| **NEIS2079** | putative integral membrane protein | Complete |
| **NEIS2080** | 30S ribosomal protein S2 | Complete |
| **NEIS2081** | elongation factor Ts | Complete |
| **NEIS2082** | uridine monophosphate kinase | Complete |
| **NEIS2103** | putative protease | Complete |
| **NEIS2104** | hypothetical protein | Complete |
| **NEIS2106** | argininosuccinate synthase | Complete |
| **NEIS2110** | serine/threonine transporter SstT | Incomplete |
| **NEIS2112** | putative outer membrane protein | Incomplete |
| **NEIS2113** | putative periplasmic protein | Incomplete |
| **NEIS2114** | peptide transporter | Complete |
| **NEIS2116** | peptide chain release factor 2 | Incomplete |
| **NEIS2118** | lipoprotein | Incomplete |

| | | |
|---|---|---|
| **NEIS2119** | putative integral membrane protein | Complete |
| **NEIS2120** | putative periplasmic protein | Complete |
| **NEIS2121** | hypothetical protein | Complete |
| **NEIS2122** | hypothetical protein | Complete |
| **NEIS2123** | RNA polymerase sigma factor | Complete |
| **NEIS2124** | lipoprotein | Incomplete |
| **NEIS2128** | hypothetical protein | Complete |
| **NEIS2129** | phosphoribosylamine--glycine ligase | Complete |
| **NEIS2130** | hypothetical protein | Complete |
| **NEIS2131** | hypothetical protein | Complete |
| **NEIS2132** | electron transfer flavoprotein alpha-subunit | Complete |
| **NEIS2133** | electron transfer flavoprotein beta-subunit | Complete |
| **NEIS2134** | Heptosyl transferase I | Incomplete |
| **NEIS2135** | putative nicotinamidase | Complete |
| **NEIS2136** | hypothetical protein | Complete |
| **NEIS2137** | glyceraldehyde 3-phosphate dehydrogenase C (EC 1.2.1.12) | Complete |
| **NEIS2138** | DNA mismatch repair protein MutS | Complete |
| **NEIS2140** | putative periplasmic protein | Complete |
| **NEIS2141** | glutamyl-tRNA synthetase | Complete |
| **NEIS2142** | putative periplasmic protein | Complete |
| **NEIS2143** | putative oxidoreductase | Complete |
| **NEIS2144** | putative periplasmic thiredoxin | Complete |
| **NEIS2145** | ABC transporter ATP-binding protein | Complete |
| **NEIS2146** | putative ABC transporter integral membrane protein | Complete |
| **NEIS2147** | hypothetical protein | Complete |
| **NEIS2148** | phosphoglycerate kinase (EC 2.7.2.3) | Incomplete |
| **NEIS2149** | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | Complete |
| **NEIS2150** | putative transmembrane transport protein | Complete |
| **NEIS2151** | putative integral membrane protein | Complete |
| **NEIS2152** | 3-deoxy-D-manno-octulosonic-acid transferase | Complete |
| **NEIS2153** | 6-phosphogluconate dehydrogenase | Complete |
| **NEIS2169** | cseE / 3-deoxy-D-manno-octulosonic acid 8-phosphate synthase | Complete |
| **NEIS2375** | sec-independent protein translocase TatA/E component | Complete |
| **NEIS2445** | hypothetical protein | Incomplete |
| **NEIS2447** | hypothetical protein | Complete |
| **NEIS2448** | hypothetical protein | Complete |
| **NEIS2515** | hypothetical protein | Complete |
| **NEIS2522** | hypothetical protein; DUF2788 | Complete |
| **NEIS2526** | conserved hypothetical protein | Complete |
| **NEIS2530** | conserved hypothetical protein | Complete |
| **NEIS2553** | conserved hypothetical protein | Complete |
| **NEIS2558** | conserved hypothetical integral membrane protein | Complete |
| **NEIS2779** | copper-containing nitrite reductase | Complete |

| | | |
|---|---|---|
| **NEIS2852** | Cbb3-type cytochrome oxidase component FixQ | Complete |
| **NEIS2903** | hypothetical protein | Complete |
| **NEIS0007** | methionyl-tRNA synthetase | Incomplete |
| **NEIS0033** | type IV pilus associated protein | Incomplete |
| **NEIS0041** | DNA transport competence protein | Incomplete |
| **NEIS0046** | glucose-1-phosphate thymidylyltransferase | Complete |
| **NEIS0047** | dTDP-D-glucose 4,6-dehydratase | Incomplete |
| **NEIS0062** | truncated galE | Complete |
| **NEIS0065** | dTDP-4-keto-6-deoxy-D-glucose-3,6-epimerase | Incomplete |
| **NEIS0096** | lipoprotein | Complete |
| **NEIS0117** | secE | Complete |
| **NEIS0139** | 50S ribosomal protein L16 | Complete |
| **NEIS0142** | 50S ribosomal protein L14 | Complete |
| **NEIS0148** | 50S ribosomal protein L18 | Complete |
| **NEIS0151** | 50S ribosomal protein L15 | Complete |
| **NEIS0153** | infA; translation initiation factor IF-1 | Complete |
| **NEIS0154** | 50S ribosomal protein L36 | Complete |
| **NEIS0156** | 30S ribosomal protein S11 | Complete |
| **NEIS0171** | UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.-) | Incomplete |
| **NEIS0194** | hypothetical protein | Complete |
| **NEIS0212** | RNA polymerase sigma factor | Complete |
| **NEIS0213** | pilin glycosyltransferase | Incomplete |
| **NEIS0214** | inner membrane transport protein | Complete |
| **NEIS0221** | MafI immunity protein | Complete |
| **NEIS0291** | LOS O-acetyltransferase | Complete |
| **NEIS0294** | hypothetical protein | Complete |
| **NEIS0308** | hypothetical protein | Incomplete |
| **NEIS0309** | hypothetical protein | Complete |
| **NEIS0332** | hypothetical protein | Complete |
| **NEIS0388** | esterase | Incomplete |
| **NEIS0428** | two-component system response regulator | Complete |
| **NEIS0499** | hypothetical protein | Complete |
| **NEIS0519** | regulatory protein | Complete |
| **NEIS0520** | hypothetical protein | Complete |
| **NEIS0535** | hypothetical protein | Incomplete |
| **NEIS0567** | putative polyamine permease substrate-binding protein | Complete |
| **NEIS0596** | MafA2 adhesin | Complete |
| **NEIS0599** | alternative toxic C-terminal extremity | Incomplete |
| **NEIS0601** | putative mafS2 cassette | Complete |
| **NEIS0626** | hypothetical protein | Complete |
| **NEIS0665** | hypothetical protein | Incomplete |
| **NEIS0667** | hypothetical protein; | Incomplete |
| **NEIS0832** | hypothetical protein | Incomplete |

| | | |
|---|---|---|
| **NEIS0916** | lipoprotein | Complete |
| **NEIS1020** | hypothetical protein | Complete |
| **NEIS1041** | ABC transporter ATP-binding protein | Complete |
| **NEIS1062** | ABC transporter ATP-binding protein | Complete |
| **NEIS1071** | hypothetical protein | Complete |
| **NEIS1088** | hypothetical protein | Incomplete |
| **NEIS1089** | hypothetical protein | Complete |
| **NEIS1204** | putative periplasmic protein | Incomplete |
| **NEIS1218** | 2-dehydro-3-deoxyphosphooctonate aldolase (EC 2.5.1.55) | Complete |
| **NEIS1222** | iron-sulfur binding protein | Complete |
| **NEIS1259** | primosomal replication protein | Complete |
| **NEIS1273** | lipoprotein | Complete |
| **NEIS1325** | hypothetical protein | Incomplete |
| **NEIS1338** | pseudo | Complete |
| **NEIS1424** | hypothetical protein | Incomplete |
| **NEIS1452** | hypothetical protein | Complete |
| **NEIS1507** | hypothetical protein | Complete |
| **NEIS1516** | putative polyamine permease substrate-binding protein | Complete |
| **NEIS1527** | two component response regulator | Complete |
| **NEIS1549** | nitrite reductase, major outer membrane copper-containing protein | Complete |
| **NEIS1573** | hypothetical protein | Incomplete |
| **NEIS1574** | DNA transport competence protein | Incomplete |
| **NEIS1615** | hypothetical protein | Complete |
| **NEIS1621** | hypothetical protein | Incomplete |
| **NEIS1623** | hypothetical protein | Incomplete |
| **NEIS1630** | hypothetical protein | Complete |
| **NEIS1672** | hypothetical protein | Incomplete |
| **NEIS1727** | acetate kinase | Complete |
| **NEIS1746** | hypothetical protein | Complete |
| **NEIS1789** | MafA adhesin | Complete |
| **NEIS1794** | putative mafS3 cassette | Incomplete |
| **NEIS1800** | alternative toxic C-terminal extremity | Complete |
| **NEIS1874** | phospho-2-dehydro-3-deoxyheptonate aldolase | Complete |
| **NEIS1875** | hypothetical protein | Incomplete |
| **NEIS1880** | DNA transport competence protein | Incomplete |
| **NEIS1885** | thiol:disulfide interchange protein DsbA2; oxidoreductase | Incomplete |
| **NEIS1901** | lacto-N-neotetraose biosynthesis glycosyl transferase | Incomplete |
| **NEIS1939** | transcriptional regulator | Incomplete |
| **NEIS1996** | DNA transport competence protein | Incomplete |
| **NEIS2005** | putative permease | Incomplete |
| **NEIS2043** | ThiF protein | Complete |
| **NEIS2068** | hypothetical protein | Incomplete |

## Supplemental Table 2: Diatabs™ reaction's interpretation guide

| Diatabs | Positive | Negative |
|---|---|---|
| **Glucose** | Yellow | Red/Orange-red |
| **Maltose** | Yellow | Red/Orange-red |
| **Sucrose** | Yellow | Red/Orange-red |
| **Lactose** | Yellow | Red/Orange-red |
| **Gamma-Glutamyl Aminopeptidase (GGA)*** | Red/Orange | Yellow |
| **Leucine Aminopeptidase (LA)*** | Orange/light orange | Yellow |
| **proline Aminopeptidase (PA) *** | Red/Orange | Yellow |
| **Beta-Galactosidase (ONPG)** | Yellow | Colourless |
| **Tributyrin** | Yellow/Yellow-orange | Red |

* Read after 4 hours. All the other tests were read after an overnight incubation

## Supplemental Table 3: API®-NH reaction's interpretation guide

| Tests | Reactions | Positive | Negative |
|---|---|---|---|
| **PEN** | Penicillinase | Yellow/ Yellow-Green/ Yellow-Blue | Blue |
| **GLU** | Glucose Acidification | Yellow/Orange | Red/Red-Orange |
| **FRU** | Fructose Acidification | Yellow/Orange | Red/Red-Orange |
| **MAL** | Maltose Acidification | Yellow/Orange | Red/Red-Orange |
| **SAC** | Saccharose Acidification | Yellow/Orange | Red/Red-Orange |
| **ODC** | Ornithine Decarboxylase | Blue | Yellow-Green/Grey-Green |
| **URE** | Urease | Pink-Purple | Yellow |
| **LIP** | Lipase | Blue* | Colourless/ Pale Grey |
| **PAL** | Alkaline Phosphatase | Yellow | Colourless/ Pale Yellow |
| **βGAL** | β-Galactosidase | Yellow | Colourless |
| **ProA** | Proline Arylamidase** | Orange | Yellow/ Pale Orange |
| **GGT** | Gamma-Glutamyl Transferase | Orange | Yellow/ Pale Orange*** |
| **IND** | Indole | Pink | Colourless |

* With precipitate
** ProA is always negative when LIP was positive,
*** Yellow-Orange if PAL was positive

## Supplemental Table 4: Two-way Average Nucleotide Identity using WGS

| | Nm | Ng | Np 1 | Np 2 | Nspp 1 | Nspp 2 | Nspp 3 | Nspp 4 | Nspp 5 | Nspp 6 | Nspp 7 | Nspp 8 | Nspp 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Nm** | | | | | | | | | | | | | |
| **Ng** | 94.4 | | | | | | | | | | | | |
| **Np 1** | 93.9 | 93.2 | | | | | | | | | | | |
| **Np 2** | 94.2 | 93.3 | 94.7 | | | | | | | | | | |
| **Nspp 1** | 93.7 | 93.5 | 94.0 | 93.9 | | | | | | | | | |
| **Nspp 2** | 93.8 | 93.6 | 93.9 | 93.9 | 97.0 | | | | | | | | |
| **Nspp 3** | 93.6 | 93.5 | 94.0 | 94.0 | 94.9 | 94.9 | | | | | | | |
| **Nspp 4** | 93.6 | 93.2 | 94.0 | 93.9 | 94.6 | 94.5 | 94.6 | | | | | | |
| **Nspp 5** | 93.7 | 93.4 | 94.1 | 93.9 | 94.4 | 94.5 | 94.4 | 94.9 | | | | | |
| **Nspp 6** | 93.6 | 93.2 | 94.2 | 94.0 | 94.2 | 94.4 | 94.2 | 94.7 | 94.3 | | | | |
| **Nspp 7** | 93.5 | 93.2 | 94.1 | 94.1 | 94.6 | 94.5 | 94.6 | 94.4 | 94.4 | 94.4 | | | |
| **Nspp 8** | 93.6 | 93.5 | 93.9 | 93.9 | 95.0 | 94.9 | 94.9 | 94.4 | 94.4 | 94.1 | 94.5 | | |
| **Nspp 9** | 93.6 | 93.5 | 93.9 | 93.7 | 95.7 | 95.7 | 94.9 | 94.5 | 94.3 | 94.2 | 94.3 | 94.9 | |

<94

>95

ANI measured in percentage are presented with a colour gradient, yellow for values <94 and red for values >95%, which is the threshold above which genomes are considered to be from the species. Nm: *N. meningitidis*; Ng: *N. gonorrhoeae*; Np: *N. polysaccharea* and Nspp: *Neisseria spp*

## Supplemental Table 5: Two-way ANI among the *N. polysaccharea* isolates based on WGS

| | Np 1 | Np 1a | Np 1b | Np 1c | Np 2 |
|---|---|---|---|---|---|
| **Np 1** | | | | | |
| **Np 1a** | 96.4 | | | | |
| **Np 1b** | 95.9 | 96.2 | | | |
| **Np 1c** | 94.6 | 94.7 | 94.6 | | |
| **Np 2** | 94.7 | 94.7 | 94.7 | 94.6 | |

<94

<95

ANI measured in percentage are presented with a colour gradient.
Np: *N. polysaccharea*

## Appendix 4: PDF of published papers