Molecular characterization of horse flies (Diptera: Tabanidae) and determination of their role in transmission of haemoparasites in southern Africa

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DEDICATION

This thesis is dedicated to my mother Matshidiso Sanna Taioe. For her encouragement, endless love and support that has sustained me throughout my life.

I LOVE YOU MA!!!

"In the middle of difficulty lies opportunity."
-Albert Einstein

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ABSTRACT

Tabanids are biting flies commonly referred to as horse flies, deer flies or clegs. They belong to the family Tabanidae composed of more than 4 400 species belonging to 114 genera with a cosmopolitan distribution. Tabanids are of economic importance worldwide due to their ability to transmit various pathogens including bacteria, viruses and protozoa. In southern Africa little has been done to characterize tabanid flies to species level using molecular techniques, and there is insufficient knowledge on the role played by tabanid flies in transmission of haemoparasites. As a result the current study was aimed at characterizing tabanid flies (Tabanidae) in selected study sites in Lesotho, South Africa and Zambia. Morphological identification and molecular techniques were used to characterize tabanid flies found in the three countries to species level. Furthermore, this study sought to detect protozoan parasites of veterinary importance harboured by the sampled tabanid species. Lastly, metagenomic analysis was conducted to determine the gut microbiota of the sampled tabanid flies in order to identify genera of medical or veterinary importance and genera involved in symbiotic associations with arthropods.

A total of 529 tabanid flies comprising of 2 from Lesotho, 307 from South Africa and 157 from Zambia, were collected. Morphological analysis revealed a total of 5 different genera collected from the sampled areas namely: *Ancala*, *Atylotus*, *Haematopota*, *Philoliche* and *Tabanus*. The overall number of members from the genus *Tabanus* was greater than all other genera combined. Morphological identification was further supported by amplification of mitochondrial *cytochrome oxidase* 1 (*CO1*) gene whereby the PCR products were sequenced and the retrived sequences matched with the above mentioned genera from the NCBI database. Phylogeny of southern African tabanid flies using *CO1* gene sequences supported monophyly in Tabanidae when compared to other tabanid flies from the NCBI database. In addition, tabanid flies from the Afrotropic region were found to be genetically distinct from those found in the Nearctic and the Neotropical regions. This is probably due to influence of variable environmental factors in different geographical areas which are probably affecting genetic makeup of the flies.

Deoxyribonucleic acid extracted from South African *Tabanus par* and *T. taeniola* tested positive for the presence of *Trypanosoma congolense* and *T. theileri* whilst one member from *T. par* was positive for the presence of *Trypanozoon* species. Deoxyribonucleic

acid extracted from Zambian tabanid flies tested positive for the presence of *Besnoitia besnoiti*, *Babesia bigemina*, *Theileria parva* and for *Trypanozoon* species at 1.27% (2/157), 5.73% (9/157), 30.11% (30/157) and 9.82% (14/157) respectively.

Analysis of gut microbes from the seven South African tabanid flies produced a total of 407 689 assembled sequences and a total of 505 operational taxonomic units (OTUs). The most abundant phylum was Proteobacteria (44.55%), followed by unclassified bacteria with 37.08%. The other important detected phyla included Tenericutes (8.91%), Firmicutes (7.33%) and Bacteroidetes (1.98%). Analysis of gut microbes associated with twelve tabanid flies from Zambia revealed 2 524 727 assembled sequences and 2 285 OTUs per fly species. A total of 12 phyla were recovered from the produced OTUs. The abundant bacterial phyla were Proteobacteria (57.81%), followed by Tenericutes with 22.67% and the least phyla detected included Planctomycetes, Gemmatimonadetes, WS3 as well as Chlamydiae. The *Spiroplasma* was the genus detected amongst all tabanid species and is suspected to be a mutual or commensal symbiont in the gut of tabanid flies. Furthermore, the following genera which has species of medical or veterinary or environmental importance were detected from the gut of tabanid flies by means of metagenomics analyses: *Enterobacter*, *Serratia*, *Klebsiella*, *Shigella*, *Escherichia*, *Proteus*, *Providencia*, *Acinetobacter*, *Zymobacter*, *Vibrio*, *Comamonas*, *Pseudomonas*, *Brochothrix*, *Bacillus*, *Staphylococcus* and *Enterococcus*. This is study has pioneered detection of bacterial genera of medical, veterinary and invironmental significance by metagenomics in tabanid flies.

This is the first report of detection of *Besnoitia besnoiti*, *Babesia bigemina*, *Theileria parva* and various trypanosome species by PCR from southern African tabanid flies. Additionally, it is for the first time gut microbes associated with tabanid flies are explored by metagenomic analysis. This study has demonstrated that there is a high abundance of different tabanid fly species in South Africa and Zambia. However, not much can be said regarding tabanid flies from Lesotho due to the fact that in the current study only 2 specimens were captured during a 3 months sampling period. Nonetheless, this study has not determined the vectorial capacity of tabanid flies for the detected protozoan parasites and bacteria. It has been reported that tabanid flies mechanically transmit some *Trypanosoma* species as well as bacterial species such as *Anaplasma marginale*, *Bacillus anthracis* and *Listeria monocytogenes.* Further studies to determine if tabanids

are capable of transmitting tick-borne parasites such as *Babesia* species and *Theileria* species are required. Transmission of *Besnoitia* species by tabanid flies is not clarified, and their association with tabanid flies needs to be further explored. Whilst a lot of research and control strategies are focused on tsetse flies and ticks, it is evident that tabanid flies need to be considered for inclusion in such efforts as well. The findings obtained in this study open doors for future studies, particularly in identifying candidate microbes that can be used in the control of tabanid flies as well as in determining the actual role played by symbiotic microbes inside the tabanid flies.

Key words: Tabanid flies, southern Africa, molecular charecterization, protozoan parasites, metagenomics, gut microbes.

CHAPTER 1

GENERAL INTRODUCTION

1.1 Background

Tabanids are robust medium to large (6 – 30 mm) biting flies commonly referred to as horse flies, deer flies or clegs (Nevill *et al*., 1994; Service, 2012). These dipterans belong to the family Tabanidae composed of more than 4 400 species belonging to 114 genera with a cosmopolitan distribution (Zumpt, 1949; Baldacchino *et al*., 2014a). A review by Usher (1972) was the first to document tabanids of southern Africa as well as their distribution. In southern Africa, there are 410 species of tabanid flies with approximately 64 species occuring in KwaZulu-Natal Province (KZN) which accounts for the highest species diversity in the country (Usher, 1972). Twelve species are endemic to KZN coastal climatic region which contributes 16% of the total endemic tabanid species to South Africa (Esterhuizen, 2006).

Vast amounts of research have been conducted on tabanid flies and it has been reported that they are capable of biologically or mechanically transmitting numerous disease causing pathogens to both humans and livestock (Zumpt, 1949; Chainey, 1993; Service, 2012). A review on medical and veterinary importance of tabanid flies by Zumpt (1949), reported that members from the genera *Tabanus*, *Haematopota* and *Chrysops* are the most important vectors in disease transmission. Additionally, recent studies conducted by Neville *et al*. (1994), Desquesnes and Dia (2003a; 2003b; 2004), reported that members of the genus *Atylotus*, *Hybomitra*, *Ancala*, *Tabanocella* and various species of *Philoliche* are capable of being mechanical vectors of blood parasites. The pathogens transmitted by tabanid flies include viruses, bacteria, protozoa and nematodes (Baldacchino *et al*., 2014a)

A study by Esterhuizen (2006) was the first to document the seasonal abundance of tabanid flies in KZN using H-traps which have been originally designed by Kappmeier (2000) for capture of tsetse flies. Additionally, in other African countries odour baited targets and traps have been employed in determining the distribution and prevalence of haematophagous dipterans and also discussed what impact the high abundance of haematophagous dipterans may have on livestock productivity and human wellbeing (Oldroyd, 1954; Okiwelu, 1975; 1976; Kappmeier, 2000; Ahmed *et al*., 2005).

In southern Africa little has been done to characterize tabanid flies to species level using molecular techniques, and there is insufficient information on the role played by tabanid flies in transmission of haemoparasites in this region. As a result the current study attempts to fill in this information gaps focusing on tabanid flies collected in South Africa, Lesotho and Zambia.

1.2 Biology of Tabanidae

1.2.1 Taxonomy

Insects are the most abundant and successful organisms in the phylum Arthropoda inhabiting fresh water and terrestrial habitats and account for approximately more than 1 million described species worldwide (Scholtz and Holm, 1998). The order Diptera (True flies) comprises of more than 85 000 described and approximately more than 70 000 undescribed species (Barraclough and Londt, 1998). They are distinguished from all other insects by the presence of one pair of mesothorasic wings and reduced hind wings called halters (Barraclough and Londt, 1998; Triplehorn and Johnson, 2005). The family Tabanidae falls under the suborder Brachycera. Based on genitalia, antennae, wing venation and other external characters the family Tabanidae is further divided into four subfamilies namely: Chrysopsinae, Pangoniinae, Scepsidinae and Tabaninae (Lessard and Yeates, 2012).

The subfamily Chrysopsinae is further divided into three tribes, namely Bouvieromyiini, Chrysopini and Rhinomyzini (Usher, 1972; Lessard and Yeates, 2012). The tribes of the subfamily Pangoniinae include Mycteromyiini, Pangoniini, Philolichini and Scionini (Lessard and Yeates, 2012). The subfamily Scepsidinae has only one tribe Scepsidini (Usher, 1972). Lastly, the largest of the subfamilies Tabaninae is composed of three tribes, namely, Diachlorini, Haematopotini and Tabanini (Usher, 1972; Lessard and Yeates, 2012). In southern Africa Scepsidinae has only 4 species, Chrysopsinae with 52 species, Pangoniinae has 50 species and lastly Tabaninae has the largest number with 121 species (Barraclough and Londt, 1998). However, for the scope of the current thesis, only members of the subfamilies Chrysopsinae and Tabaninae as well as a few species from the tribe Philolichini will be of focus due to their ability to transmit disease causing agents to susceptible hosts. The taxonomic summary of southern African Tabanidae up to genus level is given below and the names of the different genera as well as the author who described the genus were obtained from Oldroyd (1954) and Usher (1972).

Kingdom : Animalia
Phylum : Arthropoda
Subphylum : Hexapoda
Class : Insecta
Order : Diptera
Suborder : Branchycera
Infraorder : Tabanomorpha
Family : Tabanidae
Subfamily : Chrysopsinae
Tribe : Bouvieromyiini
Genus : *Erodiorhynchus* Macquart, 1838
: *Mesomyia* Macquart, 1950
Tribe : Chrysopini
Genus : *Chrysops* Meigen, 1803
Tribe : Rhinomyzini
Genus : *Hinea* Adams, 1905
: *Sphecodemyia* Adams, 1937
: *Tabanocella* Bigot, 1856
: *Thriambeutes* Grünberg, 1906
Subfamily : Pangoniinae
Tribe : Mycteromyiini
Genus : *Mycteromyia* Philippi, 1865
Tribe : Pangoniini
Genus : *Stuckenbergina* Oldroyd, 1962 replaced to *Stuckenberginiella* Zwick and Mary-Sasal, 2010
Genus : *Apatolestes* Williston, 1885
: *Brennania* Radford, 1954
Tribe : Philolichini
Genus : *Philoliche* Wiedemann, 1828
Tribe : Scionini
Genus : *Goniops* Unknown

Subfamily : Scepsidinae
Tribe : Scepsidini
Genus : *Adersia* Austen, 1912
: *Braunsiomyia* Bequaert, 1921
Subfamily : Tabaninae
Tribe : Diachlorini
Genus : *Amanella* Oldroyd, 1956
: *Limata* Oldroyd, 1954
: *Neavella* Oldroyd, 1954
Tribe : Tabanini
Genus : *Ancala* Enderlein, 1922
: *Atylotus* Osten-Sacken, 1828
: *Euncala* Enderlein, 1922
: *Tabanus* Linnaeus, 1758
Tribe : Haematopotini
Genus : *Hippocentrum* Unknown
: *Haematopota* Meigen, 1803

1.2.2 Morphology of adult flies

Identification and classification of insects into different orders is based on the various anatomical structural features and understanding these variations is essential (Triplehorn and Johnson, 2005; de Villiers, 2008). The insect body is divided into a series of segments which are grouped into three distinct regions or tagmata namely; the head, thorax and abdomen (Triplehorn and Johnson, 2005; de Villiers, 2008). The head's primary function is for accumulation of food, sensory protection and coordination of bodily activities (de Villiers, 2008). The thorax is a locomotory tagma which bares legs and wings and contains flight muscles (de Villiers, 2008). Lastly, the abdomen houses most of the visceral organs which include organs for digestive, excretory, reproduction as well as blood circulation and respiration (Triplehorn and Johnson, 2005; de Villiers, 2008).

In the family Tabanidae, the head is generally large and may be as wide as the mesonotum (Barraclough and Londt, 1998). They have brightly coloured compound eyes which are holoptic. In male flies the eyes are touching each other medially and dichoptic. In female flies they are separated by a frontal stripe and the presence of ocelli on the frons with the exception of the tribe Tabaninae which have no ocelli (Baldachinno *et al*., 2014a). However, in some species the eyes are narrowly separated and in very few species the males have similar eyes to females. In most species males have upper facets on the eyes which are often dark centrally and surrounded by a pale area.

Antennae of tabanid flies are divided into three parts, namely the scape, pedicel and flagellum is normally the longest segment of the antenna. The flagellum has 3 - 8 flagellomeres (Barraclough and Londt, 1998; Baldacchino *et al*., 2014a). In Tabaninae the basal flagellomeres are enlarged and flat with a dorsal projections (often referred to as “tooth”) and a short pedicel whereas in Chrysopsinae, Pangoniinae and Haematoponiti the flagellomeres and pedicels are elongated and slender.

In most species the mouthparts of males differ from those of females. The proboscis of females are adapted for blood-feeding with well developed blade-like mandibles and maxillae made up of a pulp and laciniae. These structures together with the hypopharynx as well as the labrum form mouthparts suitable for blood-feeding.

The thorax bears the legs, which have paired apical spurs on the mid tibia and in some species on the hind tibia. Wings have a hyaline or are distinctly patterned with large basal medial (*bm*) and radial cells (*br*) and the distal cell (*d*) invariably present in most members of Tabanidae (Barraclough and Londt, 1998).

The abdomen in males is generally simple and uniform below tribal level of classification. It is composed of gonocoxite which is fused with the hypandrium and a single gonostylus (Barraclough and Londt, 1998). Generally, Tabanidae are characterized by having an elongated third antennal segment which bears a coarse annulated style and separated from other similar sized Diptera by the structure of the pulvilliform empodium, the wing venation and absence of setae on the body and legs as well as distinct abdominal colour patterns (Barraclough and Londt, 1998).

1.2.3 Reproduction

Members of the family Tabanidae commonly breed in or near aquatic environments and in moist places in the absence of water bodies (Chainey, 1993). Like other Diptera tabanid flies have a holometabolous life cycle which includes eggs, larvae, pupa and adult stage (de Villiers, 2008). An individual female may lay eggs ranging from one hundred to one thousand either on the water edge, overhanging vegetation or rocks. Embryogenesis requires two to 21 days depending on the species involved and climatic conditions (Foil and Hogsette, 1994; Service, 2008; Roberts and Janovy, 2009; Bladacchino *et al*., 2014a).

After 5 to14 days, depending on the temperature and species, the emerging larvae may either fall or crawl in water and then burrow in mud, during winter in some localities, where they remain active for a few weeks to three years (Service, 2008; Roberts and Janovy, 2009). During this period tabanid larvae are both predators and cannibals, feeding on other insect larvae including own kind, annelids and even amphibians (Chainey, 1993; Foil and Hogsette, 1994; Roberts and Janovy, 2009; Bladacchino *et al*., 2014a). In some species particularly *Chrysops*, the larvae are scavengers and feed mainly on detritus as well as dead or decaying animal or plant matter (Service, 2008). Pupation occurs underground and the pupa is positioned vertically. Before pupation, the larvae of some African tabanid flies make hollow mud cylinders underground. By doing this, the pupae is protected from being exposed when cracks form in the mud and also enables the pupa to move deeper in the ground away from the surface when temperatures are too high (Chainey, 1993). Normally, it takes one to three weeks for a larva to complete metamorphosis (Roberts and Janovy, 2009; Bladacchino *et al*., 2014a).

Adults emerge after pupation at a sex ratio of 1:1 though males emerge earlier than females (Bladacchino *et al*., 2014a). A complete life cycle of the reproduction of these flies is demonstrated in Figure 1. Both sexes feed on nectar and other plant fluids to obtain energy for body maintenance, flight and mating (Chainey, 1993). In all species of Tabanidae mating occurs in flight mainly in the morning. Most females will seek a blood meal after mating for oviposition which will occur three to eleven days after blood consumption (Foil and Hogsette, 1994; Bladacchino *et al*., 2014a). Females of the subfamily Tabaninae particularly feed on large animals such as cattle, horses or deer, whereas *Chrysops* spp. and *Haematopota* spp. have a wider variety of hosts including humans (Bladacchino *et al.*, 2014a). A complete life cycle of a tabanid fly is shown in Figure 1 below.

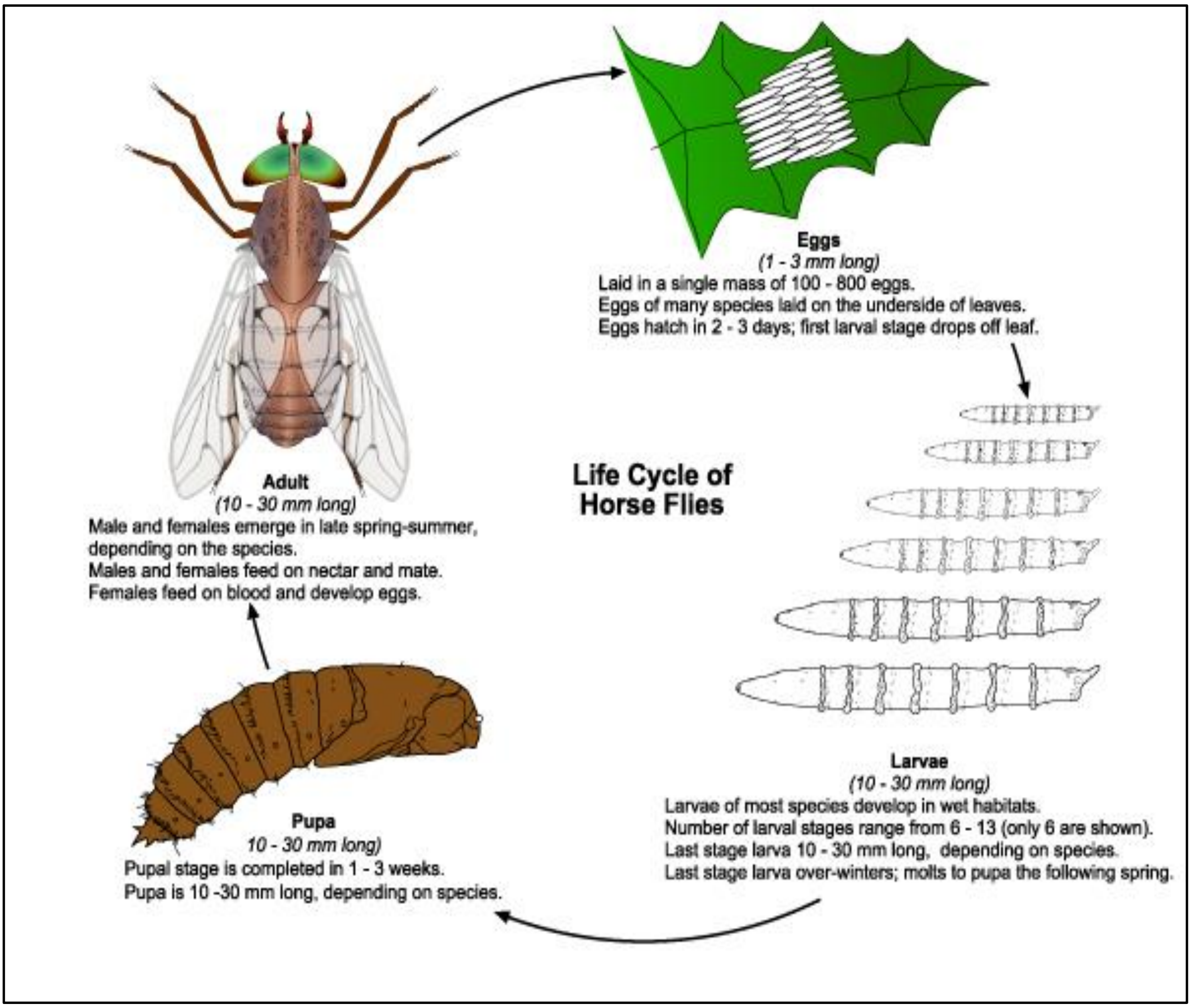

Figure 1: A complete life cycle of a tabanid fly (Muzari, 2010)

1.2.4 Behaviour

Feeding and behavioural patterns of arthropods aid to determine their potential in mechanical transmission of pathogens (Foil and Gorham, 2000). For female tabanid flies, feeding occurs in daytime, mainly during the sunniest hours of the day although a few species are crepuscular and some feed at night (Service, 2012). These female flies use odours, shape, movement, brightness, colour of the host and by the linear polarization of the host-reflected light to actively search for their feeding host (Service, 2012; Blahó *et al*., 2013). Tabanids are strong and fast fliers, characterized by their painful biting behaviour and annoyance to their hosts (Barros and Foil, 2007). As a result they induce their host defensive mechanism due to their bite intensity hence they never complete a blood-meal from a single fleeding session (Baldacchino *et al*., 2014a). However, most species exhibit behaviour of pursuing a single host until they are engorged a phenomenon known as feeding persistence as they take several small blood-meals from a single host. In contrast, some species are easily dislodged by their host defensive mechanism and thus may transfer between hosts more often however, depending on the abundance and availability of susceptible hosts (Baldacchino *et al*., 2014a).

Tabanids are telmophagous (pool-feeders) and their interrupted feeding behaviour is the most important factor in determining their role as effective mechanical transmitters of pathogens (Foil and Gorham, 2000). The quality of blood-meal residue that remains on the mouthparts following an interrupted feed may also have an influence on the amount of infectious material transmitted between hosts (Foil and Gorham, 2000; Baldacchino *et al*., 2014a). Smaller sized tabanid flies carry less residual blood and are therefore less effective mechanical vectors as compared to larger flies with larger mouthparts which often feed continuously until engorged (Oldroyd, 1954; Baldacchino *et al*., 2014a). It has also been shown that unfed tabanid flies cover greater distances in search for a blood-meal as compared to fully fed flies and this may also contribute to mechanical transmission by the flies (Barros and Foil, 2007). As a result, the behaviour of flies infected with pathogens is often altered by the parasites as compared to uninfected flies. Infected flies tend to change their preferred habitat, humidity and temperature choices (Moore, 1993). Additionally, infected flies exhibit a change in response to visual stimuli such as colour and light preference, as a result infected flies tend to forage for longer periods as compared to uninfected flies (Moore, 1993).

Despite these behavioural observations it is noted that the occurrence of adult tabanid flies is seasonal in both temperate and tropical areas. In temperate countries adults usually die off at the end of the summer and a new population emerges in the following spring or summer (Service, 2012).

1.3 Economic, medical and veterinary importance of Tabanidae

1.3.1 Tabanids as plant pollinators

In order to obtain energy and sustain their daily activities, both males and females in the family Tabanidae, require nectar and other plant fluids (Service, 2012; Baldacchino *et al*., 2014a). Most species of Tabanidae have relatively short, wider and robust piercing-proboscis which is suitable for blood-sucking (Krenn and Aspök, 2012). However, members of the tribe Philolichini have evolved specialized mouthparts which have reduced mandibles for nectar feeding and some species of the genus *Philoliche* are capable of feeding on both nectar and blood (Morita, 2008). Several members of the genus *Philoliche* have been shown to play a role in pollinator-mediated speciation of flowering plants (Morita, 2008). In the Cape floristic region it has been shown that *Philoliche* species are among the primary pollinators of about 25% of species of *Pelargonium*, about 10% of the regional Iridaceae and Orchidaceae (Combs and Pauw, 2009). However, in Orchidaceae, species of the *Disa draconis* complex are non-rewarding and rely on floral mimicry to attract pollinators. As a result the pollinator flies are never rewarded with nectar but aid in pollination of the plant (Johnson and Morita, 2006; Combs and Pauw, 2009).

1.3.2 Tabanids as vectors of pathogens

On a global scale, tabanid flies are among major livestock pests despite some species of *Philoliche* being plant pollinators. Due to their persistent painful biting behaviour and global distribution, tabanids have been described to be mechanical vectors of more than 35 pathogenic agents of livestock (Foil and Hogsette, 1994).

Tabanids are vectors of pathogens causing diseases such as anaplasmosis, anthrax, animal trypanosomiasis, bovine viral leukosis, equine infectious anaemia virus and filarial worms, tularaemia, hog cholera as well as vesicular stomatitis (Zumpt, 1949; Foil and Hogsette, 1994; Esterhuizen, 2006; Service, 2012; Baldacchino *et al*., 2014a). These pathogens may either be biologically or mechanically transmitted to susceptible hosts during interrupted feeding by horse flies (Baldacchino *et al.*, 2014a). It has been reported that losses in beef cattle production due to tabanid attacks amounted to more than US$30 million back in 1965 in the United States of America (Foil and Hogsette, 1994).

Tabanids are also responsible for the spread of anthrax infections in both humans and livestock, with horses and cattle being the most affected by this infection (Zumpt, 1949). In certain areas in Russia tabanids were responsible for 80% of cases of anthrax infections in horses and cattle in the summer months where transmission occurs through contaminated or infected faeces with the anthrax causing bacteria (Zumpt, 1949). Baldacchino *et al*. (2014a), made a summary of all the other major pathogens mechanically transmitted by tabanids which include Bovine leucosis virus, Equine infectious anaemia virus or swamp fever, *Brucella* spp., *Listeria monocytogenes* and *Erysipelothrinx rhusiopathiae*. Biologically they transmit *Haemoproteus metchnikovi*, filarial nematodes (*Loa loa*), *Elaephora schneideri* as well as *Dirophora repens* and the distribution of these pathogens is restricted to Central Africa, North America, Europe and Asia respectively (Baldacchino *et al*., 2014a).

1.4 Justification of the study

Tabanids are irritant fly pests that affect people and livestock by their noisy flying and persistent painful bite (Baldacchino *et al*., 2014a). Only female tabanid flies are haematophagous and are pool feeders that are responsible for transmitting various pathogens to both humans and livestock. Members from the subfamilies Chrysopsinae and Tabaninae are responsible for most biologically or mechanically transmitted pathogens in heavily infested areas (Service, 2012).

Due to the lack of detailed studies conducted in southern Africa. The actual threat that tabanid flies pose along with the parasites and symbiotic fauna they are habouring and are likely transmit to both humans and livestock has not been fully explored in most southern African countries. As a result the current study sought to determine which protozoan parasites southern African tabanid flies harbour as well as their symbiotic bacteria which may be identified as candidates to control the fly populations.

1.4 2 Diseases of interest in the current study

1.4.2.1 Babesiosis

Bovine babesiosis is a tick-borne disease found in tropical and subtropical regions of the world and caused by protozoan parasites of the genus *Babesia*, order Piroplasmida, phylum Apicomplexa (OIE, 2010; Iseki *et al*., 2007; Mtshali *et al*., 2014). The disease is caused by *Babesia bovis* and *B. bigemina* in susceptible mammalian hosts mainly cattle and sheep in Africa, Asia, Australia, and Central and South America whereas in some parts of Europe *B. divergens* is the economically most important species (OIE, 2010). Bovine babesiosis is biologically transmitted by ticks. *Babesia bovis* and *B. bigemina* are transmitted by *Rhipicephalus microplus*, *R. annulatus*, *R. decoloratus*, *R. geigyi* and *R. evertsi evertsi* ticks to susceptible mammalian hosts. On the other hand *B. divergens* is transmitted by *Ixodes ricinus* (Hunfeld *et al*., 2008; OIE, 2010). The lifecycle of this parasite involves two hosts which primarily comprises of a rodent (for example *Peromyscus leucopus*) and a tick from the genus *Ixodes* (OIE, 2010). Sporozoites are introduced to the rodent host where they enter erythrocytes and reproduce by budding. Additionally, in the blood, some parasites differentiate into male and female gametes to be subsequently ingested by the definitive host tick. In the tick host the gametes unite and undergo a sporogonic cycle resulting in infective sporozoites (OIE, 2010). Humans and domestic animals get infected during a blood meal from an infected tick. Humans usually are dead-end hosts. Human-to-human transmission is also is reported to occur via contaminated blood transfusions (OIE, 2010). Molecular and serological assays have been conducted to detect the disease from the host animals as well as in the tick vectors in affected nations around the world (Ryan *et al*., 2001; Hunfeld *et al*., 2008; Ica *et al*., 2007; Iseki *et al*., 2007; Mtshali *et al*., 2014; Sivakumar *et al*., 2014a). There is however, no information on any association of *Babesia* parasites and flies, tabanids in particular. As a result the current study was aimed at determining if there is any relationship between the two organisms.

1.4.2.2 Besnoitiosis

Bovine besnoitiosis is a protozoan disease caused by the cyst-forming coccidia of the genus *Besnoitia,* family Sarcocystidae and phylum Apicomplexa (EFSA, 2010; Baldacchino *et al.,* 2013; Hornok *et al*., 2014). The disease has a cosmopolitan distribution and *Besnoitia besnoiti* is most pathogenic to both domestic and wild ruminants. It is mechanically transmitted by blood-sucking dipterans such as tabanid and *Stomoxys* flies. However, the definitive host of this disease is still unknown to date (Bigalke and Prozesky, 2004; Baldacchino *et al.,* 2013; Baldacchino *et al.,* 2014a; Hornok *et al.,* 2014). In Africa the disease has been reported to cause major economic losses in Angola, Cameroon, Botswana, Kenya, Namibia, South Africa, Sudan, Swaziland, Zaire and Zimbabwe. In South Africa cases of the disease have been documented from the Free State, KwaZulu-Natal, Limpopo, Mpumalanga, North-West and Western Cape Province (Bigalke and Prozesky, 2004). Due to the prevalence of this disease in southern Africa the current study aimed to determine which tabanid species are capable of transmitting this parasite in this region.

1.4.2.3 Theileriosis

Theileriosis is a tick-borne disease found in tropical and subtropical regions of the world and is caused by protozoan parasites of the genus *Theileria*, order Piroplasmida, phylum Apicomplexa (Ica *et al*., 2007; Mans *et al*., 2015). The disease affects both domestic and wild ruminants. It has been reported that, different species of *Theileria* causes different diseases in different susceptible hosts (Yusufmia *et al*., 2010; Sivakumar *et al*., 2014b; Mans *et al*., 2015). *Theileria parva* causes a fatal disease known as East Coast Fever (ECF) to infected cattle, in eastern Africa. The disease in South Africa and in Zimbabwe is known as Zimbabwe theileriosis or January fever. The *T. annulata* causes Tropical theileriosis in cattle (Yusufmia *et al*., 2010; Mans *et al*. 2015). Goats and sheep are infected by *T. lestoquardi* which causes a disease known as malignant theileriosis (Mans *et al*., 2015). Additionally, *Theileria* species such as *T. separata*, *T. uilenbergi*, *T. luwenshuni*, *T. capreoli*, and *T. ovis* have also been reported to infect small ruminants (Sivakumar *et al*., 2014b). These parasites are known to be biologically transmitted by ixodid ticks of the genera *Amblyomma*, *Haemaphysalis*, *Hyalomma* and *Rhipicephalus* (Mans *et al*., 2015). As far as the life cycle is concerned, *Theileria* sporozoites are transmitted to susceptible host animals via the saliva of the feeding tick (OIE, 2008). However, an infected tick must be attached to a susceptible host for 48 to 72 hours before it can become infective. If environmental temperatures are high, the infective sporozoites can develop within the tick while it is unattached on the ground and may enter the host within hours of attachment. Inside the infected host, *Theileria* sporozoites undertake a multipart lifecycle involving the replication of schizonts in leukocytes and piroplasms in erythrocytes (OIE, 2008). In South Africa, the Kruger National Park and Hluhluwe-Imfolozi game reserves have been considered as endemic areas for buffalo derived *T. parva* parasites (Yusufmia *et al.*, 2010). Pienaar *et al.* (2014), reported on the presence of *Theileria* infections in southern African countries, which are well known to be transmitted by ticks. There is no known association in terms of transmission of *Theileria* parasites by tabanid flies in these theileriosis endemic areas. Hence, the current study seeks to determine whether tabanid flies are capable of harboring *Theileria* parasites.

1.4.2.4 Trypanosomiasis

African animal trypanosomiasis (AAT) or nagana is a fatal disease caused by protozoan parasites of the genus *Trypanosoma* which are mainly cyclically transmitted to wild and domestic animals by tsetse flies of the genus *Glossina* (Roberts and Janovy, 2009; OIE, 2013; Votýpka *et al.*, 2015). Tsetse flies are restricted to sub-Saharan Africa and limited to the north eastern parts of KwaZulu-Natal Province in South Africa (Leak, 1999; Service, 2008). Nagana in Africa is caused by *Trypanosoma congolense*, *T. vivax*, *T. brucei brucei* whereas *T. evansi* and *T. equiperdum* causes surra and dourine in equines respectively (Leak, 1999; OIE, 2013). Unlike the other trypanosome parasites, *T. evansi*, *T. equiperdum*, *T. theileri* and *T. vivax* are not restricted to the African continent only and have wider distribution extending to Asia and some parts of Europe as well as South America (Desquesnes *et al.*, 2013). *Trypanosoma equiperdum* is venereally transmitted and therefore does not require an arthropod vector like the other trypanosome parasites (Taylor and Authié, 2004). On the other hand *T. evansi* and the less pathogenic *T. theileri* require arthropod vectors to be transmitted to susceptible hosts and due to their wider distribution outside the African continent. Studies by Desquesnes and Dia (2003a; 2003b; 2004) have experimentally demonstrated that mechanical transmission of *T. vivax* and *T. congolense* is possible by the tabanid fly species namely, *Atylotus agrestis* and *A. fuscipes*. *Trypanosoma evansi* on the other hand is known to be mechanically transmitted by biting flies including *Stomoxys* and tabanid flies (Sumba *et al.*, 1998; Gutierrez *et al.*, 2010; Desquesnes *et al.*, 2013). The current study seeks to detect *Trypanosoma* species in tabanid flies collected from selected countries in southern Africa.

1.4.2.5 Symbiotic associations in haematophagous insects

The relationship between prokaryotes and insects is well-known. Symbiotic relationship is defined as the interaction between the microbe and the insect host in the acquisition and maintenance of metabolic pathways (Dillon and Dillon, 2004). The relationship may either be mutualistic where the bacteria play a crucial role in the development or fitness of the host insect or the association may be harmful or lethal in the case of parasites and pathogens (Kikuchi, 2009). In most circumstances the symbiotic bacteria reside within the body of the host and lead to spatially intimate interactions between partners (Kikuchi, 2009). Such interactions are observed in insects that thrive on specialized restricted diets such as plant sap, vertebrate blood, wood or decaying material (Kikuchi, 2009; Sabree and Moran, 2014). These bacterial symbionts range from mutualistic (both host and bacteria mutually benefit from the association), commensalistic (only the bacteria benefits from the association but the host is neither helped nor harmed) and parasitic (the bacteria benefits from the association and the host is negatively affected) (Dillon and Dillon, 2004). Mutualistic associations may either be obligate (both the bacteria and host insect may not survive without the other) or facultative (not essential for survival or fecundity of the host) (Kikuchi, 2009).

Bacterial communities of haematophagous insects such as mosquitos, tsetse flies and triatomid bugs have been extensively explored due to the impact that these insects have in the transmission of haemoparasites. However, it has been found that the genome size of most mutualistic bacteria has been reduced to less than 7 Mb due to long-term association with these insects (Dillon and Dillon, 2004; Kikuchi, 2009). Some of these symbionts are maternally inherited by transovarial transmission whereby the symbionts directly infect the embryos within the maternal body (Kikuchi, 2009; Engel and Moran, 2013; Sabree and Moran, 2014). Mutualistic bacteria are known to recide in haematophagous insects due to their lack of balanced diet and the need for metabolic integration (Engel and Moran, 2013). Furthermore, other than playing a vital role in supplementing the insects with vitamins, these bacteria are also known to have a role in the host fitness of these haematophagous insects, either enabling them to be more resistant to parasites or prolonging their survival (Kikuchi, 2009; Engel and Moran, 2013; Sabree and Moran, 2014). Nonetheless, tabanid flies have received little attention in regard to their association with microbes despite the fact that they are responsible for transmission of a wide variety of pathogens to both animals and humans. As a result the current study investigated the gut bacteria harboured by tabanid flies and because most of these microbes are unculturable, in the current study next generation technology was used to address this challenge.

Protozoan diseases such as animal trypanosomiasis, babesiosis, besnoitiosis and theileriosis are caused by parasites transmitted by arthropod vectors, in particular, biting flies and ticks. Most studies in South Africa and Zambia have focused on tsetse fly and ticks which are vectors of trypanosomes and piroplasmid parasites of livestock respectively. Most of the control strategies are also formulated at controling these vectors. Baldacchino *et al*. (2014a) reported that tabanids may also act as mechanical vectors of various protozoan parasites including livestock trypanosomes, although there is also a suspicion of biological transmission by these flies (Böse and Heister, 1993). Tabanid flies are mechanical vectors of a wide variety of pathogens to livestock and pose serious threat to domestic animals in affected areas and therefore have a negative impact on the agricultural sector and the economy of the affected nations. In Lesotho however, there are no documented records of studies on diseases caused by protozoan parasites or vectors including ticks and tabanid species found in the area. The symbiotic or parasitic association between tabanid flies and their gut microbiota in southern Africa is unknown and there is insufficient literature of this association globally.

The current study focused on the characterization of tabanid flies (Tabanidae) in selected study sites in Lesotho, South Africa and Zambia. Here, morphological identification and molecular techniques were used to characterize tabanid flies found in the three countries to species level. Furthermore, this study detected protozoan parasites of agricultural and economic importance infecting tabanid flies. Lastly, metagenomic diagnosis was employed to determine the microbiota of the sampled tabanid flies. Data obtained from this study highlighted the need for scientists, veterinary and livestock farming sector to also focus on possibilities of including the neglected tabanid flies in control strategies formulated to reduce infections of haemoparasites and bacteria to livestock.

1.7 Aims and objectives

1.7.1. Aims

The aim of this study was to identify and determine the diversity of tabanid flies found in the sampled areas in Lesotho, South Africa and Zambia, as well as to determine the protozoan parasites and gut bacterial communities harboured by these flies.

1.7.2 Objectives

- To identify tabanid flies from KwaZulu-Natal Province in South Africa, Maseru in Lesotho as well as from Mfuwe and Itezhi-tezhi in Zambia by morphological characteristics and molecular techniques.

- To detect by means of PCR, protozoan parasites of medical and veterinary importance harboured by tabanid flies from the three countries.

- To determine gut bacterial populations harboured by different tabanid flies using *16S rRNA* metabarcoding analysis.

CHAPTER 2

MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF TABANID FLIES FROM LESOTHO, SOUTH AFRICA AND ZAMBIA

2.1 Introduction

Class Insecta is divided into two subclasses namely, Apterygota and Pterygota. Apterygota includes all primitively wingless insects that are characterized by having an ametabolous development, meaning the immature stages share the same habitat and behave in much the same manner as adults (de Villiers, 2008). The subclass Pterygota, comprises of all other insect orders and is further divided into two infra classes Paleoptera and Neoptera (de Villiers, 2008). The order Diptera falls under Neoptera which are characterized from other insects by the presence of two membranous wings (Barraclough and Londont, 2008). The dipteran order is further divided into three suborders namely, the Nematocera, Brachycera as well as Cyclorrhapha and this division is mainly based on imaginal characters such as the shape of the antenna and the developmental stage with particular reference to the pupal stage (Hackman and Väisänen, 1982; Barraclough and Londont, 2008).

Phylogeny of the order Diptera was previously based on morphological characters focusing on shared derived features, a process known as synapomorphies or homologies (Yeates and Wiegmann, 1999). Based on synapomorphies which include the transformation of the hind wings to halters and the development of mouthpart features for sponging liquids, dipteran flies are believed to have evolved during the middle Triassic period (230 million years ago) and they are monophyletic (Yeates and Wiegmann, 1999; Yeates *et al*., 2007). The suborder Brachycera is phylogenetically divided into four monophyletic infraorders namely: Xylophagomorpha, Tabanomorpha, Stratiomyomorpha and Muscomorpha based on the posterior portions of larval head capsule which is elongated posteriorly into prothorax as well as the reduction of antennal flagellomeres of eight or less in adult flies (Yeates and Wiegmann, 1999; Wiegmann *et al*., 2003).

The infraorder Tabanomorpha, is composed of members from the family Tabanidae, Pelecorhynchidae, Athericidae, Rhagionidae and Vermileonidae (Wiegmann *et al.*, 2000). Most adult flies from this infraorder feed on nectar and pollen, however majority of females from Tabanidae and a few species from the family Rhagionidae are haematophagous for oviposition and as a result are vectors of pathogens that are of medical and veterinary importance to both humans and domestic animals (Foil and Gorham, 2000; Wiegmann *et al*., 2000). Monophyly in Tabanomorpha is based on three morphological synapomorphies which include the presence of a brush above the larval antennae (mandibular brush), the larval head is retractile and in adult flies the clypeus is convex and swollen, however these features do not support some members of the family Vermileonidae (Wiegmann *et al.*, 2000).

The early evolution of Tabanidae, particularly the adaptive specialization of their mouthparts is potentially linked to the diversification of angiosperm flowers during the late Triassic period (Morita *et al.*, 2016). However, the taxonomy of Tabanidae below tribal level has been challenging in the past decades due to the generalized morphology of tabanids whereby, the scarcity of male specimens and genital characters do not show much variation at genus as well as species level (Lessard *et al*., 2013; Morita *et al*., 2016). As a result the phylogeny of tabanids was poorly understood until molecular data were introduced. Recent studies using both morphology and molecular evidence targeting the nuclear *28S rRNA* gene, the cytochrome oxidase subunit one (*CO1*) and the first fragment of the nuclear protein-coding gene carbamoyl-phosphate synthetase-aspartate transcarbamoylase-dihydroorotase (*CAD1*) have supported monophyly in Tabanidae as well as within each subfamily (Wiegmann *et al*., 2000; 2003; Lessard *et al*., 2013; Morita *et al*., 2016).

The current study sought to document information on occurrence of tabanid flies in selected countries of southern Africa by use of morphological characters and molecular analysis. The study further seeks to determine the phylogenetic position of southern African tabanid flies in comparison to other related species around the world. Due to recent advances in diagnosis, morphological and molecular techniques were used to address this challenge in samples collected from three countries, namely, Lesotho, South Africa and Zambia. The choice of these countries was based solely on lack of information on the phylogeny as well as detailed descriptions of tabanid flies. To address the proposed challenge the following hypothesis was formulated: There will be variation in the abundance of tabanid fly populations from the sampled localities due to differences in climate and vegetation in the three countries. To achieve this hypothesis the following objectives were formulated:

- To identify the captured tabanid flies from Lesotho, South Africa and Zambia to species level using morphological and molecular techniques.

- To determine and compare the abundance of the different fly species captured in Lesotho, South Africa and Zambia

- To determine the phylogenetic position of tabanid flies from Lesotho, South Africa and Zambia.

2.2 Materials and methods

2.2.1 Study area

Samples were collected from three countries in southern Africa namely Lesotho, South Africa and Zambia (Figure 2). The overall landscape size, seasonal climatic conditions as well as vegetation in the three sampled countries varies significantly and as a result the abundance, distribution and species diversity of tabanid flies is considerably different. A brief description of the dominant vegetation and climatic conditions of the sampled areas is given below.

2.2.1.1 The Kingdom of Lesotho

Samples were collected in Maseru district (29°19'21'' S; 027°28'9'' E) (Figure 3). Lesotho occupies an area of 30 355 square kilometres (km^2) and its completely surrounded by the Republic of South Africa (Ministry of Agriculture, 1995). The country is divided into four agro-ecological zones, namely the mountains (59%), foot-hills (15%), lowlands (17%) and Orange-River-Valley (9%) with an average altitude ranging from 1 500 m to 3 000 m (Ministry of Agriculture, 1995). The agro-ecological zone of the current study area lies within the foot-hills which occupies 15% of the land cover. According to Mucina and Rutherford (2006), the Maseru district falls under the grassland biome known as the Basotho Montane Shrubland which spreads from the Free State Province, Lesotho and marginally into KwaZulu-Natal Province. The climate around these areas is composed of hot (20°C to 32°C) and wet summer months with dry and cold winters (-6.3°C to 5.1°C) that are accompanied by frequent frost. The main vegetation of these areas includes tall shrubs such as *Buddleja salviifolia*, *Euclea crispa ovata*, *Olea europa africana*, *Diospyros whytena* and *Rhus dentana;* graminoids such as *Aristida congesta*, *Eragrostis chloromela*, *E. capensis*, *E. plana*, *E. racemosa*, *Hyparrhenia hirta*, *Microchloa caffra*, *Themeda triandra* and *Harpochloa falx* among others (Mucina and Rutherford, 2006). The mean annual precipitation (MAP) of these areas is 720 mm while patches close to the Maloti Mountain range receive 1 400 mm MAP (Mucina and Rutherford, 2006).

2.2.1.2 The Republic of South Africa (RSA)

The north-eastern parts of KwaZulu-Natal Province was of interest due to the presence of animal trypanosomiasis in the area (Esterhuizen *et al*., 2005; Van den Bossche *et al*., 2006; Esterhuizen, 2006; Mamabolo *et al*., 2009; Gillingwater *et al*., 2010; Motloang *et* *al.,* 2014). Three game reserves in north-eastern KwaZulu-Natal (Figure 4), namely, Charters Creek (28°13'37"S; 032°24'1"E), Hluhluwe-Imfolozi (28°9'50"S; 032°12'15"E) and Phinda Private Game Reserve (27°46'39"S; 032°20'57"E) all situated in the Umkhanyakude district were sampled.

The first two game reserves namely Hluhluwe-Imfolozi and Phinda Private Game Reserve fall under the Zululand lowveld vegetation type which extends from south of Mkhuze, Hluhluwe, Ulundi and small patches in Mpumalanga Province as well as in Swaziland (Mucina and Rutherford, 2006). The climatic conditions around these areas are composed of summer rainfall with light rain in winter. The mean annual precipitation ranges from 500 mm to 900 mm and the mean monthly maximum and minimum are 38.5°C and 7.8°C with no frost (Mucina and Rutherford, 2006). The main vegetation in these areas include tall trees such as *Acacia burkei*, *A. nigrescence*, *Sclerocarya birrea*; small trees such as *Acacia tortilis heteracantha*, *A. gerrardi*, *A. natalitia*, *A. nolitica*, *A. senegal*, *Spirostachys africana*. Tall shrubs like *Dichrostachys cinerea*, *Euclea divinorum*, *E. crispa crispa, E. schimperi*. Succulent trees such as *Aloe marlothi marlothi*, *Euphorbia grandidens* and *E. ingens* among others. Graminoids such as *Dactyloctenium australe*, *Eragrostis capensis*, *E. curvular*, *E. racemosa*, *Heteropogon contortus*, *Sporobolus pyramidalis* and *Themeda triandra* are also common (Mucina and Rutherford, 2006).

The third game reserve Charters Creek game reserve falls under the Zululand coastal thornveld which extends from Mtubatuba to Empangeni and has summer and winter rainfall with the highest MAP in the Savanna vegetation of 800 mm to 1 050 mm and frost is frequent in winter (Mucina and Rutherford, 2006). The main vegetation in the area is similar to that of the Zululand lowveld with main difference being that no tall trees are present and the presence of geophytic herbs such as *Hypoxis rigidula* and *Pelargonium luridum* (Mucina and Rutherford, 2006).

2.2.1.3 Zambia

Tabanid fly samples were collected in the Eastern and Central Provinces of Zambia. In the Eastern Province, tabanid fly samples were collected from Mambwe district in the South Luangwa National Park (13°10'0.2''S, 31°29'59.8''E) whereas in the Central Province samples were collected from the Itezhi-tezhi district in the Kafue National Park

(14°28’52.9’’S, 26°13’17.7’’E) (Figure 5). The climatic conditions in these areas are basically tropical, but occasionally unpleasantly hot, except in the valleys (Zambezi and Luangwa) which are humid and excessively hot with temperatures exceeding 36°C. Basically, there are three seasons namely: Cool dry season (April to July), hot dry season (August to November) and warm wet season (December to March) (Mwale *et al.*, 2005; Phiri, 2005; Aregheore, 2009). During the cool dry season temperatures range from 10°C to 27°C and during the hot wet season temperatures range from 27°C to 38°C (Mwale *et al*., 1995). The MAP during the hot wet season is ~508 mm in the southern parts, ~1 200 mm in the eastern parts, ~1 270 mm in the northern parts and ~1 400 mm in the western parts of the country (Aregheore, 2009). There are four main vegetation types in Zambia namely: the closed forests, woodlands or open forests, *Termitaria* and grasslands. Both study areas are based in the woodlands with sub vegetation types of Miombo and Mopane woodland (Sekeli and Phiri, 2002). The Miombo woodlands are the most economically important vegetation type which covers about 352 million hectares of land in the country and the dominant genera include *Brachystegia*, *Isoberlinia* and *Julbernadia* as well as species such as *Marquesia macroura*, *Pericopisis angolensis*, *Erythophleum africanum* and *Parianri curatelifolia* whereas the Mopane woodlands are dominated by *Colophospermum mopane* (Sekeli and Phiri, 2002).

2.2.2 Collection of samples

Two H-traps (Figure 6a) were used to sample tabanid flies and they were placed in areas around cattle kraals and horse stables in Lesotho. The traps were placed for two weeks per site and monitored daily during the 3 months sampling period.

A total of 18 (6 traps per game reserves) H-traps were used to sample tabanid flies from the selected three game reserves in South Africa. The traps were placed for one week at 100 m apart in all three game reserves and monitored daily to collect the captured flies.

A total of 11 Epsilon traps (Figure 6b) were used per district and placed 200 m apart to cover a larger range in the sampled areas in Zambia. All traps were placed at sampling sites for one week and monitored daily for tabanid flies. Captured tabanid flies were placed in 1.5 ml Eppendorf tubes for further analysis in the laboratory.

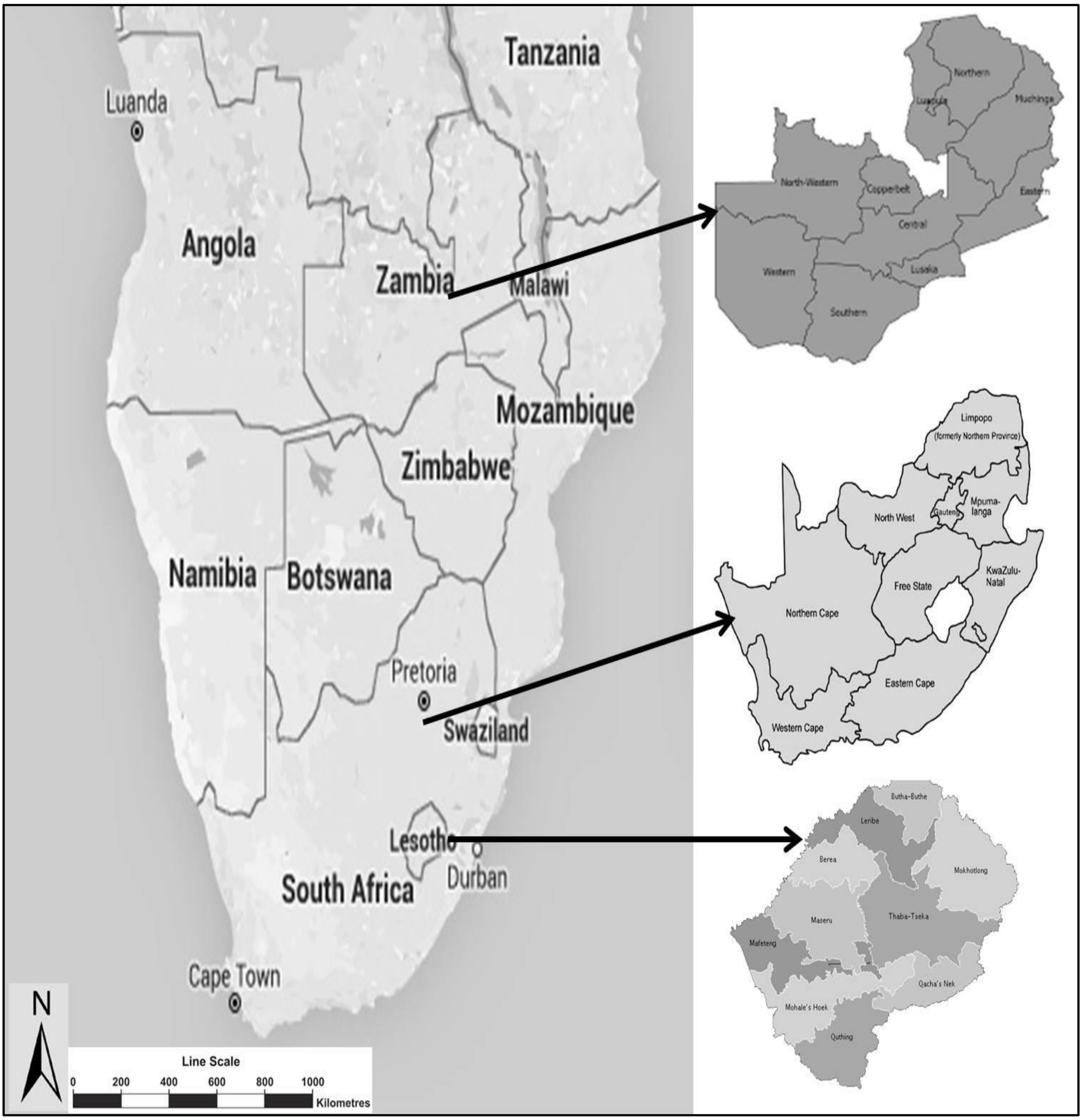

Figure 2: Map of southern Africa showing the three sampled countries namely: Lesotho, South Africa and Zambia.

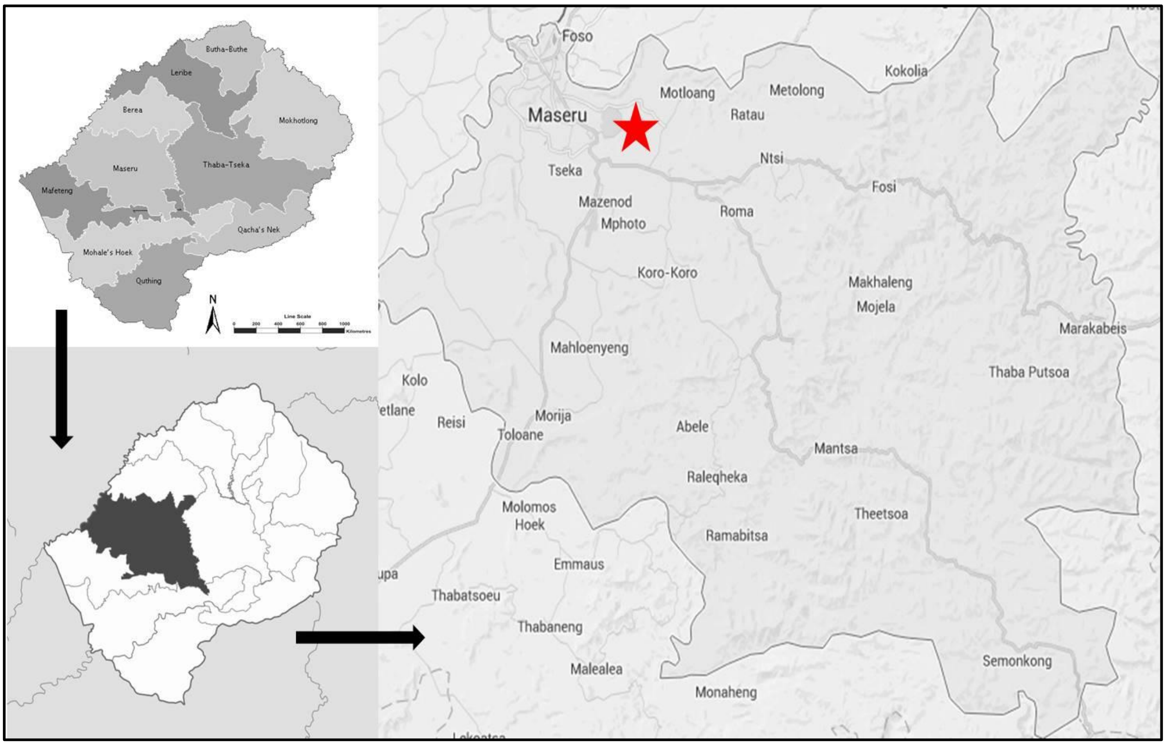

Figure 3: Map of the Lesotho showing the Maseru district. The the red star show the locality where the insect traps were placed.

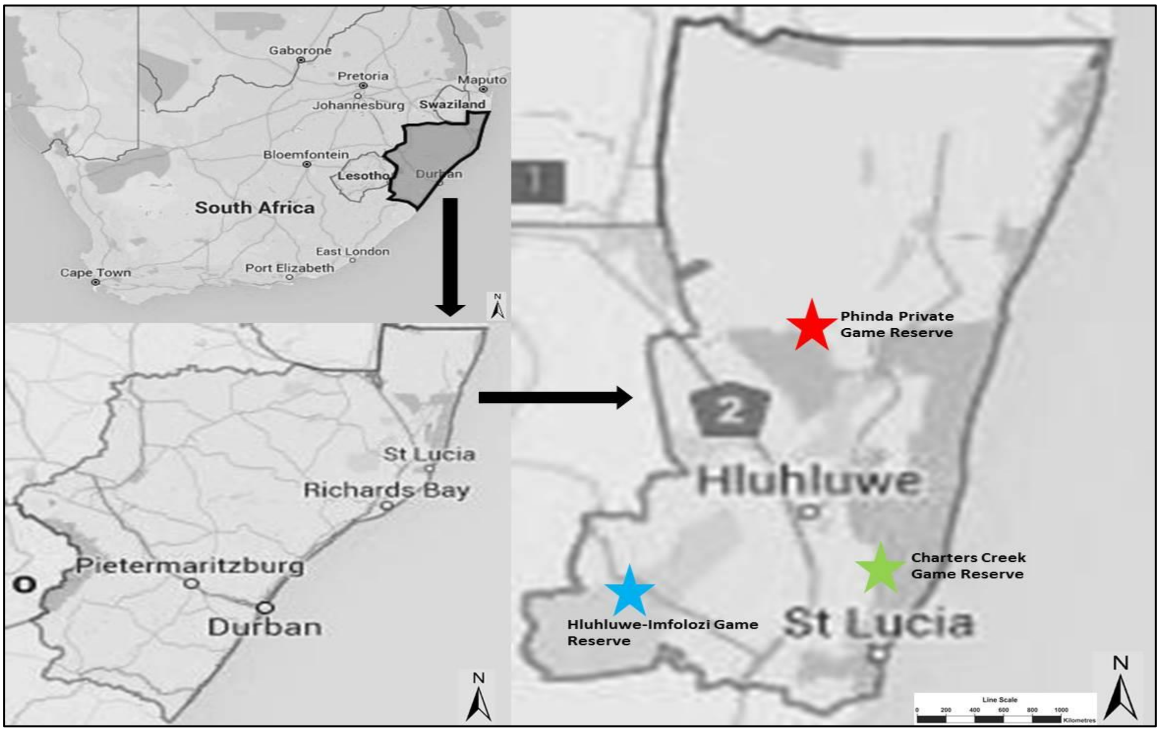

Figure 4: Map of South Africa showing KwaZulu-Natal Province and the three sampled game reserves. The blue star represents Hluhluwe-Imfolozi Game Reserve, red star represents Phinda Private Game Reserve and green star represents Charters Creek Game Reserve.

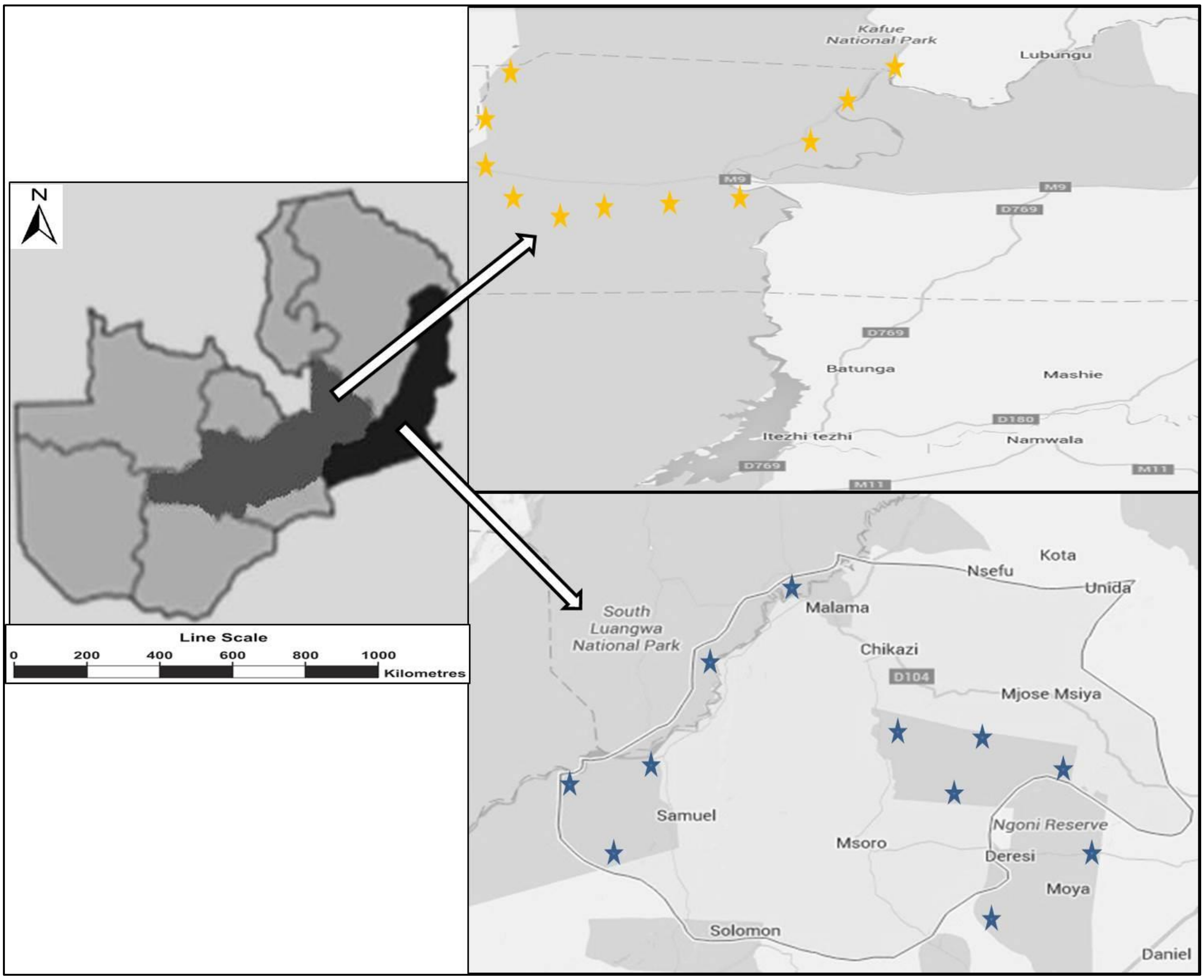

Figure 5: Map of Zambia highlighting the Eastern (Mambwe district) and Central provinces (Itezhi tezhi district). The stars show the exact locations of where the traps were placed.

Figure 6a: H-trap used to capture tabanid flies in Lesotho and in South Africa.

Figure 6b: Epsilon trap used to capture tabanid flies in Central and Eastern Provinces of Zambia.

2.2.3 Identification and characterization of tabanid flies

The Nikon AZ 100 M multi zoom microscope (Nikon Inc., Tokyo, Japan) was used to capture sequential photographs of different features of the flies. The flies were then identified to species level by discerning unique characters that differentiated between species with reference to literatures of Oldroyd (1954), Yagi (1964), Veer (1999) and Morita (2008). Usher (1972) was used to confirm the distribution and occurrence of the tabanid flies in South Africa. For tabanid flies collected from Lesotho and Zambia only the identification keys were used as there is no documented literature about the distribution of the tabanid flies in the two countries.

2.2.4 DNA extraction from tabanid flies

The wings and legs of all flies were removed to prevent excess exoskeletons that might affect the enzymatic activity of the subsequent reaction steps (Mekata *et al*., 2008). Thereafter, the whole fly was homogenised as described by Diallo *et al*. (1997) and genomic DNA was extracted using the Zymo insect DNA extraction kit following the manufacturer's protocol (Zymo Research Corporation, California, USA) Briefly, the fly specimen were placed in the ZR BashingBead^{TM} Lysis Tube and 750 µl lysis solution was added. The lysis tube was vortexed for 10 minutes at maximum speed and then centrifuged at 7 000 revolutions per minute (rpm) for 1 minute. About 400 µl of the supernatant was transferred into a Zymo-Spin^{TM} IV Spin Filter with orange cap in a collection tube and centrifuged again at 7 000 rpm for 1 minute. A total of 1200 µl of genomic lysis buffer was added to the filtrate in the collection tube and mixed. About 800 µl of the mixture was transferred into a Zymo-Spin^{TM} IIC Column with a new collection tube and centrifuged for 1 minute at 10 000 rpm. The flow through from the collection tubes was discarded and the previous step was repeated. Two hundred microliters of DNA pre-wash buffer was added to the Zymo-Spin^{TM} IIC Column and centrifuged for 1 minute at 10 000 rpm. A total of 500 µl of g-DNA wash buffer was added to the Zymo-Spin^{TM} IIC Column and centrifuged at 10 000 rpm for 1 minute. The Zymo-Spin^{TM} IIC Column was transferred to a clean 1.5 ml tube and 50 µl of DNA Elusion Buffer was added then centrifuged at 10 000 rpm for 30 seconds. The extracted DNA was then stored in a freezer until used.

2.2.5 Molecular amplification of *cytochrome oxidase 1* (*CO1*) gene

PCR targeting the *CO1* gene was conducted to identify tabanid flies to species level. This PCR was to supplement morphological analysis in characterising the captured tabanid flies and to determine their phylogenetic position when compared to other related taxa. The 911 (TTT CTA CAA ATC ATA AAG ATA TTG G) and 912 (TAA ACT TCA GGG TGA CCA AAA AAT CA) primers which amplified approximately 653 base pairs (bp) of the target gene were used (Sari *et al*., 2012). The PCR contained a final volume of 25 µl which was composed of 12.5 µl AmpliTaq Gold® 360 PCR Master Mix (AmpliTaq Gold® DNA Polymerase 0.05 units/ µl, Gold buffer [30 mM Tris/HCl pH 8.05, 100 mM KCl], 400 mM of each dNTP and 5 mM $MgCl_2$) (Applied Biosystems, California, USA). Then 2.5 mM of each primer, 2 µl of template DNA and double distilled water (ddH_2O) was added to make the final volume. The PCR conditions were set as follows: initial denaturation at 95°C for 10 minutes, followed 35 cycles of 95°C for 30 seconds, annealing at 55°C for 30 seconds, elongation at 72°C for 30 seconds and final elongation at 72°C for 1 minute. PCR products were electrophorized on a 1% agarose gel then visualised under UV light. Positive PCR products were purified using the QIAquick® Gel Extraction Kit (QIAGEN, Hilden, Germany).

2.2.6 Purification of PCR amplicons

Initially, a 1% agarose gel stained with ethidium bromide was prepared. Thereafter, 20 µl of PCR amplicon was resolved by gel electrophoresis at 100 volts for 30 minutes. Subsequently, the gels having the DNA fragments were cut with a clean sharp scalpel and the gel slices were placed into 1.5 ml Eppendorf tubes. Then 600 µl of QG buffer was added. To dissolve the sliced DNA fragments in QG buffer the Eppendorf tubes were heated at 50°C for 10 minutes on a heating block. The tubes were vortexed every 2 minutes during the incubation period. Then 200 µl of isopropanol was added to increase the DNA yield. The mixture was transferred into QIAquick spin column with a 2 ml collection tube. To bind the DNA the spin columns were centrifuged for 1 minute at 13 000 rpm. The flow through in the collection tubes was discarded and an additional 500 µl of QC buffer was added to the QIAquick column and centrifuged for 1 minute at 13 000 rpm. The purified DNA in the QIAquick column was then washed with 750 µl of PE buffer that contained 99% absolute ethanol and centrifuged again at 13 000 rpm for 1 minute. The flow through was discarded and the QIAquick column centrifuged to remove excess ethanol in the PE buffer. The QIAspin columns were transferred into new clean 1.5 ml tubes and 50 µl of EB buffer was used to elute the DNA. The purified DNA was stored at -20°C until they were sequenced at the sequencing facility of the Unit of Environmental Sciences and Management at North-West University (NWU)-Potchefstroom campus.

2.2.7 Sequencing and BLASTn

Purified PCR products were subjected to sequencing PCR with the final volume of 5 µl which was composed of 1 µl template DNA, 1 µl of either forward or reverse primer (1 pmol/µl) and 2 µl of premix BigDye®. Thereafter, 1µl of double distilled water (ddH$_2$O) was added to make the final volume. (Applied Biosystems, California, USA). The sequencing PCR conditions were initial denaturation at 96°C for 60 seconds, followed by 25 cycles entailing a 96°C for 10 seconds denaturation, annealing at 50°C for 5 seconds, and extension at 60°C for 4 minutes and holding temperature at 4°C (Applied Biosystems, California, USA). Ethanol precipitation subsequently followed and the reactions were prepared in a 1.5 ml Eppendorf tubes whereby, 25 µl of 99% ethanol, 1 µl of 3M sodium acetate and 8.75 µl of ddH$_2$O were mixed in the 1.5 ml tube. Thereafter, the tubes were vortexed and left at room temperature (20°C to 25°C) for 15 minutes to precipitate. The contents were then centrifuged at 15 000 rpm for 20 minutes at room temperature and the supernatant was discarded. The pellet was then washed with 100 µl of 70% ethanol and vortexed briefly. The tubes were again centrifuged at 15 000 rpm at room temperature and the supernatant was again discarded. The pellets were air dried for 30 minutes, afterwards 20 µl of formamide was added and the tubes were then placed on ice for 2 minutes and centrifuged for 2 minutes. Subsequently, reaction mixture was transferred into a 96-well plate and heat shocked at 95°C for 2 minutes and then placed on ice again. The eluent was placed in an ABI Prism 3100 Genetic Analyzer, where sequencing electrophoresis occurred using a 36 cm capillary array and POP-7™polymer (Applied Biosystems, California, USA). Analysis of the data was done using the Sequence Analyzer software version 1.7.1 (http://informagen.com/SA/).

2.2.8 Statistical analysis

The prevalence of each tabanid fly species was presented in proportions and summarized tables according to independent variables such as tabanid fly species as well as the locality where the fly was collected. The Kruskal–Wallis χ^2 analysis of variance by ranks at a significance of 95% was used to determine the significance in the overall distribution of the tabanid flies throughout the sampled countries

2.2.9 Phylogenetic analysis

Retrieved gene sequences obtained from all positively tested amplicons were edited using BioEdit to remove any degenerate base pairs (Hall, 1999) and saved as FASTA format. To confirm sequences obtained from *CO1* analysis, the nucleotide basic local alignment search tool (BLASTn) was used. Only gene sequences with 98% to 100% similarity match score were considered as significant. Gene sequences of species closely related to tabanid flies in the current study from the BLASTn search results were downloaded from NCBI database.

The *CO1* gene sequences were aligned by Clustal W using the multiple alignment fast fourier transform (MAFFT) program to conduct multiple and pair-wise sequence alignments (Katoh and Standley, 2013). Thereafter, the aligned sequences were trimmed using TrimAl version 1.4 to remove the uneven ends from the aligned sequences. The trimmed alignment was subsequently transferred to MEGA 6 for Maximum likelihood (ML) and to Geneious (Ver. 7.1) bioinformatics software package for Bayesian inference (BI) analyses. The alignment consisted of a total of 51 gene sequences (636 bp long) whereby 20 were obtained in the current study and 31 were downloaded from NCBI GenBank. For ML analysis 100 000 bootstrap replicates were used. The BI phylogeny was constructed using MrBayes Ver. 3.2.1 plugin on Geneious (Ver. 7.1) and the parameters were set as described by Morita *et al*. (2016).

2.3 Results

A total of 529 tabanid flies were collected from the three sampled countries. Morphological analysis revealed a total of 5 different genera collected from the sampled areas namely: *Ancala*, *Atylotus*, *Haematopota*, *Philoliche* and *Tabanus*. A total of 14 different species were collected whereby, 10 were from South Africa, 8 species were from Zambia and in Lesotho only 2 specimens from the same genus were captured.

2.3.1 Tabanids from Lesotho

Only 2 specimens were captured from Lesotho and both of these were *Atylotus nigromaculatus* (n = 2). Due to low sample size no statistical analysis was conducted for samples collected from Lesotho.

2.3.2 Tabanids from South Africa

A total of 370 tabanid flies were captured from South Africa and the collection comprised of *Ancala africana*, *Atylotus agrestis*, *A. fuscipes*, *A. nigromaculatus*, *Philoliche aethiopica*, *Tabanus gratus*, *T. taeniatus*, *T. laverani*, *T. par* and *T. taeniola.* The dominant species from the three sampled game reserves were *Tabanus par* (41.6%) and *T. taeniola* (38.4%), whilst *Tabanus gratus* (0.8%) was the least. Charters Creek Game Reserve (55.7%) had the highest species abundance followed by Hluhluwe-Imfolozi Game Reserve (29.4%) and Phinda Private Game Reserve (14.9%) with the least number of flies captured (Table 2). There was a significant difference at $p = 0.03$ (Kruskal–Wallis $\chi^2 = 7,032$, df = 2) in the overall distribution of the tabanid fly population throughout the three sampled game reserves in KwaZulu-Natal Province, South Africa.

2.3.3 Tabanids from Zambia

A total of 157 tabanid flies were collected from Zambia and these included *Atylotus agrestis*, *A. diurnus, Haematopota longa*, *Tabanus taeniatus*, *T. conformis*, *T. conspicuus*, *T. par* and *T. taeniola.* The most dominant species captured from the two provinces was *Tabanus taeniatus* (49.0%) followed by *T. taeniola* (26.1%) and the least from the collection was *T. conspicuus* (0.6%). Majority of the samples were collected from Mambwe district in the Eastern Province (94.3%) and the Itezhi-tezhi district from the Central Province (5.7%) yielded the lowest numbers (Table 3). There was significant difference at $p = 0.01$ (Kruskal–Wallis $\chi^2 = 6.893$, df = 1) in the overall distribution of the tabanid fly population throughout the two sampled provinces in Zambia. Additionally, a summary representing other insects as by-catch that are not included in the analysis of the current study are given in table 4.

Table 1: Captured tabanid flies from South Africa

Tabanid fly species	Game Reserve sampled Hluhluwe-Imfolozi (%)*	 Charters Creek (%)*	 Phinda Private (%)*	Total number of fly individuals
1. *Ancala Africana*	5 (38.5)	7 (53.8)	1 (7.7)	13
2. *Atylotus agrestis*	7 (63.6)	4 (36.4)	0 (0)	11
3. *Atylotus fuscipes*	6 (60.0)	4 (40.0)	0 (0)	10
4. *Atylotus nigromaculatus*	5 (41.7)	4 (33.3)	3 (25.0)	12
5. *Philoliche aethiopica*	2 (33.3)	4 (66.7)	0(0)	6
6. *Tabanus gratus*	3 (100)	0 (0)	0 (0)	3
7. *Tabanus taeniatus*	4 (28.6)	10 (71.4)	0 (0)	14
8. *Tabanus laverani*	4 (80.0)	1 (20.0)	0 (0)	5
9. *Tabunus par*	43 (27.9)	87 (56.5)	24 (15.6)	154
10. *Tabanus taeniola*	30 (21.1)	85 (59.9)	27 (19.0)	142
Total	**109 (29.46)**	**206 (55.68)**	**55 (14.86)**	**370**

***Indicates the relative abundance of the tabanid flies found per sampled game reserves from South Africa in percentages

Table 2: Captured tabanid flies from Zambia

Species	Central Province (%)*	Eastern Province (%)*	Total number of fly samples
1. *Atylotus agrestis*	1 (6.25)	15 (93.75)	16
2. *Atylotus diurnus*	1 (14.3)	6 (85.7)	7
3. *Haematopota longa*	0 (0)	3 (100)	3
4. *Tabanus taeniatus*	0 (0)	77 (100)	77
5. *Tabanus taeniola*	3 (7.3)	38 (92.7)	41
6. *Tabanus par*	1 (12.5)	7 (87.5)	8
7. *Tabanus conspicuous*	1 (100)	0 (0)	1
8. *Tabanus conformis*	0 (0)	4 (4)	4
Total	**7 (4.46)**	**150 (95.54)**	**157**

***Indicates the relative abundance of the tabanid flies found per sampled game reserves from Zambia in percentages

Table 3: Insects caught as by-catch from all sampled countries

Country	Order	Family	Species	Total number
Lesotho	Diptera	Muscidae	*Musca domestica*	36
			Stomoxys calcitrans	56
		Sarcophagidae	*Sarcophaga harpax*	4
	Lepidoptera	Erebidae	*Caenurgina erechtea*	2
	Hymenoptera	Sphecidae	*Sceliphron caementarium*	2
		Formicidae	*Lasius niger*	85
South Africa	Diptera	Glossinidae	*Glossina brevipalpis*	256
			Glossina austeni	1
Zambia	Diptera	Muscidae	*Musca domestica*	44
			Stomoxys calcitrans	9
		Glossinidae	*Glossina pallidipes*	24
Total				**519**

2.4 Morphological analysis

Identification of several tabanid fly species was based on their morphological characteristics and reference to the authors whom described the flies is provided as follows:

Ancala africana Gray, 1922

This species was only collected from South Africa. It was identified according to the characteristics described by Oldroyd (1954) and Yagi (1964). Accordingly, the specimen had an average body length of 17 mm. The eyes were greenish with no bands in living specimens and black on dried specimens (Figure 7A1). The callus was dark brown and had a quadrate shape with a trace of a median extension (Figure 7A1 (i)). The facial area was yellow covered with golden hairs. The antennae were blackish in pigmentation. It had an orange yellowish thorax with no patterns (Figure 7A2). The dorsum of abdomen was orange with black hair patches on the margins of all tergites ventrally and the last segment was completely black (Figure 7A3 (ii)). The wing membrane had broad transverse brown band shading crossing the distal cell but not reaching the hind margin and extends to the tips of the wing veins R_{2+3} and R_4 (Figure 7A4).

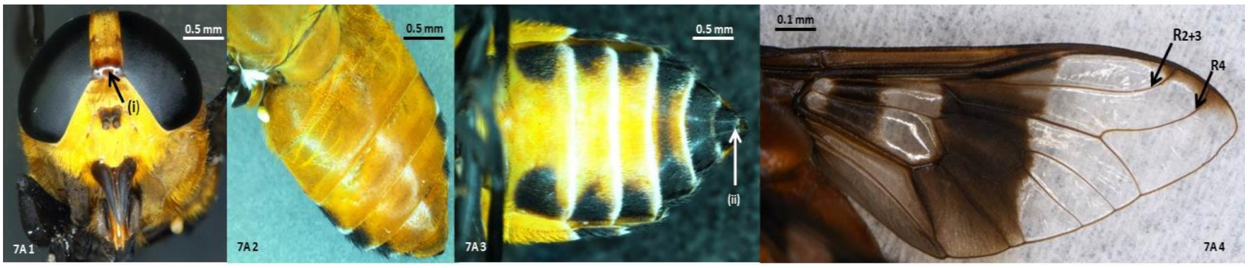

Figure 7A: Sequential images of *Ancala africana* where A1 is the head, A2-A3 is the dorsal and ventral sides of the abdomen respectively, A4 is the wing.

Atylotus agrestis Wiedemann, 1828

This species was collected from both South Africa and Zambia. It was identified by characteristics described by Oldroyd (1954), Yagi (1964) and Veer (1999). The specimen had an average body length of 14 mm. The eyes were rusty brown with a trace of a single purple band in dried specimen and reddish black in living specimen (Figure 7B1). The frons was grey and yellow towards the vertex. The proboscis and first segment of the antennae were light orange in colour and the rest of the antennae were bright yellow (Figure 7B1 (ii)). The upper and lower calli were circular and shining brown in colour (Figure 7B1 (i)). Face and parafacials were white with long white hairs (Figure 7B1). The thorax was black with slight traces of four brown longitudinal sublateral stripes. The scutellum was uniformly brownish in colour (Figure 7B2 (ii)). The abdomen was black with two orange sub lateral stripes and yellow ground colour (Figure 7B2). The veins and costa of the wings were pale yellow and only the stigma was slightly brownish (Figure 7B4 (iv)).

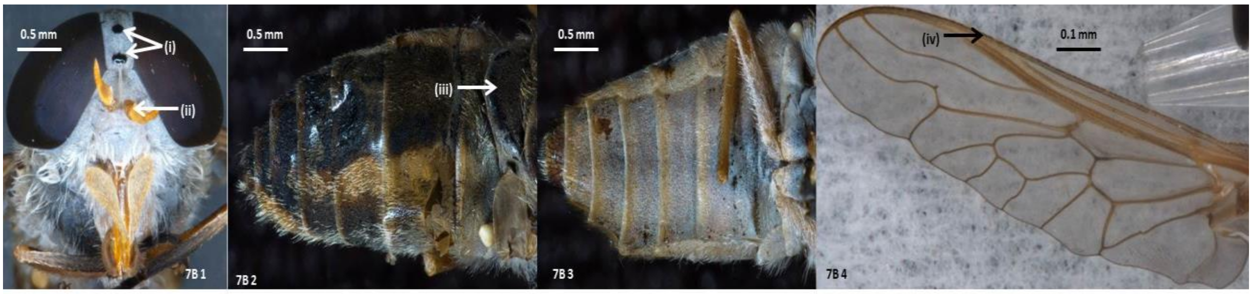

Figure 7B: Sequential images of *Atylotus agrestis* where B1 is the head, B2-B3 is the dorsal and ventral sides of the abdomen respectively, B4 is the wing.

Atylotus diurnus Walker, 1850

This species was only collected from Zambia. It was identified by characteristics described by Oldroyd (1954). The specimen had an average body length of 15 mm. The eyes were reddish black with no traces of bands on both living and dried specimens (Figure 7C1). The frons had yellow-grey fine hairs and a fairly large yellowish triangle at the vertex (Figure 7C1 (i)). Calli were dark brown with the upper callus was slightly elongated and the subcallus flat (Figure 7C1 (ii)). The face and parafacials had yellowish grey tomentum. The antennae were yellowish orange from the scape and more light yellow towards the tips (Figure 7C1 (iii)). The proboscis was dark-brown and stalky. The thorax had a black mesonotum with no patterns and covered with thin ashy-grey hairs. The dorsum of the abdomen was ashy-grey with clear patterns made up of black and golden hairs with three longitudinal stripes (Figure 7C3). The wings were clear with a bit of yellow colouration towards the ends and the stigma (Figure 7C4 (iv)).

Figure 7C: Sequential images of *Atylotus diurnus* where C1 is the head, C2-C3 is the dorsal and ventral sides of the abdomen respectively, C4 is the wing.

Atylotus fuscipes Ricardo, 1908

This species was only collected from South Africa. It was identified by characteristics described by Oldroyd (1954), Yagi (1964) and Veer (1999).The average body length of this specimen was 14 mm. Eyes of the dried specimen were reddish brown on living and dried specimens (Figure 7D1). The frons was yellowish grey with a yellow triangular shape at the vertex and a distinct median ocellus (Figure 7D1 (i)). The calli were black, ovate to quadrate in shape. The proboscis was brownish. The antennae were pale yellowish at the first segment with black hairs and more orange at the terminal (Figure 7D1 (ii)). The thorax was ashy grey with a narrow dark brown median stripe and mere traces of sublateral stripes. The abdomen was dorsum black with two orange sublateral stripes that end on the fifth tergite. The orange stripes were more broad at the first two segments (Figure 7D2 (iii)) and had golden hairs. The wings were clear with brownish veins (Figure 7D4 (iv)).

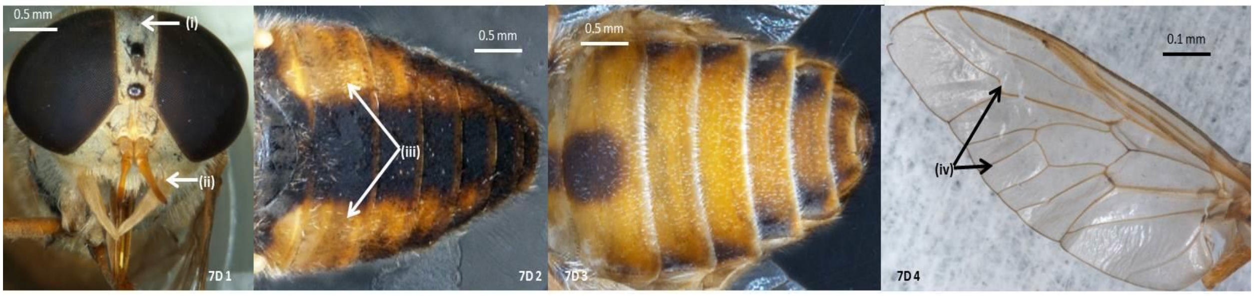

Figure 7D: Sequential images of *Atylotus fuscipes* where D1 is the head, D2-D3 is the dorsal and ventral sides of the abdomen respectively, D4 is the wing.

Atylotus nigromaculatus Ricardo, 1900

This species was only collected from South Africa. It was identified by characteristics described by Oldroyd (1954). The specimens had an average body length of 13 mm. The eyes were reddish brown on living specimen and yellowish with a trace single purple band on dried specimen on dried specimen. The frons was slightly converted with yellowish grey hairs and large black V-shaped calli at the vertex (Figure 7E1 (i)). Hairs around the head were mainly yellow and mixed with some few black ones. The face and parafacials had white fine hairs. The palpi were white and swollen at the base (Figure 7E1 (ii)). The proboscis was black-brown in colour. The thorax was black with a thin ashy grey-brown tomentum and fairly distinct narrow yellowish grey longitudinal stripes. The scutellum was ashy grey-brown (Figure 7E2 (iii)). The abdomen dorsally, was black-brown with a little reddish colour on the sides of the first two segments with three prominent yellowish grey longitudinal parallel sided stripes (Figure 7E2). The wings were clear with pale yellow stigma and yellowish veins that darken towards the margins (Figure 7E4)

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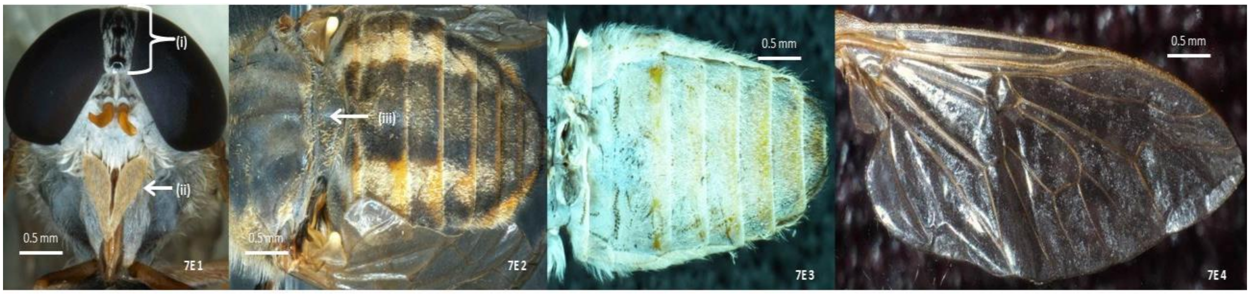


Figure 7E: Sequential images of *Atylotus nigromaculatus* where E1 is the head, E2-E3 is the dorsal and ventral sides of the abdomen respectively, E4 is the wing.

Philoliche aethiopica Thunbrg, 1789

This species was only collected from South Africa. The specimen was identified by characteristics described by Morita (2008). The average body length of the specimen was 14 mm. The head was black with black eyes (Figure 7F1). The frons was strongly divergent towards antennae and mahogany brown in colour (Figure 7F1 (i)). The first two segments of the antennae were brown with black hairs. The proboscis was black and equal to the body length (Figure 7F1 (ii)). The inner eye margins had an obtuse angle (Figure 7F1 (iii)). The thorax was dark brown with no sublateral stripes. The abdomen was bright reddish orange with small blue-black medial spots on the first four tergites dorsally and ventrally (Figure 7F2 and Figure 7F3). The wings were slightly smoky and darkened slightly at cross-veins (Figure 7F4).

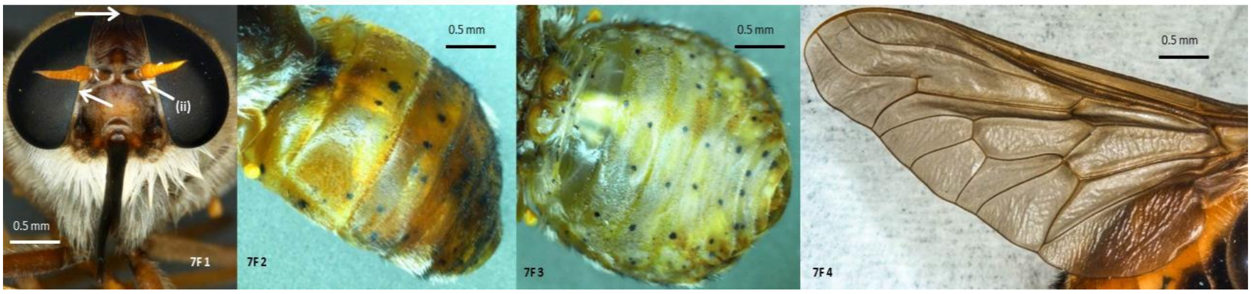


Figure 7F: Sequential images of *Philoliche aethiopica* where F1 is the head, F2-F3 is the dorsal and ventral sides of the abdomen respectively, F4 is the wing.

Tabanus taeniatus Macquart, 1834

This species was collected from both South Africa and Zambia. The specimen was identified by characteristics described by Oldroyd (1954). The average body length of these specimens were 12 mm. The eyes were green violet without bands on living specimens but appeared brownish black on dried specimens (Figure 7G1). The frons was honey-brown with black hairs and yellow hairs towards the margins of the eyes. The upper and lower calli were irregular and black in colour (Figure 7G1 (i)). The proboscis was blackish with orange yellowish palpi. The thorax had ashy black hairs and a faint narrow brown median line (Figure 7G1 (ii)). The scutellum was blackish brown with patches of grey on the sides (Figure 7G2 (iii)). The dorsum of the abdomen was ashy black with three whitish grey longitudinal stripes (Figure 7G2 (iv)). The two sublateral stripes ended on the seventh tergite which was completely greyish. The hairs were black on the dark areas of the abdomen and whitish yellow on the grey stripes. The wings were clear with pale yellow veins and stigma (Figure 7G4).

Figure 7G: Sequential images of *Tabanus taeniatus* where G1 is the head, G2-G3 is the dorsal and ventral sides of the abdomen respectively, G4 is the wing.

Tabanus gratus Loew, 1858

This species was only collected from South Africa. The specimen was identified by means of characteristics described by Oldroyd (1954). The average body length of these specimens was 12 mm. The eyes were green with three crimson bands in both living and dry specimens (Figure 7H1). The tomentum of the frons was yellowish grey and whitish towards the vertex. The calli were separated whereby, the lower callus was slightly square in shape and upper callus was oval and both were honey brown in colour (Figure 7H1 (i)). The first two segments of the antennae were whitish and the rest orange. The face and parafacials were white with whitish hairs. The proboscis was brown (Figure 7H1). The thorax had dark brown fine hairs with white median and sublateral stripes. The dorsum of the abdomen was dark brown with three clearly defined white stripes (Figure 7H2). The median stripe was narrow on the second segment, becoming broadest on the hind margin of the forth segment and narrowing again towards the posterior (Figure 7H2 (ii)). The wings were clear with yellow veins and an almost invisible stigma (Figure 7H4).

Figure 7H: Sequential images of *Tabanus gratus* where H1 is the head, H2-H3 is the dorsal and ventral sides of the abdomen respectively, H4 is the wing.

Tabanus laverani Surcouf, 1907

This species was only collected from South Africa. The specimen was identified by means of characteristics described by Oldroyd (1954). The average body length of these specimens was 14 mm. The eyes were black greenish on dried specimen and banded in living specimen (Figure 7I1). The tomentum of the frons was light grey with black patches on the vertex and the upper callus. The palpi were covered with white hairs and the proboscis was dark brown. The first two segments of the antennae were reddish and the rest were bright orange with black hairs. The thorax had a bark brown thin hairs with a pair of faint light grey sublateral stripes which continued across the sides of the scutellum (Figure 7I1 (i)). The knobs of the halters were whitish yellow (Figure 7I2 (ii)). The dorsum of the abdomen was light brown on the first two tergites and the rest was dark brown with a bold parallel sided whitish median stripe (Figure 7I2). The lateral margins were greyish with no patterns (Figure 7I2 (iii)). The wings were clear with a dark brown stigma (Figure 7I4 (iv)).

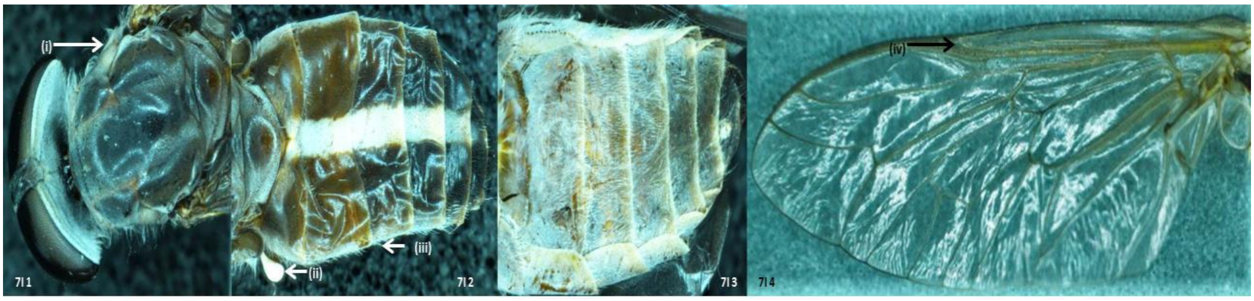


Figure 7I: Sequential images of Tabanus *laverani* where I1 is the head, I2-I3 is the dorsal and ventral sides of the abdomen respectively, I4 is the wing.

Tabanus par Walker, 1858

This species was collected from both South Africa and Zambia. The specimen was identified by characteristics described by Oldroyd (1954). The average body length of these specimens was 12 mm. The eyes were emerald green and without bands on both living and dry specimens (Figure 7J1). The tomentum of the frons was golden yellow with black hairs. The calli was yellowish brown and broadly united into an elongated, onion shape figure (Figure 7J1 (i)). The subcallus, face and parafacials were lemon yellow with yellow hairs. The palpi were yellow with black and pale yellow hairs. The proboscis was yellow orange in colour (Figure 7J1). The first two segments of the antennae were yellow with yellow hairs and the rest were bright orange (Figure 7J1 (ii)). The thorax was without any patterns and scutellum was black in ground colour. The dorsum of the abdomen was orange without any patterns and clothed with a mixture of black and golden yellow fine hairs (Figure 7J2). The wings were clear with yellow veins and stigma (Figure 7J4).

Figure 7J: Sequential images of *Tabanus par* where J1 is the head, J2-J3 is the dorsal and ventral sides of the abdomen respectively, J4 is the wing.

Tabanus taeniola Palisto de Beavios, 1807

This species was collected from both South Africa and Zambia. The specimen was identified on characteristics described by Oldroyd (1954). The average body length of these specimens was 16 mm. The eyes were reddish brown on dried specimen and dull copper green in living specimens with short and sparse pubescence (Figure 7K1). The facets were equal in size with no visible bands. The frons was reddish brown with a thin tomentum covered mostly by white hairs. The calli was reddish brown (Figure 7K1 (i)) and the proboscis was black (Figure 7K1). The first segment of the the antenna was whitish grey, the second a bit reddish with black hairs and the rest were blackish (Figure 7K1 (ii)). The thorax was black and the tomentum reddish brown on the sides. The scutellum was dull reddish with grey tomentum on the sides and grey medially. The abdomen was dorsally reddish brown at the first four tergites and the fifth to seventh tergites are dark brown (Figure 7K2). On the abdomen there were three conspicuous longitudinal whitish stripes (Figure 7K2). The median stripes were triangular and appeared to be fused (Figure 7K2 (iii)). The wings were clear with a pale stigma (Figure 7K4).

Figure 7K: Sequential images of *Tabanus taeniola* where K1 is the head, K2-K3 is the dorsal and ventral sides of the abdomen respectively, K4 is the wing.

Haematopota longa Ricardo, 1906

This species was only collected in Zambia. The specimen was identified by characteristics described by Oldroyd (1952). The average body length of these specimens was 10 mm. Eyes on living and dry specimens were reddish black (Figure 7L1). The frons was square, pale yellow and slightly grey on the sides. The specimen had circular black paired spots and not touching the eye margins (Figure 7L1 (i)). The callus was transverse, low, without median extensions and black in colour (Figure 7L1 (ii)). The first segment of the antennae were cylindrical and elongated and as long as the frons and without subapical notches (Figure 7L1 (iii)). The rest of the antennae were reddish brown and the last segment was black. The face and parafacials were whitish grey. The thorax was light brown in colour with greyish brown distinct patterns at the end of sublateral stripes and a median grey stripe (Figure 7L1 (iv)). The dorsum of the abdomen was dark brown with pale side margins. The wings were light brown with dark brown to black rosettes covering the whole wing (Figure 7L4 (v)).

Figure 7L: Sequential images of *Haematopota longa* where L1 is the head, L2-L3 is the dorsal and ventral sides of the abdomen respectively, L4 is the wing.

Tabanus conformis Walker, 1848

This species was only collected from Zambia. The specimen was identified by characteristics described by Oldroyd (1954). This specimen was fairly large with an average length of 12 mm. The eyes were dark purplish with no bands on both living and dry specimens (Figure 7M 1). Tomentum of the frons was dark brown in the middle and greyish towards the vertex and lower callus (Figure 7M1 (i)). Sub-callus and parafacials were light brown and the proboscis was black-brown (Figure 7M1 (ii)). The thorax had brown fine hairs and an ashy-grey pigment towards the edges with faint greyish sublateral stripes (Figure 7M2). The dorsum of the abdomen was orange with short black hairs which give it a brown colour to the naked eye (Figure 7M2 (iii)). There was a grey-yellowish median stripe that is clearly prominent covered with yellow hairs (Figure 7M3). The wings were smoky grey becoming more brownish towards the margins (Figure 7M4).

Figure 7M: Sequential images of *Tabanus conformis* where M1 is the head, M2-M3 is the dorsal and ventral sides of the abdomen respectively, M4 is the wing.

Tabanus conspicuus Ricardo, 1908

This species was only collected from Zambia. The specimen was identified by characteristics described by Oldroyd (1954). The body of this specimen was large with 19 mm in average length. The eyes were dark reddish brown with no bands on both living and dry specimens (Figure 7N1). The tomentum of the frons was yellowish grey to reddish brown (Figure 7N1 (i)) and the proboscis was black-brown. The thorax had yellow fine hairs with a brown tomentum between lateral stripes (Figure 7N1 (ii)). The scutellum was yellow-brown with a red tip (Figure 7N (iii)). The dorsum of the abdomen was predominantly yellow with a very broad median stripe with triangles united into a notched stripe and brown in colour giving the appearance of a yellow abdomen with two narrow brown stripes (Figure 7N2). The wings were slightly smoky with distinct colourings along the veins (Figure 7N4).

Figure 7N: Sequential images of *Tabanus conspicuus* where N1 is the head, N2-N3 is the dorsal and ventral sides of the abdomen respectively, N4 is the wing.

2.5 Phylogeny of tabanids from southern Africa

Sequences used for both Maximum Likelihood (ML) and Bayesian inference (BI) phylogenetic analyses were from members of the genera *Atylotus*, *Hybomitra*, *Tabanus*, *Haematopota* and *Philoliche* as well as *Chrysops* representing three tribes from the family Tabanidae*. Symphoromyia* [JN582255] from the family Rhagionidae was used as an out-group in both analyses (Figure. 8a and b) and there was a total of 29 sequences used. All tabanid *CO1* gene sequences generated in this study clustered with corresponding congener. In both tree topologies monophyly within the family Tabanidae is well supported. The ML (Figure. 8a) tree topology revealed 7 major clades (I – VII) with strong bootstrap support values, namely, Clade I - *Tabanus* 1 spp.; Clade II – *Hybomitra* spp.; Clade III – *Tabanus* 2 spp.; Clade IV – *Haematopota* spp.; Clade V – *Atylotus* spp.; Clade VI – *Chrysops* spp. and Clade VII – *Philoliche* spp. All *Tabanus* sequences clustered together in clade III except for two specimens from Zambia namely, *T. conspicuus* and *T. par.* The BI (Figure. 8b) analysis also produced 7 clades namely, Clade I - *Philoliche* spp.; Clade II - *Chrysops* spp.; Clade III - *Atylotus* spp.; Clade IV - *Haematopota* spp.; Clade V - *Tabanus* 2 spp.; Clade VI - *Hybomitra* spp. and Clade VII -- *Tabanus* 1 spp. respectively. Additionally, in both tree topologies, sequences generated in this study are in bold font and were all submitted to the NCBI database under the accession numbers KY555737-KY555755 (Appendix II). Whereby, the accession numbers of *T. par* are KY555737, KY555738, KY555739, KY555740, KY555741, KY555742 and KY555743 respectively. The remaining are from *Tabanus taeniatus* [KY555744], *A. diurnus* [KY555745, KY555749, KY555750], *A. agrestis* [KY555746, KY555747, KY555748], *T. gratus* [KY555751], *H. longa* [KY555752, KY555753], *T. laverani* [KY555754] and *T. taeniola* [KY555755].

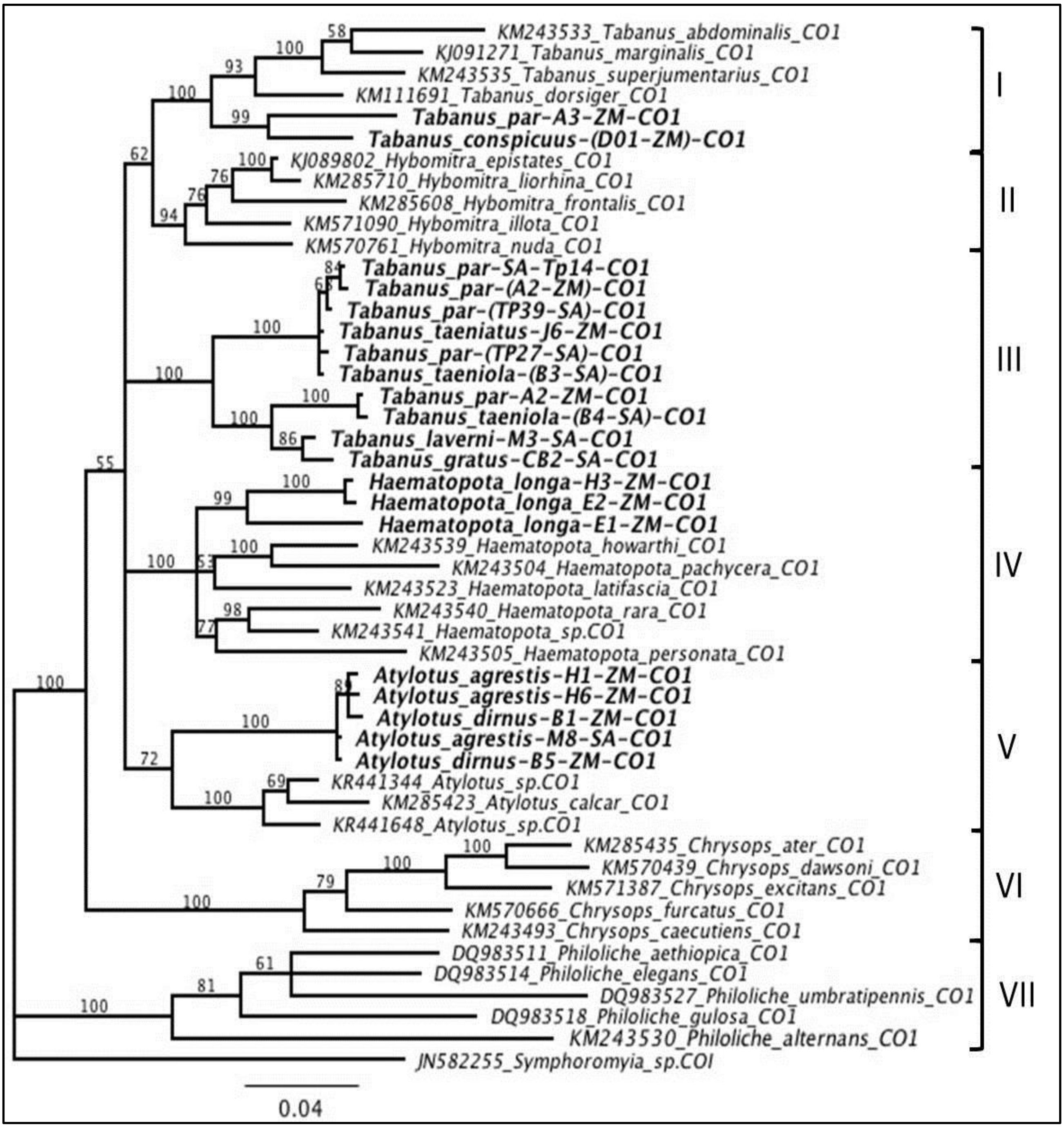


Figure 8a: Phylogenetic analysis by Maximum Likelihood (ML) method. The tree highlights the position of South African and Zambian tabanid flies. The tree has the highest log likelihood (-2596.4237). A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.2658)). The rate variation model allowed for some sites to be evolutionarily invariable ([+I], 57.6169% sites). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 29 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 637 positions in the final dataset. Evolutionary analyses were conducted in MEGA 6 (Tamura *et al.*, 2013).

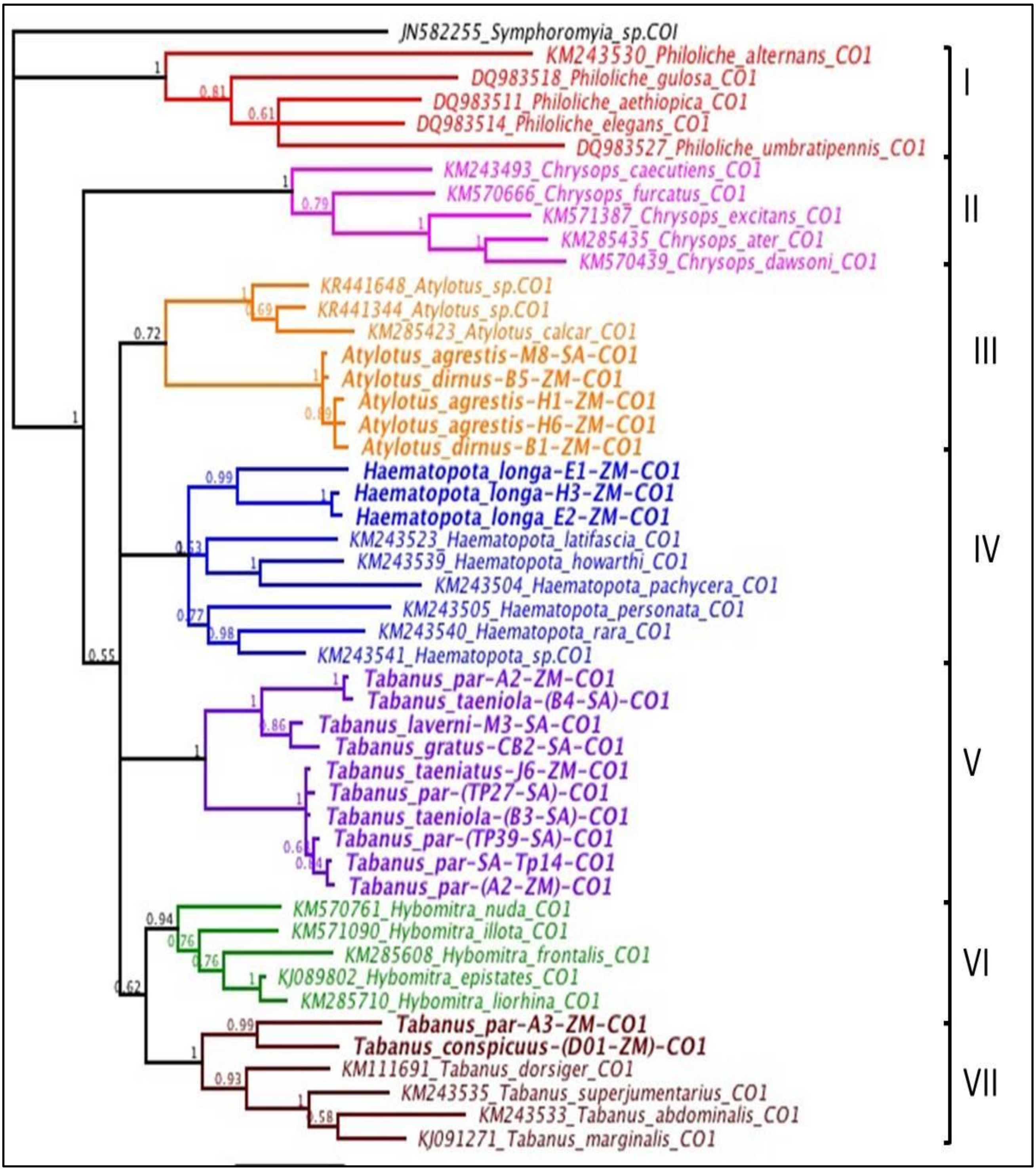


Figure 8b: Phylogenetic analysis by Bayesian inference (BI) constructed using MrBayes. Distinct clades are represented in different colours whereby *Tabanus* spp. 1 is represented by brown, *Hybomitra* spp. by green, *Tabanus* spp. 2 represented by purple, *Atylotus* spp. by orange, *Chrysops* by pink, *Haematopota* spp. by blue and members of *Philoliche* spp. by red colour respectively.

2.6 Discussion

Horse flies (Tabanids) belonging to 5 different genera representing 14 species were recorded in the current study namely: *Ancala*, *Atylotus*, *Haematopota*, *Philoliche* and *Tabanus*. The overall number of members from the genus *Tabanus* was greater than all other genera combined. Generally, members of the tribe Tabanini found in this study differ prominently from one another. In the genus *Ancala* members are easily recognised by their banded wings, a pattern-less thorax and greenish or red-yellowish abdomen with distinctive black patterns or none at all (Oldroyd, 1954). The genus *Atylotus* on the other hand is easily distinguished by its hemispherical head, rusty brown eyes which often show a narrow purple band on eyes of dried specimens and frons with isolated spot-like calli. Lastly, the genus *Tabanus* which has several different species is arranged into species-groups. These include (i) the marmorosus-group, which has streaked veined wings, (ii) the sufis-group in which the upper and lower calli are separated but not reduced as in *Atylotus*, (iii) the insignis-group which is moderately sized (ranging from 10 mm to 17 mm) and is composed of black and white species with a bold thoracic and abdominal pattern, (iv) the pullulus-group with a swollen subcallus, (v) the ruficrus-group with a fairly larger size than all species however, according to Oldroyd (1954) this group can only be described merely by their large size (vi) the plain-group with no patterns on the thorax, abdomen and wings and lastly (vii) the patterned-group which are composed of small to moderately sized species with segmented patterns on the abdomen whereas some have no patterns but indefinite markings towards the tip of the abdomen.

In the current study, species of *Chrysops* and *Hybomitra,* as well as species from the subfamily Scepsidinae were not encountered from the sampled countries. In a study of seasonal abundance of horse flies conducted for a period of 4 years in north eastern KwaZulu-Natal province by Esterhuizen (2006), no members from Scepsidinae were recorded. The last record of Scepsidinae members in southern Africa were reported by Usher (1972). Furthermore, Esterhuizen (2006) recorded only two species from the genus *Chrysops* from four years of sampling, which indicates that species from the genus *Chrysops* are uncommon in sampled regions. Likewise, in the studies conducted by Okiwelu (1975; 1976) on tabanids from Zambia in the miombo woodlands, *Chrysops* species were not reported. Additionally, the effectiveness of the traps used in all sampled countries is questioned as in the study by Okiwelu (1976), Malaise traps baited with CO_2 were used and these traps were more efficient in attracting *Chrysops* species as compared to acetone baited traps used in the current study. Despite the scarcity of *Chrysops* in the sampled countries, there have been reports of *Chrysops* and the role they play in transmission of *Loa loa* in western and central Africa (Ahmed *et al.,* 2005).

The small sample size encountered in the current study in Lesotho and Zambia where samples were collected in early months of 2016 in Lesotho and late months of 2015 in Zambia may have resulted from variation in temperature and rainfall patterns. Additionally, southern Africa has been experiencing the *El Niño* phenomenon between 2015 and 2016, *El Niño* is defined as a local warming of surface waters that takes place in the entire equatorial zone of the central and eastern Pacific Ocean of the Peruvian coast and which affects the atmospheric circulation worldwide (Rojas *et al.,* 2014; WHO, 2016). In Africa this phenomenon affected rainfall patterns and temperatures in many parts of the continent resulting in dry, humid and extremly hot climatic conditions in southern Africa. This condition had a major impact on the abundance of tabanid fly populations. Vast amounts of research conducted on the seasonal abundance of tabanid flies mostly concluded that high numbers of flies are observed during the summer months or rainy season (Barros 2001; Ahmed *et al.,* 2005; Esterhuizen, 2006; Itina *et al.,* 2013; Baldacchino *et al.,* 2014a).

Generally, the sample size of tabanid flies was higher in South Africa as compared to other sampled countries mainly because samples were collected during 2014 where there was no *El Niño* phenomenon. Additionally, Ahmed *et al.* (2005) has been reported that, higher collections of tabanid flies were made in the vicinity of natural hosts like livestock and wild animals hence there were more samples collected from the region. In Lesotho, there are no nature reserves or conserved areas which partly explains the low capture success of tabanid flies. Esterhuizen (2006) stated that, the acetone odour-baited traps are only active in the visual and olfactory whereby attracting only the flies in close range to the traps. This might be another possibility of the low fly catches observed in this study. Furthermore, the absence of tall indigenous tress in Lesotho might have an effect on the abundance of tabanid flies as it was noted by Usher (1972), that tabanid flies normally prefer well shaded habitats whereas Lesotho is dominated by tall shrubs and not trees. Lastly, it has been reported that in the tropics tabanids may not completely disappear in the dry months, but their numbers are normally reduced and maximum numbers of biting flies usually appear towards the beginning of the rainy season (Service, 2012).

Observations made from both tree topologies of maximun likelihood (ML) and Bayesian inference (BI) showed 7 major clades which support monophyly within the family Tabanidae. Similar observation was reported previously where morphological analysis derived from genitalia and external characters as well as molecular techniques targeting mitochondrial (*CO1*) and nuclear (*28S rRNA*) genes also supported monophyly in Tabanidae (Lessard and Yeates, 2012; Lessard *et al.,* 2013; Morita *et al*., 2016). All species used clustered with corresponding congenera. Sequences from the genus *Atylotus* from this study formed a sister group with those from GenBank as observed in clade V, figure 8a and clade III in figure 8b. The genus *Haematopota* in both ML (clade IV) and BI (clade V) analyses was monophyletic and these findings correspond to those by Morita and colleagues (2016). Additionally, as observed by Morita *et al*. (2016) members from the subfamily Chrysopsinae appeared to be paraphyletic as shown in clade II of figure 8a and clade VI of figure 8b. In both tree topologies the genus *Tabanus* had two genetically distinct clades as sequences from the current study clustered on their own. As such, it is therefore suggested that this splitting might be a result of different ecozones. *Tabanus* sequences from this study are from the Afrotropic region and genetically distinct from those found in the Nearctic and the Neotropical regions from GenBank. Only two sequences of *T. par* and *T. conspicuus* from Zambia clustered with those from GenBank suggesting that possible horizontal gene transfer may have occurred in the two sequences hence their position in both tree topologies. It has also been suggested that, in most phylogenetic analysis of tabanid flies and other closely related species, there are usually uncertainties with the position of most species due to weak support observed from internal relationships (Yeates *et al.,* 2007; Morita *et al*., 2016). The same conclusion can be drawn from the current study about the positioning of the two *Tabanus* sequences from Zambia as well as the splitting of members from the genus *Atylotus.* Analysis generated in this study show that southern African tabanid flies do form well supported clades with corresponding congener, however they somehow appear to be genetically distinct from other related species as they formed monophyletic clusters with each other and as such, more extensive analysis on the phylogeny of tabanid flies as well as population genetics studies are required.

CHAPTER 3

MOLECULAR DETECTION OF HAEMOPARASITES INFECTING TABANID FLIES IN LESOTHO, SOUTH AFRICA AND ZAMBIA

3.1 Introduction

One of the most simplest and effective modes of pathogen transmission by haematophagous insects is mechanical transmission. This mode of transmission appears to occur either through contamination of mouthparts or regurgitation (Foil and Gorham, 2000; Baldacchino *et al*., 2013). Regurgitation is an important process in most dipterans as they are unable to consume solid food without liquefying it down using enzyme loaded saliva and as a result may be responsible for the transmission of most bacterium associated pathogens (Foil and Gorham, 2000). Defecation is also significant as pathogens may be ingested and deposited on food or other surfaces, however if the pathogens do not multiply within the alimentary canal of the insect then this is defined as mechanical transmission (Foil and Gorham, 2000). Contamination of mouthparts by haematophagous insects is the most common form of mechanical transmission of pathogens however, this is determined by the pathogen involved in the blood or tissue fluid as well as the size and form of mouthparts associated with blood feeding (Foil and Gorham, 2000; Baldacchino *et al.*, 2014b). Most pathogens can survive for more 24 hours in the crop if ingested during a blood meal by haematophagous insects before being passed on to the next host either by defecation or regurgitation before a new blood meal (Neville *et al*., 1994; Desquesnes and Dia, 2003a; Baldacchino *et al*., 2013; Baldacchino *et al.*, 2014a).

The telmophagous feeding behavior of tabanid flies enable them to be effective mechanical transmitters of pathogens due to their body size and type of mouthparts. Pathogens ingested by these flies can survive in the crop or gut for more than 5 days until transmitted to a new host during the next blood meal (Baldacchino *et al*., 2013). As a result tabanid flies are responsible for mechanical transmission of various pathogens ranging from bacteria, viruses and parasites to both animals and humans (Zumpt, 1949; Foil and Hogsette, 1994; Foil and Gorham, 2000; Desquesnes and Dia, 2003a; 2003b; 2004; Esterhuizen, 2006; Service, 2012; Baldacchino *et al*., 2013; 2014a; Hornok *et al.,* 2014).

Protozoans are among the most important parasites transmitted by tabanid flies and they include *Trypanosoma* and *Besnoitia* species (Baldacchino *et al*., 2014a). However, this study seeks to detect *Babesia* and *Theileria* species which are also known to be transmitted by ticks. All these protozoan parasites exhibit antigenic variation which enables them to evade their host immune response and as a result enables the parasites to be more virulent and difficult to treat (Sivakumar *et al*., 2014a). These pathogens result in various diseases in infected hosts, however, their clinical symptoms are similar but their pathogenicity differs per parasite species and host involved.

Livestock infected with either *Babesia* or *Theileria* parasites have clinical symptoms that are acute to chronic in susceptible hosts. These include fever, anorexia, weakness, severe anaemia, nasal discharge and reduced milk production (Ica *et al.,* 2007; Hunfeld *et al.,* 2008; OIE, 2010; Sahinduran, 2012). Additionally, in cases where theileriosis is involved, enlarged superficial lymph nodes, inappetence, diarrhoea, and haemorrhage in submucous, emaciation as well as jaundice may be observed (Sahinduran, 2012). Where babesiosis is involved, abortion in pregnant livestock is observed. If the disease manifests in the brain, leading to cerebral babesiosis hyperxcitability, convulsions, opisthotonos, coma and death occurs in the case where the infection is caused by either *Babesia bovis* or *B. bigemina* (OIE, 2010; Sahinduran, 2012). These two diseases have been extensively studied using microscopy, serology and molecular techniques in perspective of the tick vectors and animal host (Ica *et al.,* 2007; Hunfeld *et al.,* 2008; Yusufmia *et al*., 2010; Sivakumar *et al*., 2014a; Mans *et al.,* 2015; Yokoyama *et al*., 2015). However, none of these studies addressed the possibility of alternative vectors that might be responsible for the transmission of these two parasites in the absence of ticks.

In the case where besnoitiosis is involved, only two species from the genus *Besnoitia* namely *B. besnoiti* for cattle and *B. caprae* for goats are of importance to the agricultural sector (EFSA, 2010; Namazi *et al.*, 2010; Sahinduran, 2012). In Africa, mechanical transmission of these two parasites by tabanid flies to susceptible livestock has been demonstrated by *Atylotus nigromaculatus* as well as *Tabanocella dentriconis* (Baldacchino *et al*., 2014a). It was also observed that *Besnoitia* parasites can survive for more than 24 hours on the mouthparts of these two tabanid species (Baldacchino *et al*., 2014a). Infected livestock with besnoitiosis show clinical symptoms that range from acute to chronic. The acute signs include fever, increased pulse and respiratory rates, swelling on the ventral aspects of the body, edema of the skin and occasionally diarrhea may occur including nasal discharge. In the chronic stage severe dermatitis is observed (Bigalke and Prozesky 2004; Sahinduran, 2012). In infected goats the clinical symptoms differ from those of infected cattle and they include thickening of the skin over the lower limbs, around the eyes, nose and scrotum with severe alopecia on all mentioned areas (Sahinduran, 2012).

African trypanosomiasis (AT) on the other hand is more problematic in both the health and the agricultural sectors and mechanical transmission of this pathogen by tabanids has been known for decades (Zumpt, 1949; Sahinduran, 2012; Baldacchino *et al*., 2014a). Tabanid flies are known to mechanically transmit various species of *Trypanosoma* parasites such as *Trypanosoma congolense*, *T. evansi*, *T. vivax* as well as *T. theileri* (Zumpt, 1949; Foil and Hogsette, 1994; Foil and Gorham, 2000; Desquesnes and Dia, 2003a; 2003b; 2004; Esterhuizen, 2006; Service, 2012; Sahinduran, 2012; Baldacchino *et al*., 2013; 2014a; Hornok *et al.,* 2014). It has also been reported that *T. evansi* is widespread in most African countries where tsetse flies are absent (Desquesnes *et al*., 2013). *Trypanosoma evansi* is distributed in northern, eastern as well as western Africa and has recently extended to the Middle East to South-East Asia where there are no tsetse flies. Furthermore, the distribution extends to Latin America in fifteen countries and up to so far, flies from the subfamily Tabaninae are considered to be responsible vectors for the wide dispersal of this parasite (Desquesnes *et al*., 2013). They further concluded that *T. vivax* is more likely to be mechanically transmitted than *T. congolense*. Their results strongly suggests that mechanical transmission plays a significant role in the epidemiology of African animal trypanosomiasis and that the potential for mechanical transmission of *A. agrestis* covers a large geographic area since it can be found from Senegal to South Africa. These observations are further supported by Sinshaw *et al*. (2006).

Livestock infected with animal trypanosomiasis show clinical symptoms that range from acute, subacute to chronic. These signs are based on the establishment of anaemia and the grade of organ impairment associated with the disease. In the acute form abortion in pregnant livestock, reduced milk yield, depression and anorexia are observed (Taylor and Authié, 2004; Sahinduran, 2012; OIE, 2013). The subacute form is characterized by weight loss, enlarged lymph nodes as well as the appearance hyperemic mucous membranes. Lastly, the chronic form symptoms range from dull, dry hair coats and inelastic skin. Lethargy and pale mucous membranes are also observed in infected livestock (Taylor and Authié, 2004; Sahinduran, 2012).

Treatment for all the above-mentioned pathogens varies between parasite species involved. In some circumstances, drugs are used to treat symptoms or remove the pathogen involved, whereas in some, dipping is used to control the insect vectors. In some, there are no specific drugs used for treatment and only the control of the vector is essential for the reduction of the pathogen numbers. For babesiosis, drugs such as diminazene aceturate (3-5 mg/kg), phenemidine diisethionate (8-13 mg/kg) imidocarb dipropionate (1-3 mg/kg) and amicarbalide diisethionate (5-10 mg/kg) may be administered to infected livestock (OIE, 2010; Sahinduran, 2012). In cases where theileriosis is involved, buparvaquone (2.5 mg\kg) is the most effective drug used. Additionally, for both babesiosis and theileriosis, effective use of acaricides at 3-week intervals is recommended to control tick populations that cause these two diseases (Sahinduran, 2012). However, in the case of besnoitiosis no known treatment is available and as such, infected animals if diagnosed early are eliminated to prevent the spread of the disease (Bigalke and Prozesky, 2004; EFSA, 2010; Sahinduran, 2012). For trypanosomiasis, drugs such as dimiazene aceturate (3.5-7 mg\kg), homidium bromide and chloride (1 mg\kg) and Isometamidium (0.25-1 mg\kg) may be used in conjunction with insecticides and traps to control fly populations and reduce the incidence of trypanosomiasis in infested areas (Sahinduran, 2012; OIE, 2013).

Effective control measures as well as the proper use of acaricides and insecticides on vectors are essential in the control and prevention of diseases mentioned above. In the current study, to better understand the prevalence of the *Besnoitia besnoiti*, bovine *Babesia* species and *Theileria* species as well as animal *Trypanosoma* species in tabanid flies, polymerase chain reaction (PCR) technique is used to detect the above-mentioned parasites in flies captured from three countries in southern Africa. To achieve this aim the following specific objective was formulated: To detect, by PCR, *Besnoitia besnoiti*, *Babesia* species, *Theileria* species as well as *Trypanozoon* species*, T. congolense, T. theileri* and *T. vivax* in tabanid flies collected in Lesotho, South Africa and Zambia.

3.2 Materials and methods

3.2.1 Sampling of tabanid flies

Samples were collected from three countries in southern Africa namely Lesotho, South Africa and Zambia (Figure 2; Chapter 2). The two different fly traps were used for this study where in Lesotho and South Africa H-traps (Figure 6a; Chapter 2) whereas in Zambia Epsilon traps (Figure 6b; Chapter 2) were utilized. In all countries the traps were placed as mentioned in Chapter 2 section 2.2.2. Briefly, two H-traps were set for 3 months in Lesotho, in South Africa 18 H-traps were set for 2 weeks and lastly in Zambia 11 Epsilon traps were set for 2 weeks.

3.2.2 DNA extraction from tabanid flies

DNA was extracted using the Zymo insect DNA extraction kit following the manufacturer's protocol. Subsequently after the tabanid fly identification using keys, the wings and legs of all captured flies were removed. This was done to prevent excess exoskeletons that might affect the enzymatic activity of the reactions to follow on a later stage (Mekata *et al*., 2008). Thereafter, the whole fly was homogenised as described by Diallo *et al*. (1997) and genomic DNA was extracted using the Zymo insect DNA extraction kit following the manufacturer's protocol (Zymo Research Corporation, California, USA). Briefly, the fly specimens were placed in the ZR BashingBead^{TM} Lysis Tube and 750 µl lysis solution was added. The lysis tube was vortexed for 10 minutes at maximum speed and then centrifuged at 7 000 revolutions per minute (rpm) for 1 minute. About 400 µl of the supernatant was transferred into a Zymo-Spin^{TM} IV Spin Filter with orange cap in a collection tube and centrifuged again at 7 000 rpm for 1 minute. A total of 1 200 µl of genomic lysis buffer was added to the filtrate in the collection tube and mixed. About 800 µl of the mixture was transferred into a Zymo-Spin^{TM} IIC Column with a new collection tube and centrifuged for 1 minute at 10 000 rpm. The flow through from the collection tubes was discarded and the previous step was repeated. Two hundred microliters of DNA pre-wash buffer was added to the Zymo-Spin^{TM} IIC Column and centrifuged for 1 minute at 10 000 rpm. A total of 500 µl of g-DNA wash buffer was added to the Zymo-Spin^{TM} IIC Column and centrifuged at 10 000 rpm for 1 minute. The Zymo-Spin^{TM} IIC Column was transferred to a clean 1.5 ml tube and 50 µl of DNA Elusion Buffer was added then centrifuged at 10 000 rpm for 30 seconds. The extracted DNA was then stored in a freezer until used.

3.2.3 Detection of protozoan parasite DNA from tabanid flies

3.2.3.1 Amplification of *Besnoitia* DNA

Species specific primers Bes-F (5’-ATT CGG ACC GTT TTG TGG-3’) and Bes-R (5’-CCT CTC GAG GCT ACA AGT CG-3’) which amplified a 1 065 bp of the *18S rRNA* gene fragment were used (Namazi *et al*., 2011). The genomic DNA of *Besnoitia besnoiti* obtained from Onderstepoort Biological Products (OBP) in Pretoria was used as a positive control and double distilled water (ddH$_2$O) was used as a negative control. The PCR reaction had the final volume of 25 µl which consisted of 12.5 µl AmpliTaq Gold® 360 PCR Master Mix [(AmpliTaq Gold® DNA Polymerase 0.05 units/ µl, Gold buffer [30 mM Tris/HCl pH 8.05, 100 mM KCl], 400 mM of each dNTP and 5 mM MgCl$_2$)] (Applied Biosystems, California, USA). Then 2.5 mM of each primer, 2 µl of template DNA and ddH$_2$O was added to make the final volume. PCR conditions included, initial denaturation at 95°C for 10 minutes, 95°C for 30 seconds, annealing at 60°C for 30 seconds, initial elongation at 72°C for 1 minute and final elongation step at 72°C for 7 minutes (Namazi *et al*., 2011).

3.2.3.2 Amplification of *Babesia/Hepatozoa/Theileria* DNA

Amplification of approximately 390-430 bp fragment of the hypervariable region V4 of the *18S rRNA* for either *Babesia* or *Theileria* parasites, genus specific primers RLB-F2 (5’-GAC ACA GGG AGG TAG TGA CAA G-3’) and RLB-R2 (5’-CTA AGA ATT TCA CCT CTG ACA GT-3’) were used (Ica *et al*., 2007; Altay *et al*., 2008). The genomic DNA of *Babesia bigemina* (Argentina strain) and *Theileria parva* (Muguga isolate) were used as positive controls whereas double distilled water (ddH$_2$O) was used as a negative control. The PCR reaction had the final volume of 25 µl which consisted of 12.5 µl AmpliTaq Gold® 360 PCR Master Mix [(AmpliTaq Gold® DNA Polymerase 0.05 units/ µl, Gold buffer [30 mM Tris/HCl pH 8.05, 100 mM KCl], 400 mM of each dNTP and 5 mM MgCl$_2$)] (Applied Biosystems, California, USA). Then 2.5 mM of each primer, 2 µl of template DNA and ddH$_2$O was added to make the final volume. PCR conditions included, initial denaturation at 95°C for 10 minutes, 95°C for 30 seconds, annealing at 58°C for 30 seconds, initial elongation at 72°C for 1 minute and final elongation step at 72°C for 7 minutes (Ica *et al*., 2007; Altay *et al*., 2008).

3.2.3.3 Amplification of *Trypanosoma* DNA

The PCR with universal trypanosome primers targeting the internal transcribed spacer 1 (*ITS1*) gene was used to detect trypanosome DNA from the tabanid flies. The primers designed by Njiru *et al*. (2005) with the following sequences were used: forward primer ITS1 CF (5'-CCG GAA GTT CAC CGA TAT TG-3') and reverse primer ITS1 BR (5'-TTG CTG CGT TCT TCA ACG AA-3'). The genomic DNAs of *T. congolense* (IL 3000); *T. b. brucei* (GUTat 3.1) and *T. theileri* (Japan Isolate) were used as positive controls and double distilled water (ddH$_2$O) as a negative control. The PCR reaction had the final volume of 25 µl which consisted of 12.5 µl AmpliTaq Gold® 360 PCR Master Mix [(AmpliTaq Gold® DNA Polymerase 0.05 units/ µl, Gold buffer [30 mM Tris/HCl pH 8.05, 100 mM KCl], 400 mM of each dNTP and 5 mM MgCl$_2$)] (Applied Biosystems, California, USA). Then 2.5 mM of each primer, 2 µl of template DNA and ddH$_2$O was added to make the final volume. PCR conditions included, initial denaturation at 95°C for 10 minutes, 95°C for 30 seconds, annealing at 58°C for 30 seconds, initial elongation at 72°C for 1 minute and final elongation step at 72°C for 7 minutes (Njiru *et al.,* 2005).

3.2.4 Purification of PCR amplicons

For all PCR reactions mentioned above, amplicons were subjected to 1% gel electrophoresis, stained with GelRed DNA stain (Biotium. Inc, USA) and visualised under UV light. Positively amplified amplicons were purified using the QIAGEN Gel Purification Kit (QIAGEN, Hilden, Germany) according to manufacturer's protocol as follows: Initially, a 1% agarose gel stained with ethidium bromide was prepared. Thereafter, 20 µl of PCR amplicons were resolved by gel electrophoresis at 80 volts for 45 minutes. Subsequently, the gels having the DNA fragments were cut with a clean sharp scalpel and the gel slices were placed into 1.5 ml Eppendorf tubes. Then 600 µl of QG buffer was added. To dissolve the sliced agarose gel containing DNA fragments in QG buffer the Eppendorf tubes were heated at 50°C for 10 minutes in a heat block. The tubes were vortexed every 2 minutes during the incubation period. Then 200 µl of isopropanol was added to increase the DNA yield. Thereafter, the mixture was transferred into QIAquick spin column with a 2 ml collection tube. To bind the DNA the spin columns were centrifuged for 1 minute at 13 000 rpm. The flow through in the collection tubes was discarded and an additional 500 µl of QC buffer was added to the QIAquick column and centrifuged for 1 minute at 13 000 rpm. The purified DNA in the

QIAquick column was then washed with 750 µl of PE buffer that contained 99% absolute ethanol and centrifuged again at 13 000 rpm for 1 minute. The flow through was discarded again and the QIAquick column was centrifuged to remove excess ethanol in the PE buffer. The QIAspin columns were transferred into new clean 1.5 ml tubes and 50 µl of EB buffer was used to elute the DNA. The newly purified DNA was stored at -20°C until they were sequenced at the sequencing facility of the Unit of Environmental Sciences and Management at North-West University (NWU)-Potchefstroom campus.

3.2.5 Sequencing and BLASTn

The purified PCR products in a final volume of 5 µl were subjected PCR for sequencing. The 5 µl reaction mixture consisted of 1 µl template DNA, 1 µl of either forward or reverse primer (1 pmol/µl), 2 µl of premix BigDye®. One microlitre of double distilled water (ddH2O) was added to make the 5 µl-final volume (Applied Biosystems, California, USA). The sequencing PCR conditions were initial denaturation at 96°C for 60 seconds, followed by 25 cycles entailing a 96°C for 10 seconds denaturation, annealing at 50°C for 5 seconds, and extension at 60°C for 4 minutes and holding temperature at 4°C (Applied Biosystems, California, USA). Ethanol precipitation subsequently followed and the reactions were prepared in a 1.5 ml Eppendorf tubes whereby, 25 µl of 99% ethanol, 1 µl of 3M sodium acetate and 8.75 µl of ddH_2O were mixed in the 1.5 ml tube. Thereafter, the tubes were vortexed and left at room temperature (20°C to 25°C) for 15 minutes to precipitate. The contents were then centrifuged at 15 000 rpm for 20 minutes at room temperature and the supernatant was discarded. The pellet was then washed with 100 µl of 70% ethanol and vortexed briefly. The tubes were again centrifuged at 15 000 rpm at room temperature and the supernatant was again discarded. The pellets were air dried for 30 minutes, afterwards 20 µl of formamide was added and the tubes were then placed on ice for 2 minutes and centrifuged for 2 minutes. Subsequently, reaction mixture was transferred into a 96-well plate and heat shocked at 95°C for 2 minutes and then placed on ice again. The eluent was placed in an ABI Prism 3100 Genetic Analyzer, where sequencing electrophoresis occurred using a 36 cm capillary array and POP-7™polymer (Applied Biosystems, California, USA). Analysis of the data was done using the Sequence Analyzer software version 1.7.1 (http://informagen.com/SA/).

Retrieved gene sequences were edited using BioEdit to remove any degenerate base pairs (Hall, 1999) and saved as FASTA format. To confirm sequences obtained from all PCR analysis basic local alignment search tool (BALSTn) was used. The gene sequences with 85% to 99% identity match score were considered as significant.

3.2.6 Phylogenetic analysis

Retrived sequences from this study were subjected to BLASTn analysis on GenBank. Thereafter, the sequences were aligned with corresponding sequences of *Babesia*, *Theileria* and *Trypanosoma* by Clustal W. Then neighbor-joining trees for all three parasites with 1000 bootstrap replicates using the *P*-distance analysis method were constructed. All neighbor-joining trees were conducted on MEGA 6.

3.2.7 Statistical analysis

The prevalence of each parasite species were presented in proportions and summarized in tables according to the dependent variables such as tabanid fly species as well as the locality where the fly was collected. Thereafter, 2 X 2 one tailed fisher's exact test which is a form of chi-square, was used to determine any significant association between the prevalences of the parasitic infections (*Besnoitia, Babesia, Theileria* and *Trypanosoma* parasites) and localities of their occurrence at $P < 0.05$.

3.3 Results

A total of 529 tabanid flies were collected during the current study. From these collections, Lesotho had only two flies while South Africa had 370 and Zambia had 157. All collected samples were analyzed by species-specific PCR assays for the presence of *Besnoitia, Babesia, Theileria* and *Trypanosoma* parasite DNAs respectively. Parasite sequences generated in this study (Appendix II) were submitted to the NCBI database under the accession numbers KX870078 to KX870086.

3.3.1 Prevalence of protozoan parasites from Lesotho tabanid flies

None of the 2 *Atylotus nigromaculatus* collected from Lesotho tested positive for the presence of *Besnoitia, Babesia, Theileria* and *Trypanosoma* DNAs by PCR.

3.3.2 Prevalence of protozoan parasites from South African tabanid flies

Of the 370 tabanid flies analysed none tested positive for the presence of *Besnoitia, Babesia* and *Theileria* DNA by PCR. Only *Trypanosoma* DNA was detected from South African tabanid flies.

Polymerase chain reaction from ITS1 primers showed that, 8.38% (31/370) of the tested samples were positive for the presence of trypanosome DNA. Only flies collected from Charters Creek 7.3% (15/206) and Hluhluwe-Imfolozi 14.7% (16/109) game reserves were positive for the presence of trypanosome DNA and none were positive from Phinda Private Game Reserve. Only members from *Tabanus par* 9.09% (14/154) and *T. taeniola* 11.97% (17/142) were positive. *Trypanosoma congolense* (Savannah) was detected in *T. par* 3.25% (5/154) and *T. taeniola* 7.04% (10/142), whilst *T. theileri* was detected in *T. par* 5.19% (8/154) and *T. taeniola* 4.61% (7/142). *Trypanozoon* DNA, was detected from only 0.65% (1/154) of *T. par* specimen from Charters Creek Game Reserve. There was no significant difference at *P* = 0.1131 (one tailed Fisher's Exact Test (FET)) in the prevalence of *T. congolense* (Savannah) as well as at *P* = 0.5650 (one tailed FET) for *T. theileri* found between *Tabanus par* and *T. taeniola* positive samples from South Africa.

Nucleotide BLAST analysis confirmed the *Trypanosoma congolense* positive samples from *Tabanus par* had 89% to 90% identity match with *T. congolense* LS25 isolate [JX910374] from the NCBI GenBank, whilst those from *T. taeniola* had 90% to 97%

identity match score with *T. congolense* isolate TS07210 [JN673389]. The *T. theileri* parasite detected from *Tabanus par* and *T. taeniola* had 80% to 90% identity match score with *Trypanosoma theileri* [ZPU2807] and [JN673396] isolates in the NCBI GenBank database. *Trypanosoma congolense* and *T. theileri* sequences obtained from this study were submitted to GenBank under the accession numbers KX870079 and KX870080 respectively.

The sequence of the *Trypanozoon* species obtained from *T. par* matched with *Trypanosoma brucei* Sezena strain [AF306775] and with *T. evansi* isolate 006 [HQ593640] by 93% identity match score when subjected to BLASTn (Figure 10). The accession number of the *Trypanozoon* sequence obtained from this study deposited to GeneBank is KX870078. The neighbour-joining tree for *Trypanosoma* sequences obtained in this study is given in figure 11. Neither *T. vivax* nor mixed infections were detected from the analysed samples.

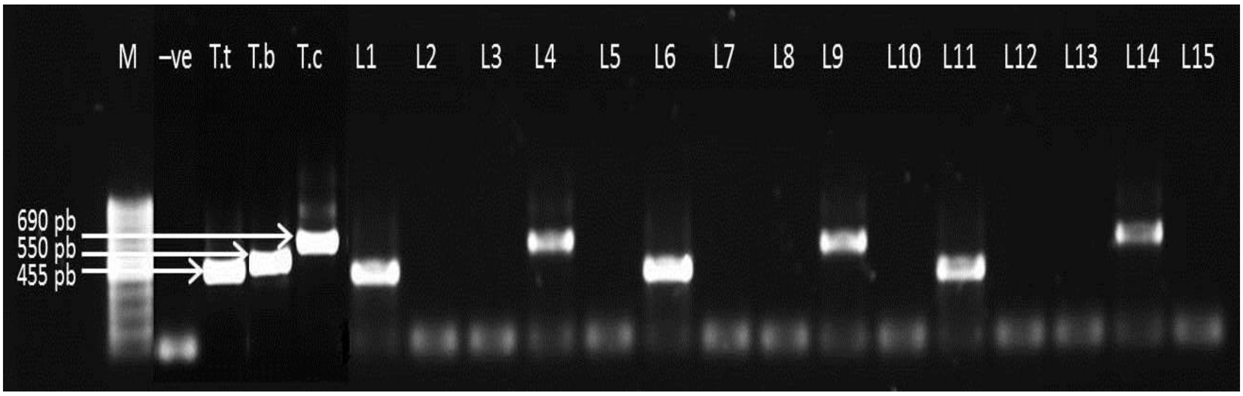
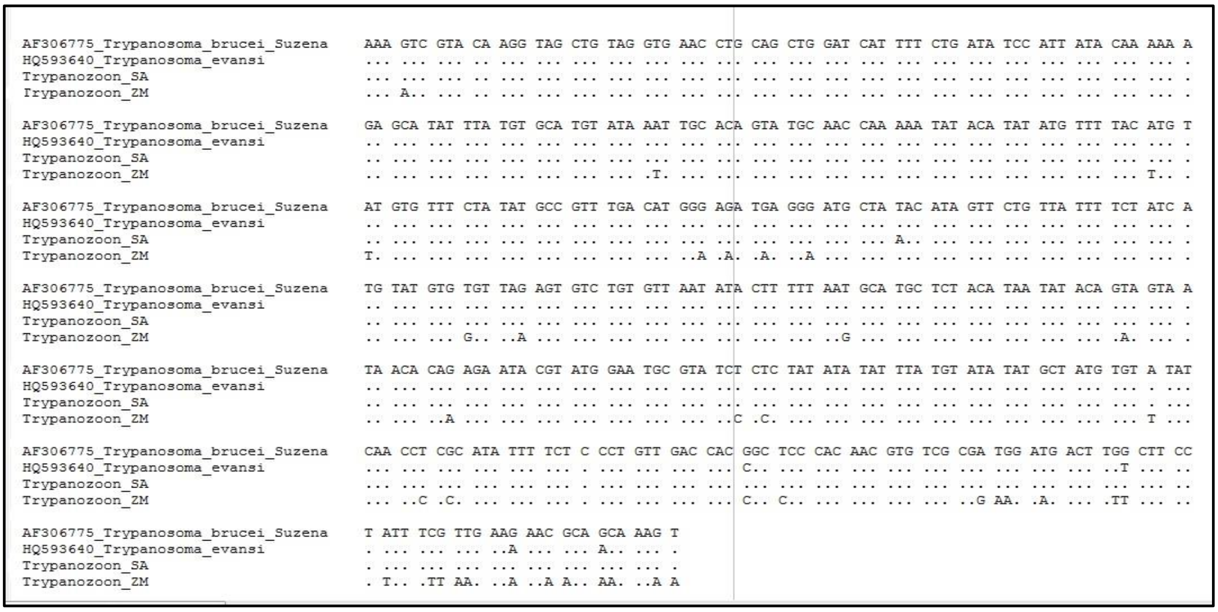


Figure 9: Gel image showing PCR amplification of *Trypanosoma* DNA from South African tabanid flies. M is the molecular marker, -ve is for the no template control, T.t is *Trypanosoma theileri* (Japan Isolate) positive control, T. b is the *T. b. brucei* (GUTat 3.1) positive control and *T. c* is the *T. congolense* (IL 3000) positive control. Lane 1, 6. And 11 show samples positive for *T. theileri.* Lane 4, 9 and 14 show samples positive for *T. congolense.*



```
AF306775_Trypanosoma_brucei_Suzena   AAA GTC GTA CA AGG TAG CTG TAG GTG AAC CTG CAG CTG GAT CAT TTT CTG ATA TCC ATT ATA CAA AAA A
HQ593640_Trypanosoma_evansi          ... ... ... .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .
Trypanozoon_SA                       ... ... ... .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .
Trypanozoon_ZM                       ... A.. ... .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .

AF306775_Trypanosoma_brucei_Suzena   GA GCA TAT TTA TGT GCA TGT ATA AAT TGC ACA GTA TGC AAC CAA AAA TAT ACA TAT ATG TTT TAC ATG T
HQ593640_Trypanosoma_evansi          .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .
Trypanozoon_SA                       .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .
Trypanozoon_ZM                       .. ... ... ... ... ... ... ... .T. ... ... ... ... ... ... ... ... ... ... ... ... ... T.. .

AF306775_Trypanosoma_brucei_Suzena   AT GTG TTT CTA TAT GCC GTT TGA CAT GGG AGA TGA GGG ATG CTA TAC ATA GTT CTG TTA TTT TCT ATC A
HQ593640_Trypanosoma_evansi          .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .
Trypanozoon_SA                       .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... A.. ... ... ... ... ... ... ... .
Trypanozoon_ZM                       T. ... ... ... ... ... ... ... ... ..A .A. .A. ..A ... ... ... ... ... ... ... ... ... ... .

AF306775_Trypanosoma_brucei_Suzena   TG TAT GTG TGT TAG AGT GTC TGT GTT AAT ATA CTT TTT AAT GCA TGC TCT ACA TAA TAT ACA GTA GTA A
HQ593640_Trypanosoma_evansi          .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .
Trypanozoon_SA                       .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .
Trypanozoon_ZM                       .. ... ... G.. ..A ... ... ... ... ... ... ... ... ..G ... ... ... ... ... ... ... .A. ... .

AF306775_Trypanosoma_brucei_Suzena   TA ACA CAG AGA ATA CGT ATG GAA TGC GTA TCT CTC TAT ATA TAT TTA TGT ATA TAT GCT ATG TGT A TAT
HQ593640_Trypanosoma_evansi          .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... . ...
Trypanozoon_SA                       .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... . ...
Trypanozoon_ZM                       .. ... ..A ... ... ... ... ... ... ... ..C .C. ... ... ... ... ... ... ... ... ... ... T ...

AF306775_Trypanosoma_brucei_Suzena   CAA CCT CGC ATA TTT TCT C CCT GTT GAC CAC GGC TCC CAC AAC GTG TCG CGA TGG ATG ACT TGG CTT CC
HQ593640_Trypanosoma_evansi          ... ... ... ... ... ... . ... ... ... ... C.. ... ... ... ... ... ... ... ... ... ..T ... ..
Trypanozoon_SA                       ... ... ... ... ... ... . ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ..
Trypanozoon_ZM                       ... ..C .C. ... ... ... . ... ... ... ... C.. C.. ... ... ... ... ..G AA. .A. ... .TT ... ..

AF306775_Trypanosoma_brucei_Suzena   T ATT TCG TTG AAG AAC GCA GCA AAG T
HQ593640_Trypanosoma_evansi          . ... ... ... ..A ... ... A.. ... .
Trypanozoon_SA                       . ... ... ... ... ... ... ... ... .
Trypanozoon_ZM                       . T.. .TT AA. ..A ..A A.. AA. ..A A
```

Figure 10: Sequence alignment for *Trypanozoon* species from South Africa and Zambia when compared to their BLASTn matches *Trypanosoma brucei* and *T. evansi* from GenBank. The dots indicate identical nucleotide sequences.

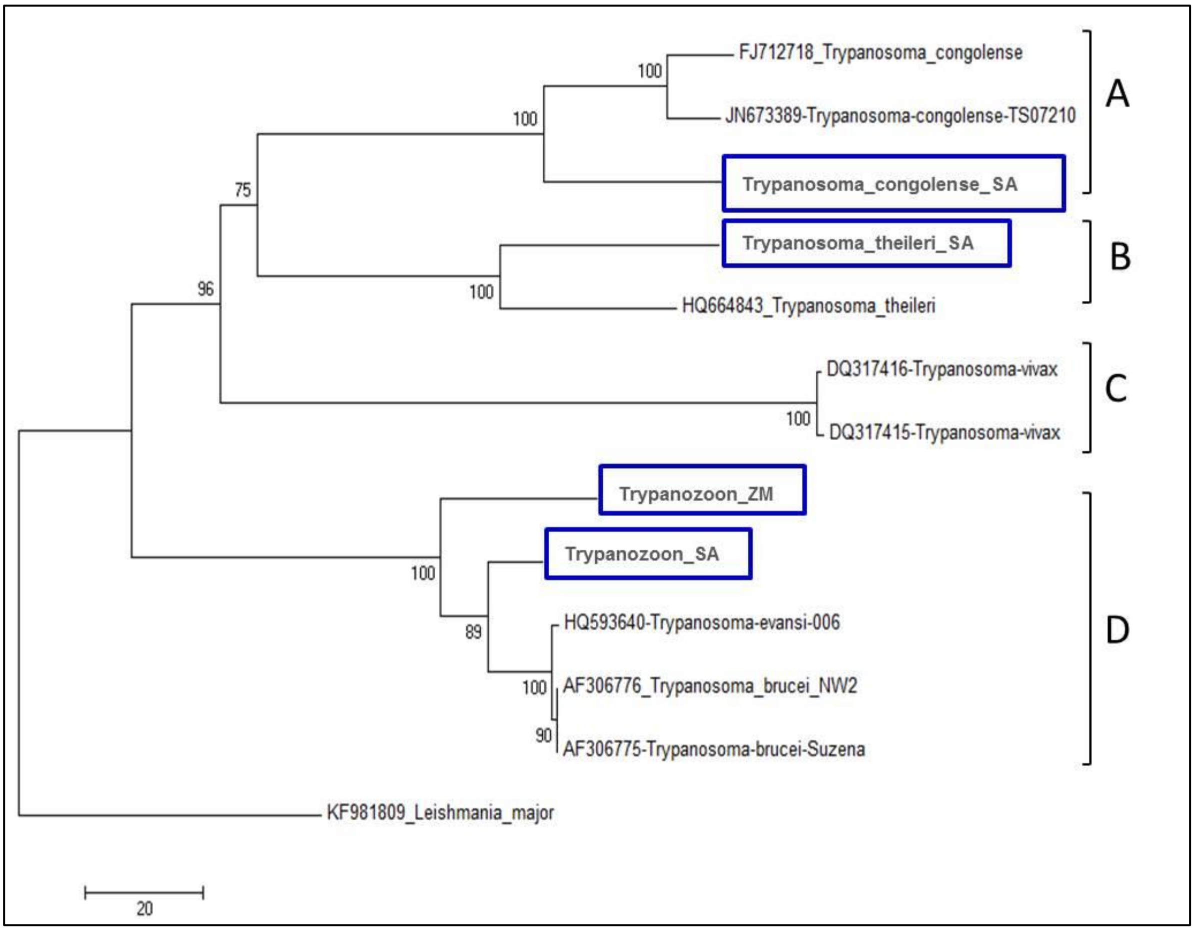


Figure 11: Neighbour-joining tree of *Trypanosoma* sequences with 1000 bootstrap replicates. Four major clades (A –D) were recovered namely, A the *Nannomonas* clade, B the *Megatrypanum* clade, C the *Duttonella* clade and D the *Trypanozoon* clade. In the blue rectangles are sequences that were obtanied in this study.

3.3.3 Detection of protozoan parasites from tabanid flies collected in Zambia

The 157 tabanid flies collected from Zambia, had a total of 35.03% (55/157) samples that tested positive for presence of *Besnoitia besnoiti* 2/157 (1.27%), *Babesia* spp. or *Theileria* spp. 39/157 (24.84%) and *Trypanosoma evansi* 14/157 (9.82%) by PCR. Only 1 sample of *Tabanus conspicuus* collected from Itezhi-tezhi district in Central Province was positive for *Babesia bigemina* and the remaining samples from Central Province were negative for the tested parasites. Eastern Province had the highest prevalence of the tested parasites with 54/156 (34.62%) from the sampled flies.

Polymerase chain reaction using *Besnoitia* species-specific primers BES-F and BES-R detected 1.27% (2/157) positive samples from the tested fly samples. Only samples from *Tabanus conformis* (2/4) were positive by PCR for the presence of *B. besnoiti* (Figure 12). Due to the low number of positively tested tabanid flies by PCR no statistical analysis was conducted for the prevalence of *B. besnoiti.* The BLASTn analysis showed that these two sequences matched with *Besnoitia besnoiti* from Israel [DQ227420] with 87% identity match score.

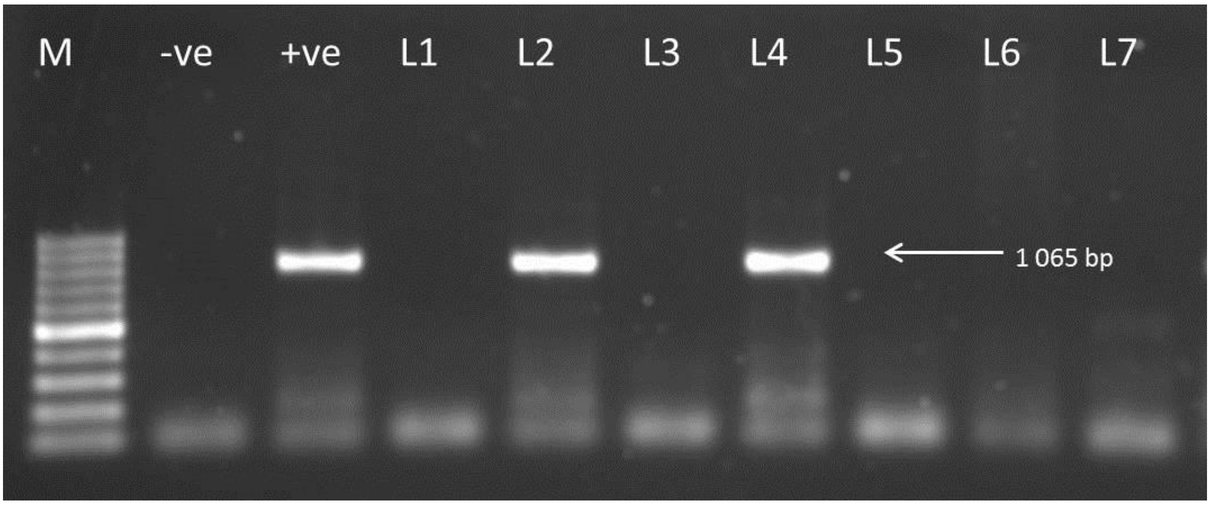


Figure 12: Gel image showing PCR amplification for *Besnoitia* DNA from Zambian tabanid flies. M is the molecular marker, -ve is for the no template control, +ve is the *Besnoitia besnoiti* positive control. L2 and L4 show the samples that tested positive for the presence of *Besnoitia* DNA. L1, L3, L5, L6 and L7 show samples that amplified below detection limit.

The haemoparasites specific primers (RLB-F2 and RLB-R2) targeting the *18S rRNA*-hypervariable region V4 of either *Babesia* or *Theileria* species was used to confirm if the two parasite species were present in the flies. Out of the 157 flies analysed, either *Babesia* or *Theileria-18S rRNA* fragment were detected in 24% (39) of the samples. In particular, *Babesia bigemina-18S rRNA* fragment was detected in 21.66% (34/157) of the flies whereas the gene fragment of *Theileria parva* was found in 3.18% (5/157) of the flies (Figure 13). All the 39 flies positive for either *B. bigemina* or *T. parva* genes were sampled from Mambwe district in Eastern Province. For *Atylotus agrestis* fly samples, 62.50% (10/16) were infected with the parasites whereas 100% (7/7) of *Atylotus diurnus* samples had the haemoparasites. Of the *Tabanus taeniola* samples analysed, 17.07% (7/41) were infected. *Tabanus taeniatus* and *Tabanus conspicuus* were the least infected with 3.90% (3/77) and 100% (1/1) respectively. There was no significant difference at *P* = 1.0994 (one tailed FET) in the prevalence of *Babesia bigemina* in all positively tested tabanid samples. The BLASTn match results showed that the *B. bigemina* sequences retrieved by RLB-PCR matched with *Babesia bigemina* isolate MT26 [KU206297] having 90% - 98% identity match score (Figure 14). The neighbour-joining tree for *Babesia* sequences obtained in this study is given in figure 15.

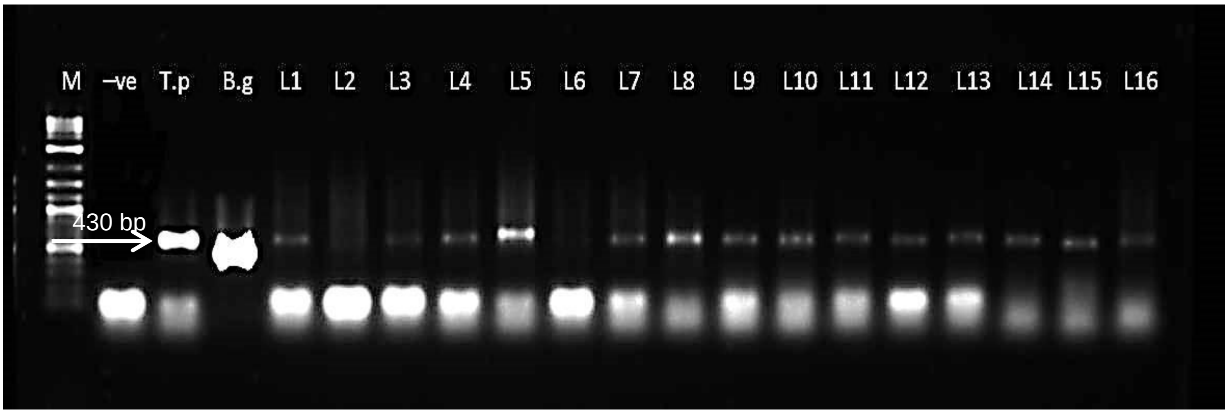
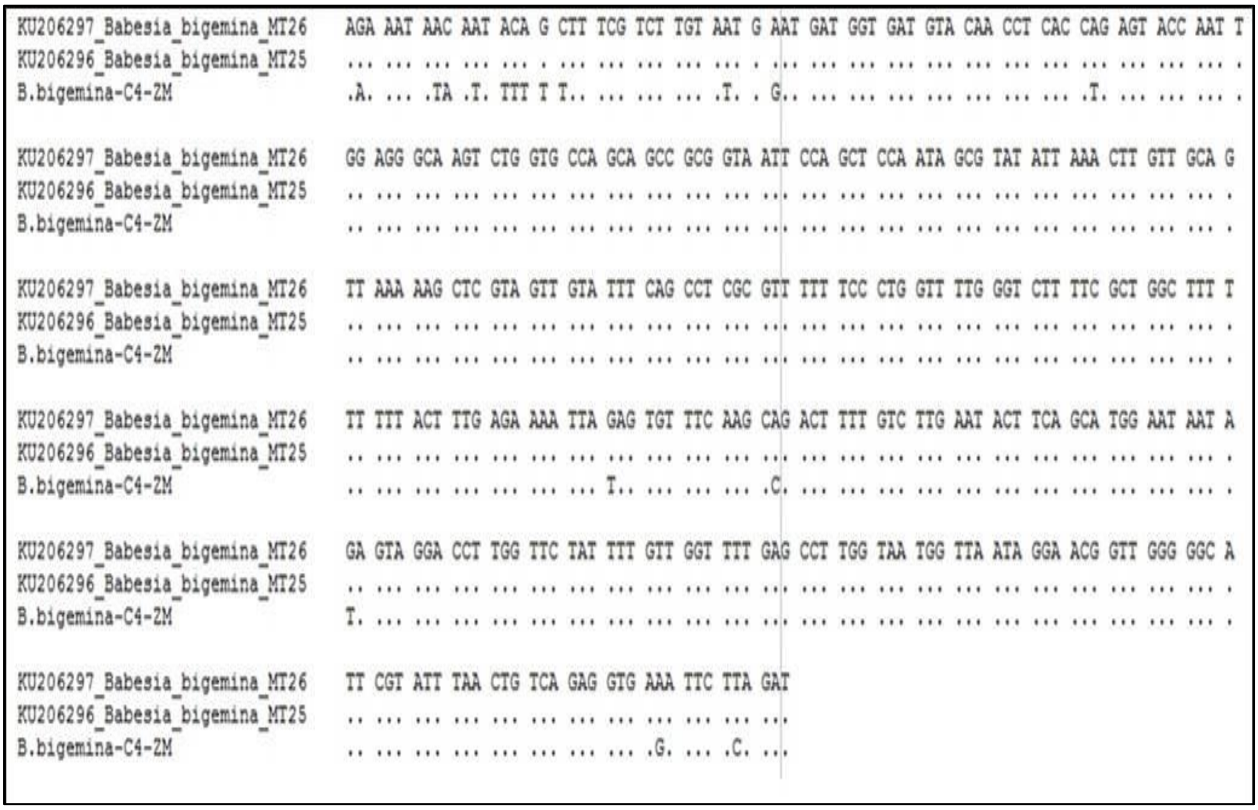


Figure 13: Gel image showing PCR amplification of piroplasmid parasite DNA. M is the molecular marker, -ve is for the no template control, T.p is the *Theileria parva* positive control and B.g is the *Babesia bigemina* positive control. L1 to L15 show samples positive for either *Babesia* or *Theileria* DNA. In L1 to L5 is *Atylotus diurnus* DNA, L6 to L10 is *A. agrestis*, L11 to L15 is *Tabanus taeniola.*



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KU206297_Babesia_bigemina_MT26   AGA AAT AAC AAT ACA G CTT TCG TCT TGT AAT G AAT GAT GGT GAT GTA CAA CCT CAC CAG AGT ACC AAT T
KU206296_Babesia_bigemina_MT25   ... ... ... ... ... . ... ... ... ... ... . ... ... ... ... ... ... ... ... ... ... ... ... .
B.bigemina-C4-ZM                 .A. ... .TA .T. TTT T T.. ... ... ... .T. . G.. ... ... ... ... ... ... ... .T. ... ... ... .

KU206297_Babesia_bigemina_MT26   GG AGG GCA AGT CTG GTG CCA GCA GCC GCG GTA ATT CCA GCT CCA ATA GCG TAT ATT AAA CTT GTT GCA G
KU206296_Babesia_bigemina_MT25   .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .
B.bigemina-C4-ZM                 .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .

KU206297_Babesia_bigemina_MT26   TT AAA AAG CTC GTA GTT GTA TTT CAG CCT CGC GTT TTT TCC CTG GTT TTG GGT CTT TTC GCT GGC TTT T
KU206296_Babesia_bigemina_MT25   .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .
B.bigemina-C4-ZM                 .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .

KU206297_Babesia_bigemina_MT26   TT TTT ACT TTG AGA AAA TTA GAG TGT TTC AAG CAG ACT TTT GTC TTG AAT ACT TCA GCA TGG AAT AAT A
KU206296_Babesia_bigemina_MT25   .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .
B.bigemina-C4-ZM                 .. ... ... ... ... ... ... T.. ... ... ... .C. ... ... ... ... ... ... ... ... ... ... ... .

KU206297_Babesia_bigemina_MT26   GA GTA GGA CCT TGG TTC TAT TTT GTT GGT TTT GAG CCT TGG TAA TGG TTA ATA GGA ACG GTT GGG GGC A
KU206296_Babesia_bigemina_MT25   .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .
B.bigemina-C4-ZM                 T. ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .

KU206297_Babesia_bigemina_MT26   TT CGT ATT TAA CTG TCA GAG GTG AAA TTC TTA GAT
KU206296_Babesia_bigemina_MT25   .. ... ... ... ... ... ... ... ... ... ... ...
B.bigemina-C4-ZM                 .. ... ... ... ... ... ... ... .G. ... .C. ...
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Figure 14: Sequence alignment for *Babesia bigemina* from Zambia when compared to other related *Babesia bigemina* strains (MT26 and MT25) from GenBank. The dots indicate identical nucleotide sequences.

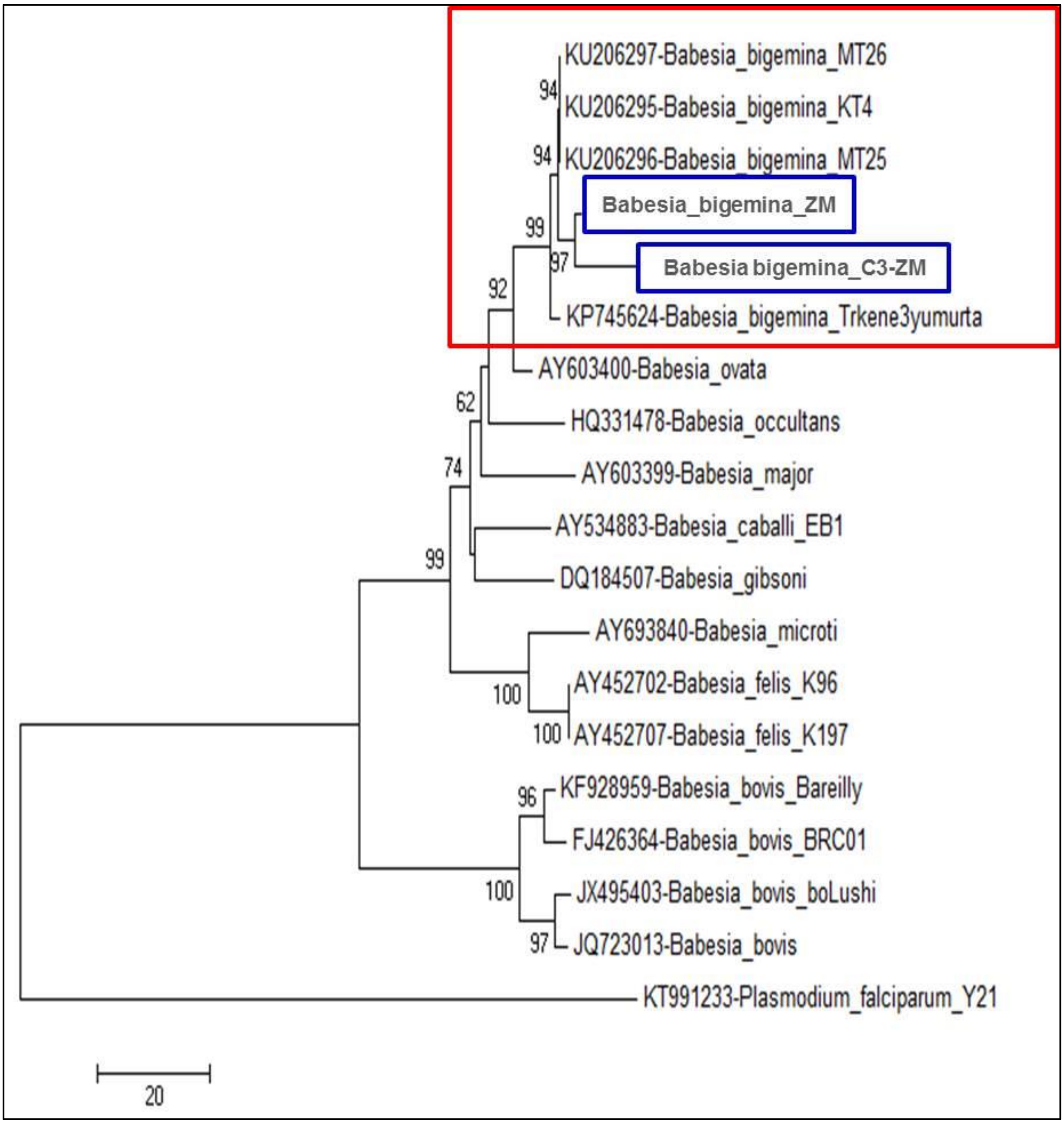
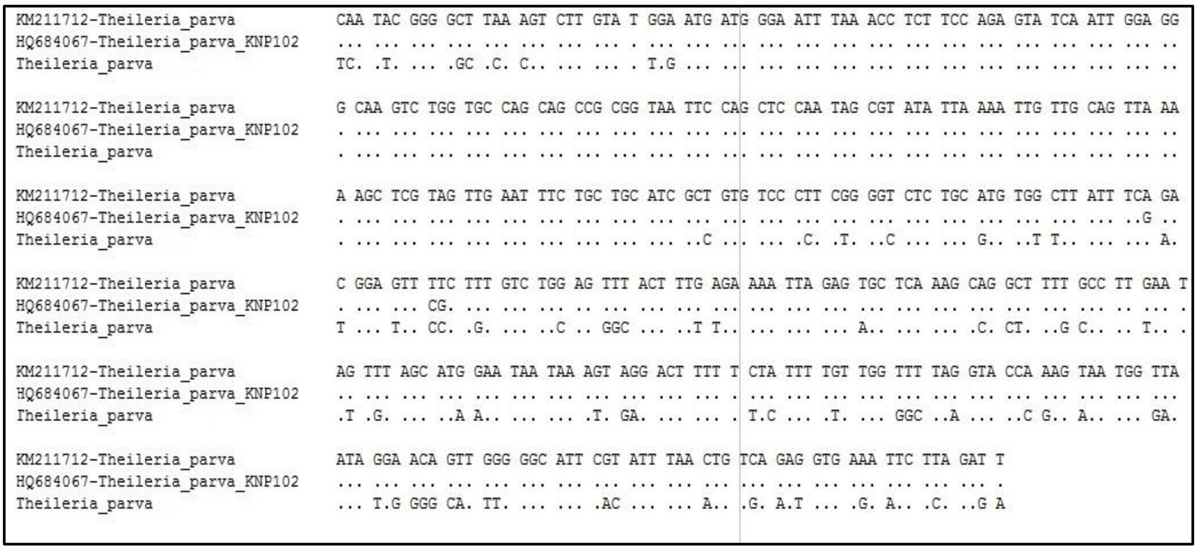


Figure 15: Neighbour-joining tree of *Babesia* sequences with 1000 bootstrap replicates. The red block indicates the cluster of *Babesia bigemina* sequences obtained from this study when compared to other *B. bigemina* from GenBank. In the blue rectangles are *B. bigemina* sequences found in this study.

Only 5 (3.81%) *Tabanus taeniola* samples tested positive for *Theileria* parasite. Therefore, because of the low number of the *T. taeniola* samples testing positive for *Theileria*, further meaningful statistical analysis was not necessary. Analysis using BLASTn confirmed sequence matches with *Theileria parva* isolate KNP102 [HQ684067] and *Theileria parva* [KM211712] with 87% to 89% identity match scores. The *T. parva*-like sequence was then aligned with the two *Theileria* sequences from GenBank to determine the identity similarities between the three sequences (Figure 16). The neighbour-joining tree for *Theileria* sequences obtained in this study is given in Figure

17. The detected piroplasmid parasites were submitted to GenBank under the accesion numbers KX870083, KX87004 and KX870085 for *B. bigemina* and KX870086 for *T. parva* respectively.



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KM211712-Theileria_parva          CAA TAC GGG GCT TAA AGT CTT GTA T GGA ATG ATG GGA ATT TAA ACC TCT TCC AGA GTA TCA ATT GGA GG
HQ684067-Theileria_parva_KNP102   ... ... ... ... ... ... ... ... . ... ... ... ... ... ... ... ... ... ... ... ... ... ... ..
Theileria_parva                   TC. .T. ... .GC .C. C.. ... ... . T.G ... ... ... ... ... ... ... ... ... ... ... ... ... ..

KM211712-Theileria_parva          G CAA GTC TGG TGC CAG CAG CCG CGG TAA TTC CAG CTC CAA TAG CGT ATA TTA AAA TTG TTG CAG TTA AA
HQ684067-Theileria_parva_KNP102   . ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ..
Theileria_parva                   . ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ..

KM211712-Theileria_parva          A AGC TCG TAG TTG AAT TTC TGC TGC ATC GCT GTG TCC CTT CGG GGT CTC TGC ATG TGG CTT ATT TCA GA
HQ684067-Theileria_parva_KNP102   . ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ..G ..
Theileria_parva                   . ... ... ... ... ... ... ... ... ... ..C ... ... .C. .T. ..C ... ... G.. ..T T.. ... ... A.

KM211712-Theileria_parva          C GGA GTT TTC TTT GTC TGG AG TTT ACT TTG AGA AAA TTA GAG TGC TCA AAG CAG GCT TTT GCC TT GAA T
HQ684067-Theileria_parva_KNP102   . ... ... CG. ... ... ... .. ... ... ... ... ... ... ... ... ... ... ... ... ... ... .. ... .
Theileria_parva                   T ... T.. CC. .G. ... ..C .. GGC ... ..T T.. ... ... ... A.. ... ... .C. CT. ..G C.. .. T.. .

KM211712-Theileria_parva          AG TTT AGC ATG GAA TAA TAA AGT AGG ACT TTT T CTA TTT TGT TGG TTT TAG GTA CCA AAG TAA TGG TTA
HQ684067-Theileria_parva_KNP102   .. ... ... ... ... ... ... ... ... ... ... . ... ... ... ... ... ... ... ... ... ... ... ...
Theileria_parva                   .T .G. ... ..A A.. ... ... .T. GA. ... ... . T.C ... .T. ... GGC ..A ... ..C G.. A.. ... GA.

KM211712-Theileria_parva          ATA GGA ACA GTT GGG GGC ATT CGT ATT TAA CTG TCA GAG GTG AAA TTC TTA GAT T
HQ684067-Theileria_parva_KNP102   ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... .
Theileria_parva                   ... T.G GGG CA. TT. ... ... .AC ... ... A.. .G. A.T ... .G. A.. .C. ..G A
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Figure 16: Sequence alignment for *Theileria parva* from Zambia when compared to other related *Theileria parva* from GenBank. The dots indicate identical *T. parva* nucleotide sequences.

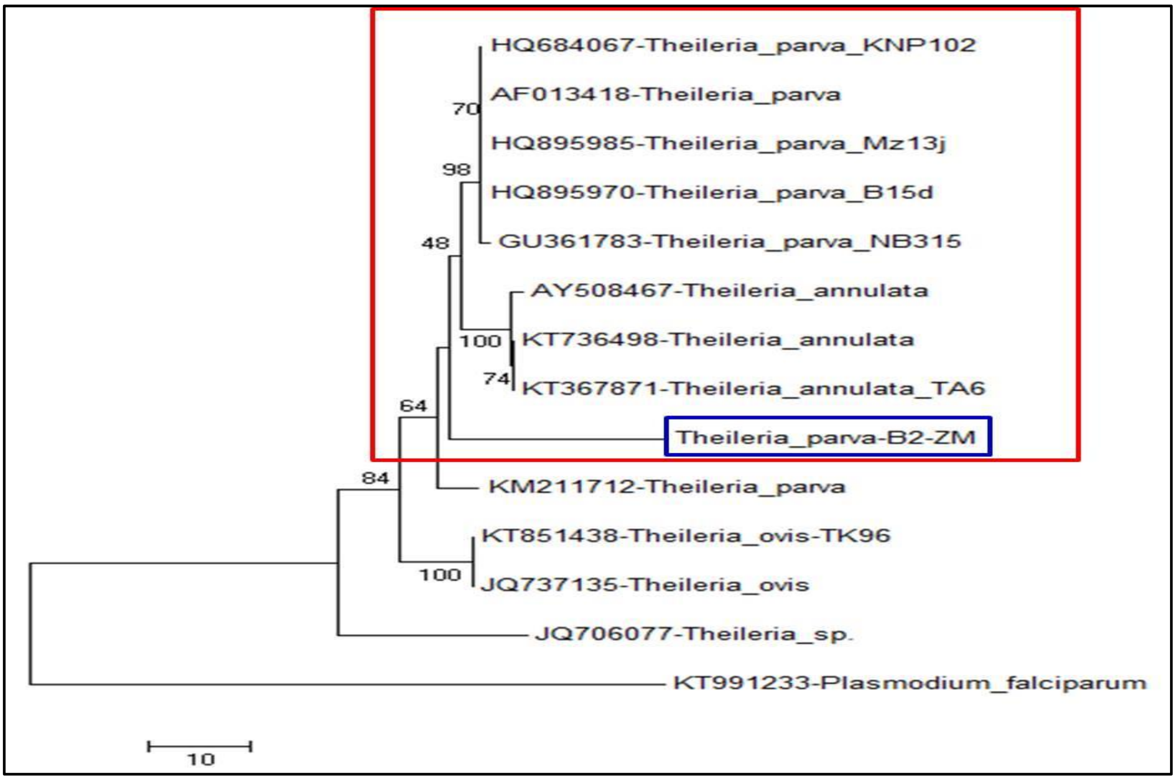

Figure 17: Neighbour-joining tree of *Theileria* sequences with 1000 bootstrap replicates. The red block indicates the phylogenetic position of *Theileria parva* sequence obtained in this study when compared to other *Theileria* sequences. In the blue rectangle is the *T. parva* seqence from this study.

PCR using trypanosome universal ITS1-CF and ITS1-BR primers had 9.82% (14/157) positive samples for the presence of *Trypanosoma* DNA. The trypanosome infections were only detected from samples collected from Eastern Province and detection was from *Tabanus taeniola* 17.07% (7/41) and *T. par* 87.50% (7/8) (Figure 18). There was a significant difference at *P* = 0.0007 (one tailed FET) in the prevalence of *Trypanosome* species in all positively tested tabanid samples*.* The BALSTn results showed that all sequences from positively tested samples by ITS-PCR matched with *Trypanosoma evansi* isolate 006 [HQ593640] with 89% to 99% identity match score (Figure 10). The *Trypanozoon* sequences from the Zambian samples were submitted to NCBI GeneBank under the accession numbers KX870081 and KX870082. A total of 75% (6/7) *Tabanus par* specimens from Zambia had mixed infections with *Babesia bigemina* and *Trypanozoon* as summarised in table 4.

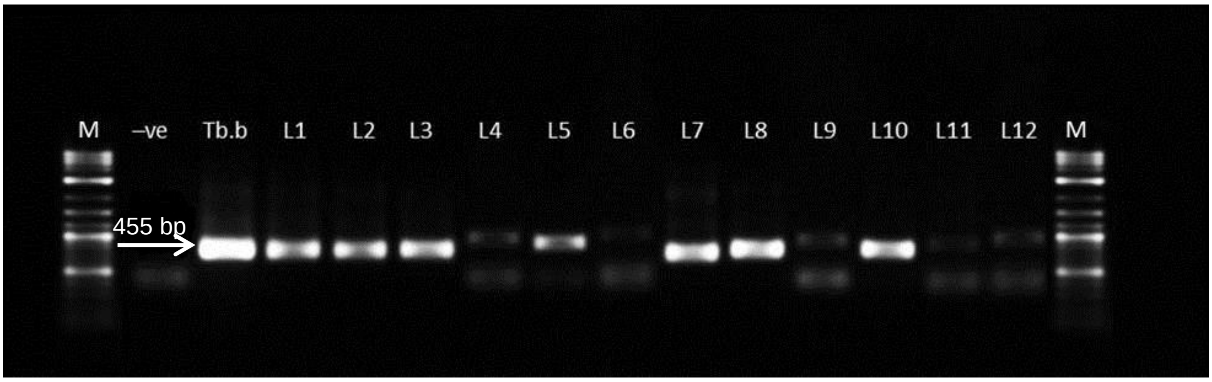

Figure 18: Gel image showing PCR amplification of *Trypanosoma* DNA from Zambian tabanid flies. M is the molecular marker, -ve is for the no template control, Tb.b is the *Trypanosoma brucei brucei* (GUTat 3.1) positive control. L1 to L12 show samples positive for presence of *Trypanosoma* DNA from Zambian samples.

Table 4: Prevalence of protozoan parasites detected from tabanid flies collected from Lesotho, South Africa and Zambia

Country	Species	*Babesia bigemina* (%)*	*Besnoitia besnoiti* (%)*	*Theileria parva* (%)*	*Trypanosoma congolense* (%)*	*Trypanozoon* species (%)*	*Trypanosoma theileri* (%)*	Total number of flies (N)*
Lesotho	*Atylotus nigromaculatus*	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2
South Africa	*Ancala africana*	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	13
	Atylotus agrestis	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	11
	Atylotus fuscipes	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	10
	Atylotus nigromaculatus	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	12
	Philoliche aethiopica	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	6
	Tabanus gratus	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	3
	Tabanus laverani	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	5
	Tabanus taeniatus	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	14
	Tabanus taeniola	0 (0)	0 (0)	0 (0)	10 (7.42)	0 (0)	7 (4.93)	142
	Tabunus par	0 (0)	0 (0)	0 (0)	6 (3.90)	1 (0.65)	8 (5.19)	154
Zambia	*Atylotus agrestis*	10 (62.50)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	16
	Atylotus diurnus	7 (100.0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	7
	Haematopota longa.	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	3
	Tabanus taeniatus	3 (3.90)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	77
	Tabanus taeniola	7 (17.07)	0 (0)	5 (12.20)	0 (0)	7 (17.07)**	0 (0)	41
	Tabanus par	6 (75.0)	0 (0)	0 (0)	0 (0)	7 (87.50)**	0 (0)	8
	Tabanus conspicuus	1 (100.0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1
	Tabanus conformis	0 (0)	2 (50.0)	0 (0)	0 (0)	0 (0)	0 (0)	4
Total								**529**

* Indicates the average prevalence of the tested pathogens from the positively tested tabanid flies

**Indicates the significance for the prevalence of the detected pathogens at $p<0.05$ calculated using Fisher's Exact Test by comparing the positively tested flies per pathogen detected.

3.4 Discussion

It is well known that tabanids are vectors of most livestock pathogens causing diseases such as anaplasmosis, anthrax, animal trypanosomiasis, bovine viral leukosis, equine infectious anaemia virus and filarial worms, tularaemia, hog cholera as well as vesicular stomatitis (Zumpt, 1949; Foil and Hogsette, 1994; Esterhuizen, 2006; Service, 2012; Baldacchino *et al*., 2014a). It has been recorded that there is a correlation between the abundance of tabanid flies and the prevalence of *Trypanosoma vivax* in Ethiopia (Sinshaw *et al*., 2006). During the 1960s in the United States of America it was reported that effects of tabanids in livestock production resulted in loses that amounted to more than US$30 million (Foil and Hogsette, 1994). This highlights the negative economic impact that these flies pose to livestock production in heavily infested areas.

In the current study four different protozoan pathogens have been detected by PCR. The first two animal parasites namely, animal *Trypanosoma* species and *Besnoitia besnoiti* are known to be mechanically transmitted by tabanid flies and *Stomoxys* flies however, the definitive host for bovine besnoitiosis is still unknown to date (Bigalke and Prozesky, 2004; Baldacchino *et al.,* 2013; Baldacchino *et al.,* 2014a; Hornok *et al.*, 2014). In Africa, bovine besnoitiosis has been reported to cause major economic losses in Angola, Cameroon, Botswana, Kenya, Namibia, South Africa, Sudan, Swaziland, Zaire and Zimbabwe. In South Africa, cases of the disease have been documented from the Free State, KwaZulu-Natal, Limpopo, Mpumalanga, North-West and Western Cape Province respectively (Bigalke and Prozesky, 2004). The detection of *Besnoitia* from only two specimens of *Tabanus conformis* may suggest that the two had fed on the same infected host prior to capture. However, despite the low prevalence of bovine besnoitiosis in Zambia and its absence from Lesotho and South African fly samples might suggest that the disease is re-emerging in the positive sampled area.

This study reports for the first time ever on the detection of *Babesia* species and *Theileria* species from tabanid flies collected in Zambia. Both parasites are known as tick-borne pathogens and their prevalence has been documented in both sampled countries (OIE, 2008; 2010; Yusufmia *et al.*, 2010; Williams *et al*., 2014). However, the latter studies were focused on the tick vectors or livestock. Furthermore, different genotypes from analysis based on the *18S rRNA* gene of these two tick-borne pathogens have been reported (Mtshali *et al*., 2014; Sivakumar *et al.*, 2014a; Mans *et* *al*., 2015). However, pathogenicity, virulence and cyclical vectors of these different variants are poorly understood.

Studies by Desquesnes and Dia (2003a; 2003b; 2004) have clearly demonstrated that mechanical transmission of *T. vivax* and *T. congolense* are highly possible by the tabanid fly *Atylotus agrestis* and *A. fuscipes*. *Trypanosoma evansi* on the other hand is known to be mechanically transmitted by biting flies and these may include *Stomoxys* and tabanids (Sumba *et al.,* 1998; Gutierrez *et al.,* 2010; Desquesnes *et al.,* 2013). It has been reported that trypanosomes can also develop within the midgut and hindgut of tabanid flies (Krinsky and Pechuman, 1975). In the current study, *T. congolense, T. theileri* and *Trypanozoon* sp. parasites were detected for the first time in *Tabanus par* and *T. taeniola* from South Africa and Zambia. The presence of *Trypanozoon* species such as *Trypanosoma brucei* and *T. evansi as* observed from BLASTn similarity matches have not been reported to occur in these countries and require further confirmation. Previous studies on the prevalence of trypanosome parasites have been conducted before in both countries however, all the analysis was focused on either tsetse flies or susceptible hosts (Van den Bossche, 2001; Mamabolo *et al*., 2009; Gillingwater *et al.,* 2010; Mwandiringana *et al.*, 2012; Motloang *et al.,* 2014). Moreover, in all studies conducted the infections were associated with the prevalence of tsetse fly as vector and excluding all other possible mechanical vectors. The prevalence of trypanosome parasites in countries where tsetse flies are absent, suggest that other haematophagous flies such as tabanid and *Stomoxys* flies are responsible for the transmission of these pathogens (Desquesnes *et al.,* 2013).

Mechanical transmission of trypanosomes by tabanid flies depends on numerous variables. Firstly, there has to be a high level parasitaemia of *Trypanosoma* in the host blood stream. Secondly, high density of potential mechanical vectors and close contact between the host animals and the vector flies (Desquesnes *et al.,* 2009). Thirdly, the biology of the flies is another contributing factor, for instance, the size of the fly mouthparts, whereby larger mouthparts of tabanid flies mechanically transmit more parasites as compared to smaller ones (Sumba *et al.,* 1998; Baldacchino *et al.,* 2013). Furthermore, the duration of parasite survival on the mouthparts is shorter (24 hours) as compared to inside the crop and the gut (5 to 7 days) and this would allow delayed transmission as the flies can regurgitate infected blood into the host (Baldacchino *et al.,* 2013). *Tabanus taeniola* has an average size of 22 mm as a result the mouthparts are fairly large and this enables them to be suitable mechanical transmission vectors. Additionally, the large size indicates that their flight patterns cover a bigger distance which further increases the chances that they can travel and transmit pathogens from one herd of animals to another.

The mere presence of *Babesia* and *Theileria* parasites DNA in tabanid flies from Zambia does not necessarily mean that they are vectors of the pathogens as any parasite can be taken up during a blood meal but factors such as the biology and size of the flies as well as the abundance of susceptible hosts may have an impact in making that particular fly a possible vector for these two pathogens that are known to be tick-borne (Azmi *et al*., 2016). This study has brought about new scientific information in the field of entomology and veterinary sciences in terms of possible neglected vectors of *Babesia*, *Besnoitia*, *Theileria*, *Trypanosoma* parasites in South Africa and Zambia. Although further studies are required this information calls for a re-evaluation of current vector control strategies as to whether tabanid flies should be monitored and included in arthropod vector control approaches.

CHAPTER 4

METAGENOMIC ANALYSIS OF GUT MICROBIOTA OF HORSE FLIES FROM SOUTH AFRICA AND ZAMBIA

4.1 Introduction

Prokaryotic organisms are by far the most abundant and diverse species on earth, estimated to be around 4 to 6 X10^{30} in total (Cowan *et al.,* 2009; Sleator *et al.*, 2008). These organisms have been known to have a significant impact on the evolution and speciation of interaction patterns in eukaryotic organisms (Kikuchi, 2009; Minard *et al.,* 2013). As a result, the interaction between arthropods and bacteria covers a broad range from symbiotic associations and strict parasitism to obligate mutualism (Minard *et al.,* 2013; Sassera *et al*., 2013).

These microbes in insects are known to alter the metabolic capacities that are not usually available to the host by (i) supplementing their nutrient poor diet which is commonly observed in haematophagous insects; (ii) aid in digestion of recalcitrant food particles as observed in cockroaches (Blattodea) or wood-feeding termites (Isoptera); and (iii) aid in protection against pathogens or parasites as in tsetse flies (Diptera) where it has been reported that the absence of *Wigglesworthia* symbionts result in an increase in trypanosome infections (Aksoy and Rio, 2005; Kikuchi, 2009; Gusmão *et al.*, 2010; Palavesam *et al.*, 2012; Engel and Moran, 2013; Sassera *et al.*, 2013). They are further known to affect the competence of insects as disease vectors and lastly they govern mating and reproductive systems (Synder *et al.*, 2010; Engel and Moran, 2013). Despite effects microbes have on insects they are also acknowledged for their role during biogeochemical cycling in natural and human-impacted ecosystems such as decomposition of plant biomass and carbon cycling as well as in rates of nitrogen fixation and nitrogen cycling (Engel and Moran, 2013).

There has been an increase in studies conducted on insect gut microbes for the past decades to better understand how these microbes influence the metabolism of insects (Engel and Moran, 2013). To achieve such analysis, culture dependent and independent methods have been utilized before (Yun *et al.*, 2014). Culture based methods are important for understanding the physiological characteristics of the bacteria (Gupta *et al.,* 2014). However, it was reported that culture dependent methods produce biased results and underestimates the bacterial diversity within insect guts, depending on the conditions and techniques employed (Gupta *et al.*, 2014; Yun *et al.*, 2014). It has additionally been suggested that in culture dependent methods, the main difficulty lies in recreating a complex physiochemical environment of the insect body hence most facilitative bacterial species are unculturable (Minard *et al.*, 2013). Nonetheless, some authors argue that the term unculturable is inappropriate in that correct culture conditions are yet to be discovered (Cowan *et al.*, 2009). As a result, recent advances in science have led to the use of insect cell lines or axenic media to culture some of the microbes from insects which were previously unculturable and leading to a revolution in studies of insect endosymbionts (Kikuchi, 2009).

Culture independent methods including quantitative PCR (qPCR), sequencing, molecular phylogenetic analysis and *in situ* hybridization as well as metagenomic analysis which targeted the *16S rRNA* gene have produced comprehensive associations between bacterial communities and insects (Schmeisser *et al.*, 2007; Kikuchi, 2009; Yun *et al.*, 2014). This resulted in an escalation of knowledge in understanding the dynamics of microbes living within insects. According to Yun and associates (2014), the utilization of recent advances in molecular biology and application of high-through-put next generation sequencing (NGS) to microbial ecology have shown that the diversity in microbial populations is significantly higher than previously estimated by culture-based and conventional methods. Unlike conventional molecular methods, metagenomics deals with the extraction, cloning into a suitable vector and sequencing analysis of the entire genetic complement of microbes of an organism or environmental sample (water, soil, gut content of vertebrates and or invertebrates), whereby it makes it possible to investigate a wide diversity of individual genes and their products as well as analysis of entire gene operations that encode for biosynthetic pathways (Handelsman, 2004; Schmeisser *et al.*, 2007).

By definition metagenomics is the study of collective genomes of members of a microbial community (Sabree *et al.*, 2009). This method involves cloning as well as analysing genomes of prokaryotes without culturing them, thereby, offering an opportunity to describe the most diverse microbial species on earth which cannot be cultured yet (Sabree *et al.*, 2009; Yun *et al.*, 2014). This novel technology initially started about a decade ago whereby it involved cloning of environmental DNA, followed by functional gene expression screening and was later supplemented by direct random shotgun sequencing of environmental DNA (Thomas *et al.*, 2012). According to Thomas and associates (2012), metagenomics provides access to functional gene composition of microbial communities and as such, offers a much broader description than phylogenetic surveys which are often based on the diversity of a single gene. Furthermore, it provides genetic information on potentially novel biocatalysts or enzymes, genomic linkages between function and phylogeny for uncultured microorganisms as well as evolutionary profiles of community function and structures (Thomas *et al.*, 2012). Metagenomic analysis is further supplemented by metatranscriptomics or metaproteomic approaches which describe the total complement RNA molecules that are present in a cell under specific conditions (Handelsman, 2004; Sabree *et al.*, 2009; Thomas *et al.*, 2012; Nijhof, 2015). In metatranscriptomics analysis, functional novel antibiotics, antibiotic resistance as well as degenerative enzymes can be expressed (Handelsman, 2004). However, a significant drawback involved with this analysis is that, not all selected metagenomic genes are expressed in any particular host bacterium selected for cloning and as a result non-expressed genes are never represented (Handelsman, 2004; Schmeisser *et al*., 2007; Nijhof, 2015). Most genes have expression requirements and may not be expressed in the *Escherichia coli* cloning vector, and this has led to an increase in the range of cloning vectors such as *Streptomyces lividans* and *Pseudomonas putida* as alternative hosts (Schmeisser *et al*., 2007).

Analyses to detect gut microbes have been conducted from most economically important insect orders namely: Archaeognatha (bristletails), Blattaria (cockroaches), Coleoptera (specifically weevils), Dermaptera (earwigs), Diptera (fruit flies), Hemiptera (assassin and stink bugs), Hymenoptera (specifically honey bees) as well as Isoptera (wood termites) and Lepidoptera (moths) to investigate the general patterns in gut microbes composition as well as their symbiotic associations in some of the above mentioned orders (Sleator *et al.*, 2008; Sabree and Moran, 2014; Yun *et al.,* 2014).

Metabarcoding analysis to detect gut microbes targeting the *16S rRNA* hypervariable region V3 – V4 from tabanid flies using an Illumina MiSeq platform was conducted in the current study. It is for the first time metagenomic sequence analysis is conducted on different tabanid flies collected from South Africa and Zambia. Despite the fact that samples were collected from two different countries and with different climatic and environmental conditions it is however hypothesised that, the microbial composition of different tabanid flies will be dominated by similar bacterial phyla. It is further hypothesised that, similar to other haematophagous flies, the tabanid flies also harbour symbiotic bacteria and as such the following specific objectives were set:

- To determine gut microbial composition of different tabanid flies collected from South Africa and Zambia using *16S rRNA* based metabarcoding on an Illumina MiSeq platform

- To identify symbiotic, commensalistic, mutualistic or parasitic gut bacteria of tabanids as well as those of medical and veterinary importance.

4.2 Materials and methods

4.2.1 Tabanid fly samples

A total of 19 tabanid flies were used in the current study, whereby, 7 fly specimens were collected in South Africa and 12 were collected in Zambia. Samples from South Africa were: *Atylotus agrestis* (n=2) (see chapter 2 Figure 7B 1-4 for images), *Tabanus gratus* (n=1) (see chapter 2 Figure 7G 1-4 for images), *T. par* (n=2) (see chapter 2 Figure 7J 1-4 for images) and *T. taeniola* (n=2) (see chapter 2 Figure 7K 1-4 for images). All flies from South Africa were caught using H-traps (see chapter 2 Figure 6a for images) at Charters Creek game reserve.

Flies from Zambia were collected from Eastern (Mambwe district) Province (see chapter 2, Figure 5 for map of sampled area). Fly specimens were captured using Epsilon traps (see chapter 2 Figure 6a for images) and they comprised of *Tabanus conformis* (n=3) (see chapter 2 Figure 7M 1-4 for images), *T. par* (n=3), *T. taeniola* (n=3) and *Atylotus diurnus* (n=3) (see chapter 2 Figure 7C 1-4 for images) respectively. No samples from Lesotho were included in this analysis due to small sample number and poor DNA quality.

4.2.2 DNA extraction

Deoxyribonucleic acid extracted from tabanid fly gut using Qiagen DNeasy Blood & Tissue Kit (QIAGEN, Hilden, Germany) was conducted according to manufacturer's instructions. Tabanid fly specimens were dissected and the whole gut removed. The gut was then washed twice with 70% ethanol and once with double distilled water (ddH$_2$O) to remove any contaminants. The gut was then homogenised in a mixture containing 180 µl of Buffer ATL and 20 µl of proteinase K, vortexed and incubated at 56°C until completely lysed. The incubated samples were vortexed occasionally during incubation thereafter the samples were vortexed for an additional 15 seconds. Two hundred microliters of Buffer AL was added, the samples mixed by vortexing and incubated at 56°C for 10 minutes. Thereafter, 200 µl of absolute ethanol was added and again the samples were mixed by vortexing. Then, the mixture was transferred into DNeasy Mini spin column placed in a 2 ml collection tube, centrifuged at 8 000 rpm for 1 min and the flow-through discarded. The 2 ml collection tube was replaced and 500 µl of Buffer AW1 was added, centrifuged at 8 000 rpm again for a minute. The flow-through and the collection tube were discarded. The spin column were transferred into new 2 ml collection tube thereafter, 500 µl of Buffer AW2 was added and the tubes were centrifuged for 3 minutes at 14 000 rpm. The flow-through was again discarded and the spin columns transferred into new 1.5 ml Eppendorf tubes where the DNA was eluted with 200 µl of Buffer AE. The samples were subsequently allowed to stand at room temperature for a minute. Subsequently the samples were then centrifuged for a minute at 8 000 rpm and this step was repeated to increase the DNA yield. The concentration of extracted DNA was measured using Qubit ® 3.0 Fluorometer (Life Technologies, California, USA) then stored at -4°C until used.

4.2.3 The *16S rRNA* library preparation workflow

4.2.3.1 Initial amplicon PCR

The initial amplicon PCR was conducted to amplify the targeted DNA out from a DNA sample using specific primers with overhanging adaptors. The PCR reaction contained 12.5 µl of 2X KAPA Hifi HotStart ReadyMix [composed of KAPA HiFi HotStart DNA Polymerase (1 U/µL), Fidelity Buffer (5X), GC Buffer (5X), high-quality dNTPs (10 mM each) and $MgCl_2$ (25 mM)] (KAPA Biosystems, Massachusetts, USA), 5 µl of each primer and lastly 2.5 µl of microbial DNA. The reaction had a final volume of 25 µl in 96-well PCR plates (Illumina, 2013). The PCR conditions involved an initial one cycle done at 95°C for 3 minutes followed by 25 cycles of denaturation at 95°C for 30 seconds, annealing at 55°C for 30 seconds and extension at 72°C for 30 seconds. Thereafter, a final one cycle of extension was done at 72°C for 5 minutes followed by a hold temperature at 4°C pending further analysis. One micro liters of the PCR product was ran using Bioanalyzer DNA 1000 (Agilent Technologies, Waldbronn, Germany) to visualize the size. The 470 bp was verified using the V3 and V4 primer pairs from the protocol. The primers included the 341F forward primer (TCG TCG GCA GCG TCA GAT GTG TAT AAG AGA CAG CCT ACG GGN GGC WGC AG) and 805R reverse primer (GTC TCG TGG GCT CGG AGA TGT GTA TAA GAG ACA GGA CTA CHV GGG TAT CTA ATC C) with added Illumina adapter overhang sequences, namely, Forward overhang: TCG TCG GCA GCG TCA GAT GTG TAT AAG AGA CAG and Reverse overhang: GTC TCG TGG GCT CGG AGA TGT GTA TAA GAG ACA G, respectively.

4.2.3.2 Initial PCR clean-up

The amplicon PCR plate was centrifuged at 3, 500 rpm for one minute at temperate of 20°C. AMPure XP beads were were exposed to room temperature and then vortexed for 30 seconds to ensure that the beads are evenly dispersed (Illumina, 2013). Twenty micro litres of AMPure XP beads were added to each PCR amplicon in the plate using a multichannel pipette. The samples were incubated at room temperature for 5 minutes without shaking. The plate was placed on a magnetic stand for 2 minutes. Subsequently, the supernatant was removed with a multichannel pipette and discarded. The amplicon PCR plate was washed twice with 200 µl of freshly prepared 80% ethanol then incubated for 30 seconds on the magnetic stand and the supernatant was discarded as before. A P20 multichannel pipette was used to remove excess ethanol. Subsequently, the amplicon PCR plate was air dried at room temperature for 10 minutes, thereafter, the amplicon PCR plate was removed from the magnetic stand and 52.5 µl of 10 mM Tris, pH 8.5 was added to each amplicon. Thereafter, the amplicon PCR plate was incubated at room temperature for 2 minutes then placed on a magnetic stand until the supernatant was dissolved. Then 50 µl of the supernatant was transferred into a new 96-well plate.

4.2.3.3 Index PCR

A total of 5 µl of the PCR amplicon was transferred into a new 96-well plate and the remaing 45 µl was stored for further analysis. The index primers 1 and 2 were arranged according to the following order; Index 2 primer tubes with white caps were vertically aligned from A to H whereas, the Index 1 primer tubes with orange caps were horizontally aligned from 1 to 12 in the TruSeq Index Plate Fixture (Illumina, 2013). Subsequently, the 96-well plate with the 5 µl re-suspended PCR amplicon were placed in the TruSeq Index Plate Fixture. Subsequently, a 50 µl mixture containing 5 µl of Nextera XT Index Primer 1 (N7xx), 5 µl Nextera XT Index Primer 2 (S5xx), 25 µl of 2X KAPA HiFi HotStart Ready Mix [composed of KAPA HiFi HotStart DNA Polymerase (1 U/µL), Fidelity Buffer (5X), GC Buffer (5X), high-quality dNTPs (10 mM each) and $MgCl_2$ (25 mM)] (KAPA Biosystems, Massachusetts, USA) and 10 µl of PCR grade water was prepared. The contents were mixed thoroughly and the plate was covered with a Micro-seal 'A' then centrifuged at 3 500 rpm for 1 minute at 20°C. The PCR conditions were set as follows; 95°C for 3 minutes followed by 8 cycles of 95°C for 30 seconds, 55°C for

30 seconds, 72°C for 30 seconds and a final elongation step of 72°C for 5 minutes with holding temperature at 4°C.

4.2.3.4 PCR clean-up 2

AMPure XP beads were used for this clean-up. The Index PCR plate was centrifuged at 2 500 rpm at 20°C for 1 minute. As done before in the first clean-up, the AMPure XP beads were vortexed for 30 seconds to ensure that they are evenly dispersed (Illunima, 2013). A total of 56 µl of AMPure XP beads were added and thoroughly mixed into each well of the Index PCR plate. The Index PCR plate was then incubated at room temperature for 5 minutes. The Index PCR plate was then placed on a magnetic stand for 2 minutes. Once again, a multichannel pipette was used to remove and discard the supernatant while the Index PCR plate was on the magnetic stand. Subsequently, the beads were washed with 200 µl of freshly prepared 80% ethanol and incubated for 30 seconds on the magnetic stand. The supernatant was then removed and discarded. The 80% ethanol wash step was repeated twice afterwhich, the Index PCR plate was air dried for 10 minutes while on the magnetic stand. The Index PCR plate was then removed and 27.5 µl of 10 mM Tris was added and mixed thoroughly into each well. The Index PCR plate was subsequently incubated at room temperature for 2 minutes and then placed on a magnetic stand for 2 minutes. About 25 µl of the supernatant from the Index PCR plate was transferred into a new 96-well plate, sealed with Micro-seal 'B' and stored at -25°C.

4.2.3.5 Library quantification, normalization and pooling

Firstly, DNA concentration was calculated and converted to nano molar (nM) as determined by an Agilent Technologies 2100 Bioanalyzer trace (Agilent Technologies, Waldbronn, Germany):

$$\frac{(\text{Concentration in ng/ml})}{(660\ \text{g/mol x average library})} \quad \text{X}\ 10^{6} = \quad \text{concentration in nM}$$

The determined concentrations were diluted with Tris pH 8.5 to 4 nM for the library preparation (Illumina, 2013). From each library, 5 µl of the diluted DNA were mixed for pooling libraries with unique indices.

4.2.3.6 Library denaturation and MiSeq sample loading

Heat block suitable for 1.7 ml microcentrifuge tubes was set to 96°C. MiSeq v3 reagent cartridge (Illumina, USA) was thawed at room temperature and ice water bath containing 3 parts of ice and 1 part of water was prepared (Illumina, 2013). Subsequently, 5 µl of freshly diluted 0.2 N NaOH was added to 5 µl of 4 nM pooled library. Samples were briefly vortexed and centrifuged at 2 500 rpm at 20°C for a minute and incubated at room temperature for 5 minutes to allow all DNA to denature into single strands. Finally, 990 µl of pre-chilled HT1 was added into 10 µl of the denatured DNA and the samples were placed on ice until final dilution stage.

4.2.3.7 Denaturation and dilution of PhiX control

During this part of the experiment, 2 µl of 10 nM PhiX library was mixed with 3 µl of 10 mM Tris pH 8.5. Thereafter, 5 µl of 4 nM PhiX library and 5 µl of 0.2 N NaOH were mixed in a microcentrifuge tube and briefly vortexed. Then the samples were incubated for 1 minute at room temperature to denature the PhiX library into single strands. To produce 20 pM PhiX library, 10 µl of denatured PhiX library was added into 990 µl of pre-chilled HT1, the samples were then mixed by inverting several times, pulse centrifuged and placed on ice. Subsequently, the two libraries were combined by adding 30 µl of the denatured and diluted PhiX control with 570 µl of denatured and diluted amplicon library, and then placed on ice (Illumina, 2013). Using a heat block the combined library and PhiX control were incubated at 96°C for 2 minutes, then inverted twice and placed on ice for 5 minutes. Samples were then loaded into MiSeq flow cell (Illumina, USA) and analysed using the MiSeq Reported Software (MRS) using the metagenomics workflow option from the MiSeq system.

4.2.4 Metagenomic data preparation

Generated metagenomic sequences were recovered in FASTQ format from the MiSeq system. FastQC Highpoint Sequence QC Report Version: 0.11.4 was used to determine the quality of the individual FASTQ sequences. For bioinformatics analysis Mothur Open Source expandable software was used (Schloss *et al.*, 2009). However, before the analysis started the following files had to be preinstalled: SILVA-based bacterial reference database and Mothur-formatted RDP set (version 9).

4.2.4.1 FASTQ sequence extraction

A spread sheet with three columns containing the sample code name in the first column, the name of the forward read in the second and the name of the reverse read in the third column was created. The excel file was then saved as a CSV comma delimited file. On Mothur, the two sets of reads for each sample were combined by first making a reverse compliment for the reverse read and subsequently, joining the contigs. The maximum length for consensus sequence reads was 470 bp long and the minimum 460 bp. Then, sequences that had ambiguous bases or were shorter than 460 bp were removed.

4.2.4.2 Processing improved sequences

All sequences that were identical to one another and considered duplicates were merged. This aided in significantly reducing the number of sequences. Retrieved sequences were aligned against a reference alignment. On the SILVA reference database, all sequences were expected to start at position 6428 and end at position 23444 against the reference sequence. Subsequently, sequences that started at or before position 6428 and end at or after position 23444 were removed from the alignment. Trimmed sequences were then split into groups and sorted by abundance from most abundant to the least. Using the UCHIME algorithm the chimeras within sequences were removed with reference to the most abundant sequences. For the final quality control step, the first step was to ensure that all sequence generated are from prokaryotes and nothing more. A Bayesian classifier was used for this analysis. Finally, the sequences were ready to be checked for error rates.

4.2.4.3 Assessing error rates

The remaining sequences were clustered into operational taxonomic units (OTUs). These OTUs are used to classify groups of closely related individuals or clusters of microorganisms grouped by sequence similarities of a specific taxonomic marker gene (Blaxter *et al.*, 2005).

4.2.4.4 Preparing for analysis

Firstly, the OTUs were clustered into phylotypes by using taxonomic information of order and family to split the sequences into bins and then cluster within each bin. Afterwards, the taxonomy for each OTU was determined. The phylotypes of the different OTUs were then arranged from Kingdom to Genus level.

4.2.5 Metagenomic data analysis

4.2.5.1 Alpha diversity measurements

Focusing on the OTU-based dataset, refraction curves describing the number of OTUs observed was calculated to measure the diversity within the analysed data. Afterwards, the Inverse Simpson diversity estimator was ran to standardize the dataset randomly selecting sequences for each sample 1000 times and calculating an average for each run.

4.2.5.2 Beta diversity measurements

The membership and structure of various samples using an OTU-based approach was compared. A heatmap of the relative abundance of each OTU across samples with log2 scaling was constructed. Subsequently, similarities between memberships and structures found in different samples were calculated. Subsequently, a Venn diagram to describe the shared bacterial species of the different sample groups to each other was constructed.

4.3 Results

4.3.1.1 Metagenomic analysis of South African tabanid fly gut DNA

Analysis of gut microbes from South African tabanid flies (n = 7) revealed a total of 407 689 assembled sequences. The sequences were then truncated to 12 915 and after aligning them to the SILVA bacteria reference alignment tool, only 11 442 reads remained with 10 586 reads revealing unique sequences (Table 5). A total of 505 OTUs were produced in the final analysis (Appendix III) and BLASTn similarity match of 97% to 100% were considered noteworthy.

Table 5: Number of sequences from South African fly samples used to produce OTUs

Tabanid fly	Tabanid name	Sample code	Number of sequences assembled	Number of sequences aligned	Total number of OTUs
1	*Atylotus agrestis*	Aagr_3or	83546	2019	505
2	*Atylotus agrestis*	Aagr_5or	77131	3046	505
3	*Tabanus gratus*	Tgra_8or	108140	2795	505
4	*Tabanus par*	Tpar_6or	21606	1324	505
5	*Tabanus par*	Tpar_7or	17533	103	505
6	*Tabanus taeniola*	Ttae_1or	62693	1599	505
7	*Tabanus taeniola*	Ttae_2or	37040	556	505
Total			**407689**	**11442**	

4.3.1.2 Classification of South African tabanid fly OTUs

There were a total of 7 phyla recovered from South African tabanid flies (Figure 19). The most abundant phylum was Proteobacteria (44.55%) followed by unclassified bacteria with 37.08%. The other important detected phyla included Tenericutes (8.91%), Firmicutes (7.33%) and Bacteroidetes (1.98%). The remaining phyla namely, Verrucomicrobia and TM7 (referred to as Saccharibacteria) had an abundance of 0.20%.

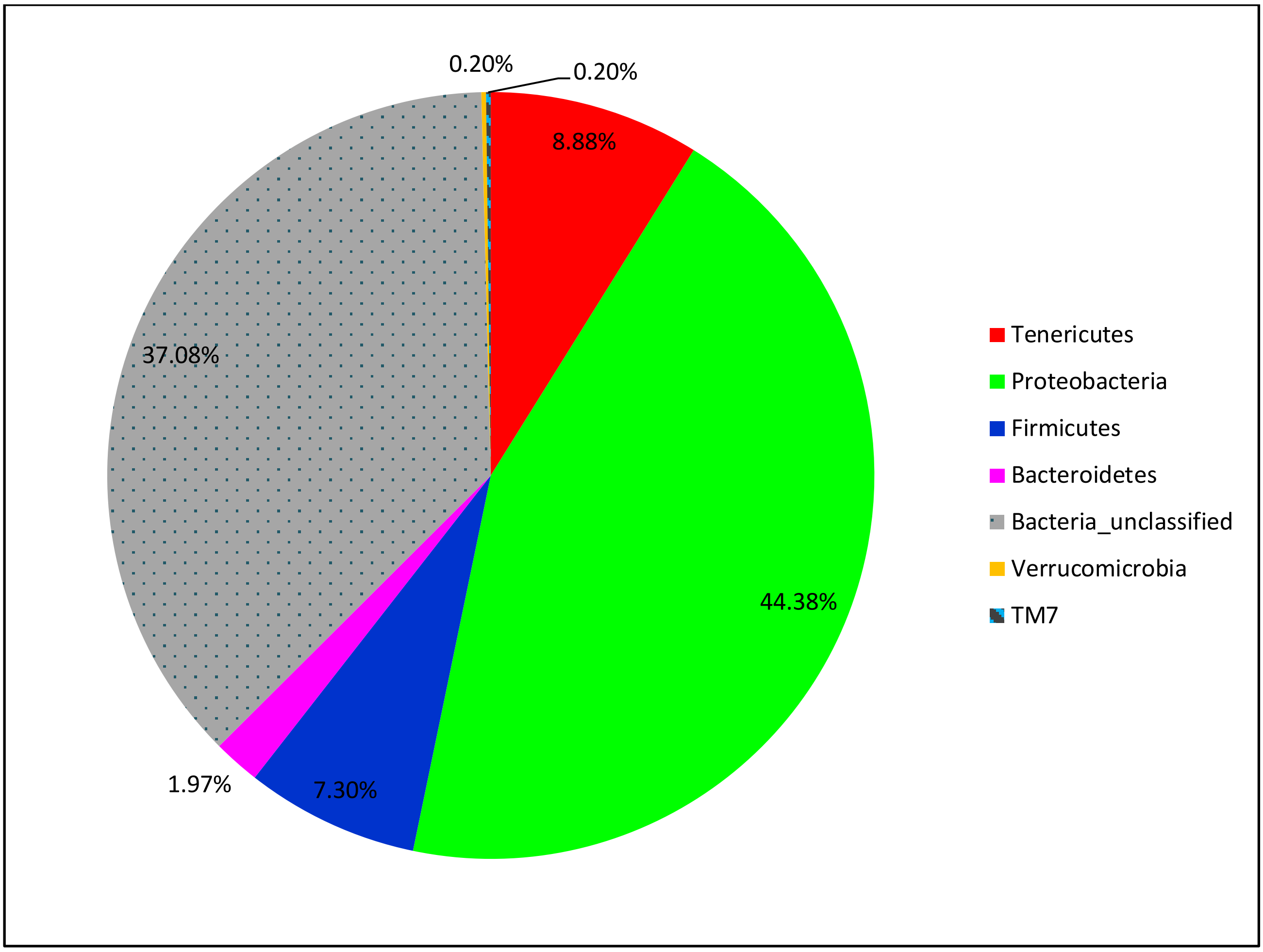

Figure 19: The proportions of bacterial phyla detected from South African tabanid flies.

A total of 13 bacterial classes with 3 classes being unclassified were obtained. The prevailing classes included Gammaproteobacteria (37.82%), Mollicutes (8.91%), Bacilli (6.73%) and Betaproteobacteria (1.78%). The unclassified bacteria contributed 37.23% followed by unclassified Proteobacteria with 4.55%. All remaining classes were relatively low ranging from 0.20% to 0.99% (Figure, 20). These less abundant bacterial classes included Bacteroidia, Opitutae and Sphingobacteria, Clostridia, Flavobacteria as well as TM7 class.

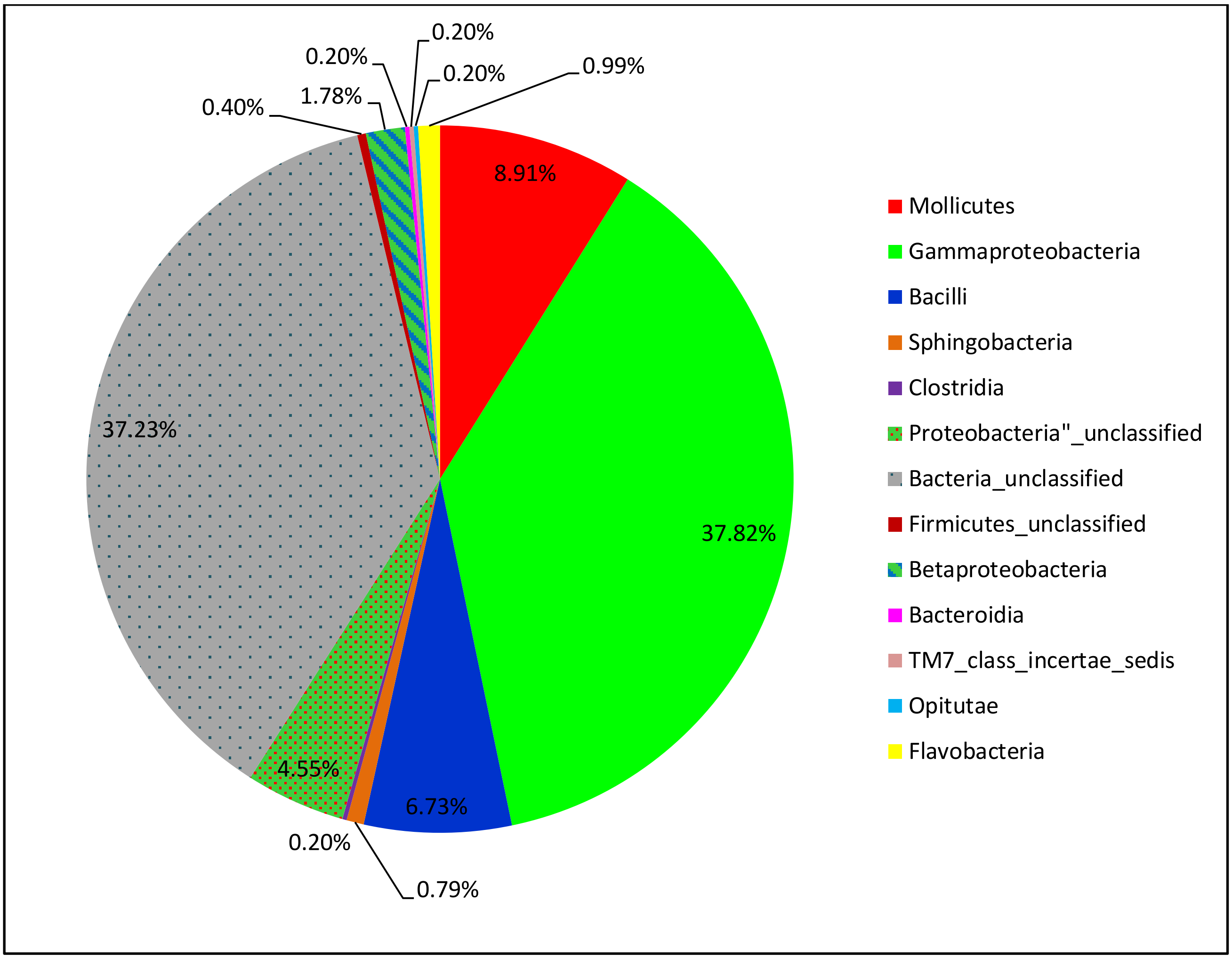

Figure 20: The proportions of bacterial classes detected from South African tabanid flies.

A total of 20 bacterial orders were obtained. The dominant bacterial orders included Enterobacteriales with 15.61% followed by Entomoplasmatales (8.67%) and Bacillales (6.17%). However, unclassified bacteria were the most abundant with 36.22%, unclassified Gammaproteobacteria (17.53%) and unclassified Proteobacteria (4.43%). All bacterial orders that had (≤ 10 members) low representatives were grouped as other and all contributed 5.63% of the total bacterial orders detected (Figure 21). These included Sphingobacteriales, Clostridiales, Oceanospirillales, Xanthomonadales, Burkholderiales, Bacteroidales, Flavobacteriales, TM7_order_incertae_sedis, Neisseriales, Opitutales as well as unclassified Firmicutes and unclassified Bacilli respectively.

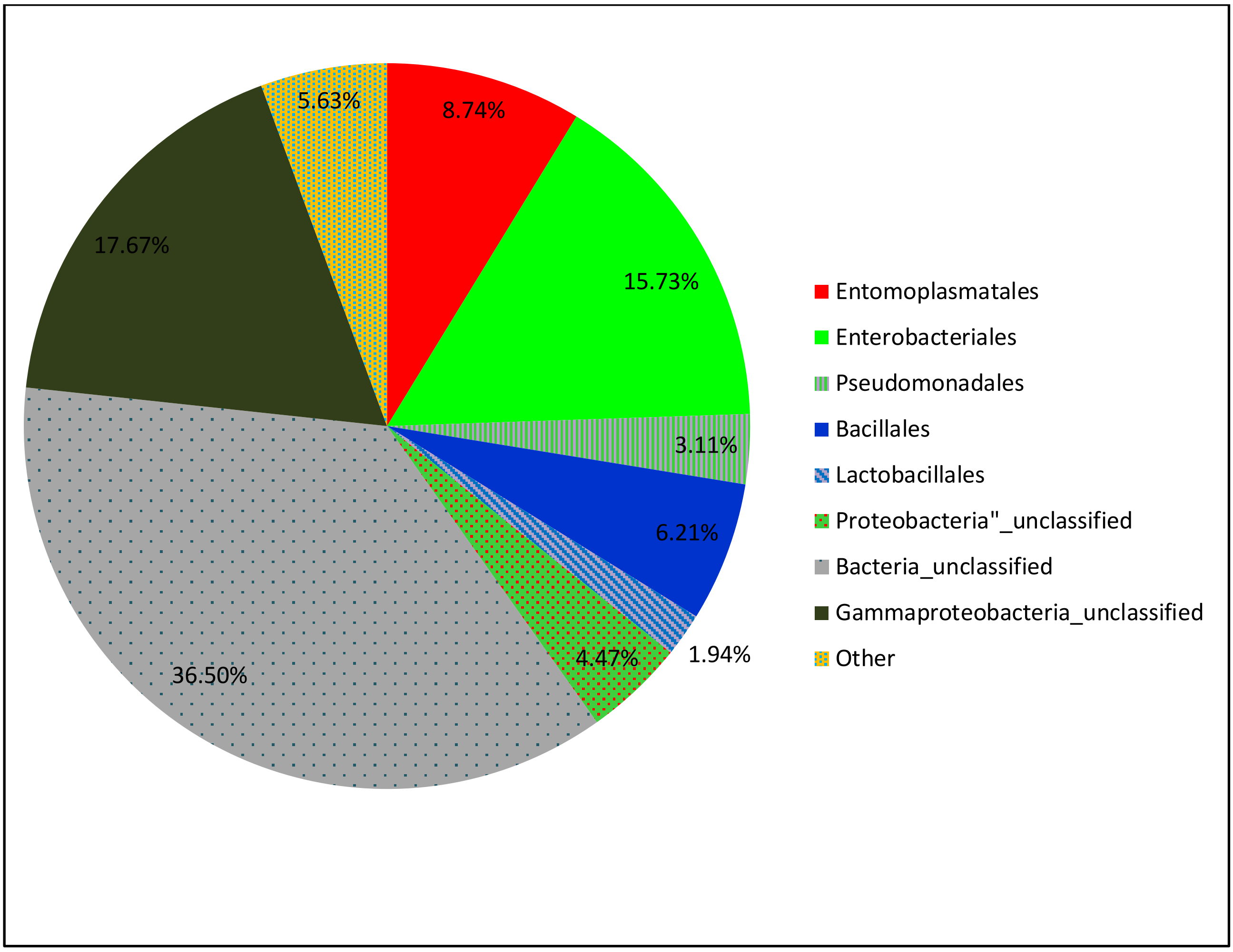

Figure 21: The proportions of bacterial orders detected from South African tabanid flies.

Abundant bacterial families detected from South African tabanid flies included Enterobacteriaceae, Spiroplasmataceae, Bacillaceae, Staphylococcaceae as well as Moraxellaceae as Pseudomonadaceae (Figure 22). Additionally, all bacterial families with ≤ 20 representative members were grouped as other and these included Comamonadaceae, Xanthomonadaceae, Halomonadaceae, Sphingobacteriaceae, Aerococcaceae, Streptococcaceae, Listeriaceae as well as Flavobacteriaceae. The unclassified families of Gammaproteobacteria, Proteobacteria and unknown bacteria were also observed. The families Enterobacteriaceae, Moraxellaceae and Spiroplasmataceae were detected in all sampled flies with variable abundance observed among all flies.

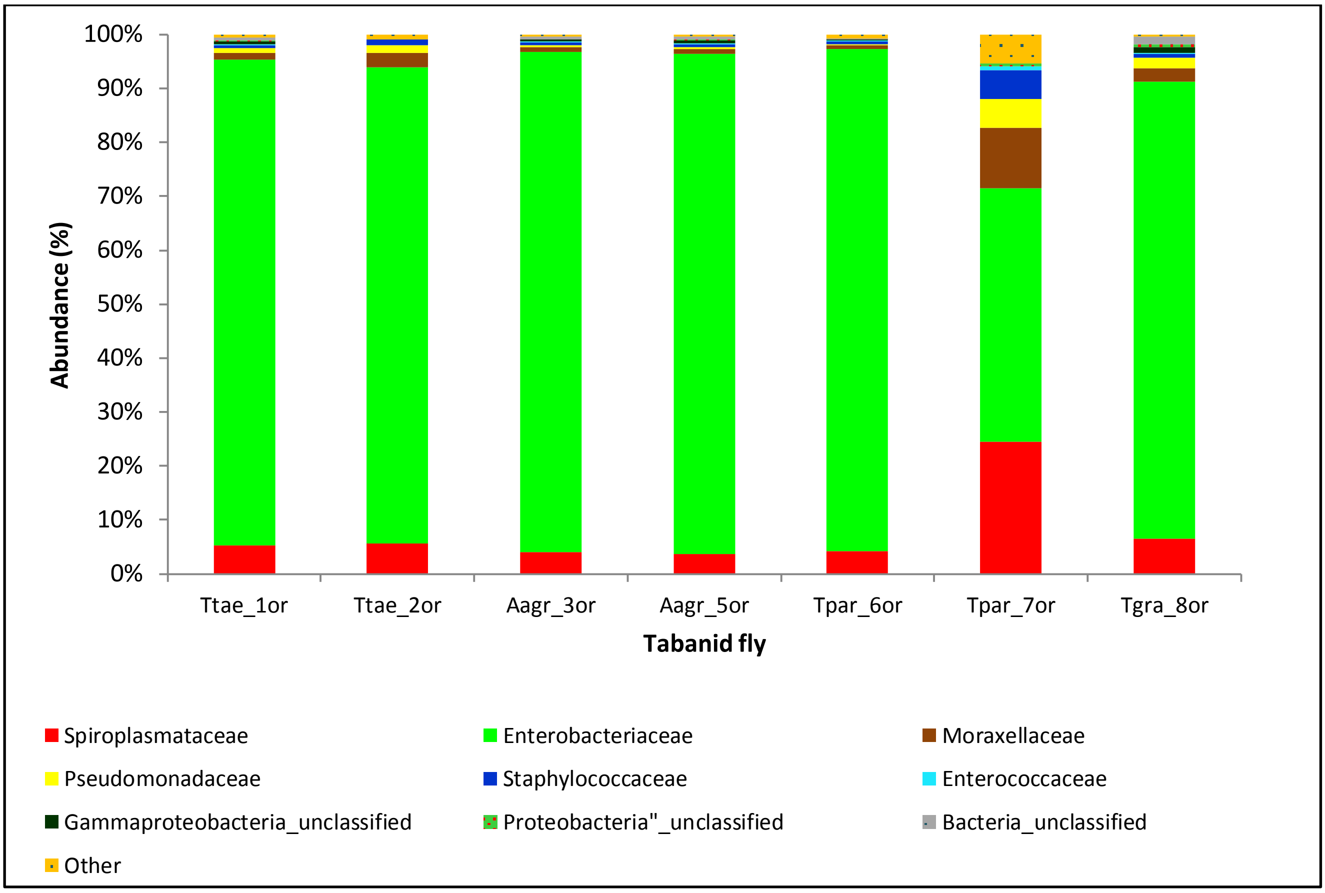

Figure 22: Abundance of bacterial families detected from South African tabanid flies.

Most of the analysed data from South African tabanid flies was restricted to family level and also included a large number of unclassified bacterial species, as observed in the produced OTUs in Appendix III. The analysis at genus level was restricted to bacterial species of medical and veterinary importance as well as those of known symbiotic association. Dominant bacterial genera which were observed from all sampled South African tabanid flies included *Spiroplasma*, *Serratia*, *Enterobacter*, *Staphylococcus, Acinetobacter* and *Pseudomonas* (Figure 23)*. Tabanus par* (Tpar_7or) had the most bacterial diversity followed by *T. taeniola* (Ttae_2or). Unclassified bacteria as well as the bacterial genera *Jeotgalicoccus*, *Stenotrophomonas*, *Comamonas*, *Alcaligenes*, *Facklamia*, *Providencia*, *Shimwellia* and *Proteus* that had few representatives (less than 10) were not included in the analysis.

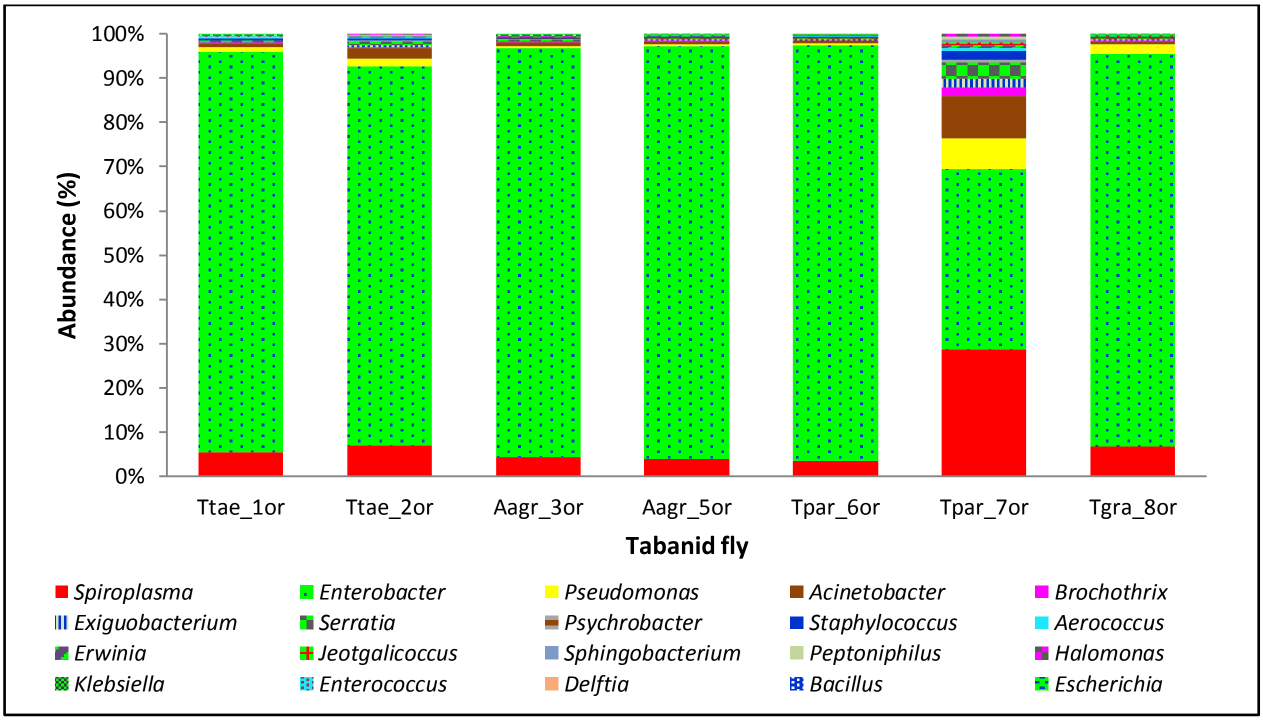

Figure 23: Abundance of bacterial genera detected from South African tabanid flies.

4.3.1.3 *Alpha* and *beta* diversity for South African tabanid flies

The *alpha* diversity analysis to determine the bacteria species richness of produced OTUs from calculated Inverse Simpson diversity index for each fly sample is shown in table 6. At 0.03 distance level and cut off value of 97%, all sequences were maintained at 500 due to the poor number of reads produced. This was done in order to maximize the good sequence coverage however, there was poor coverage observed except in *Tabanus gratus* (Tgar_8or) which had the good coverage score of 73.5%. All other sequences ranged between 16.2% and 54.8% respectively. The number of observed OTUs was also poor as all members scored ≤ 2. The same scenario was also observed in the inverse Simpson index.

Table 6: Alpha-diversity indices based on Illumina MiSeq data from South African tabanid flies

Species	**Sample code**	**N_{seqs}**	**Coverage**	**S_{obs}**	**invSimpson**
Tabanus taeniola	Ttae_1or	50	0.471000	1.53	1.000000
Tabanus taeniola	Ttae_2or	50	0.548000	1.45	1.000000
Atylotus agrestis	Aagr_3or	50	0.389000	1.61	1.000000
Atylotus agrestis	Aagr_5or	50	0.323000	1.68	1.000000
Tabanus par	Tpar_6or	50	0.162000	1.84	1.000000
Tabanus par	Tpar_7or	50	0.278000	1.72	1.000000
Tabanus gratus	Tgra_8or	50	0.735000	1.27	1.000001

** N_{seq} = number of sequences; S_{obs} = number of observed OTUs; invSimpson = inverted Simpson's index

The *beta* diversity analysis was conducted to determine the relative abundance for the produced OTUs at class and geneus levels. The Venn diagram was produced to show the shared species richness between different sampled tabanid flies. In Figure 24a it is clearly shown that there was high degree of relative abundance of bacteria classes at 0.03 distance level among different species of tabanid flies collected from South Africa. The relative abundance between species based on the colour intensity ranged between 0.048 to 0.191. However, the relative abundance between *Tabanus par* (Tpar_7or) and *Tabanus gratus* (Tgra_8or) was the lowest at 0.048.

In Figure 24b the relative abundance at genus level is demonstrated. Despite the low number of OTUs produced at genus level there was some degree of relative abundance shared between different tabanid species (0.000 - 0.993). There was a significantly high relative abundance between the two species of *Atylotus agrestis* (Aagr_3or and Aagr_5or) with *Tabanus taeniola* (Ttae_1or and Ttae_2or) (0.794 - 0.993). *Tabanus gratus* (Tgar_8or) and *T. par* (Tpar_7or) had low relative abundance when compared to other species (0.000 – 0.199). Abundance of bacterial classes shared between different tabanid from South Africa is demonstrated and sharing between different groups is apparent despite its low intensities at genus level.

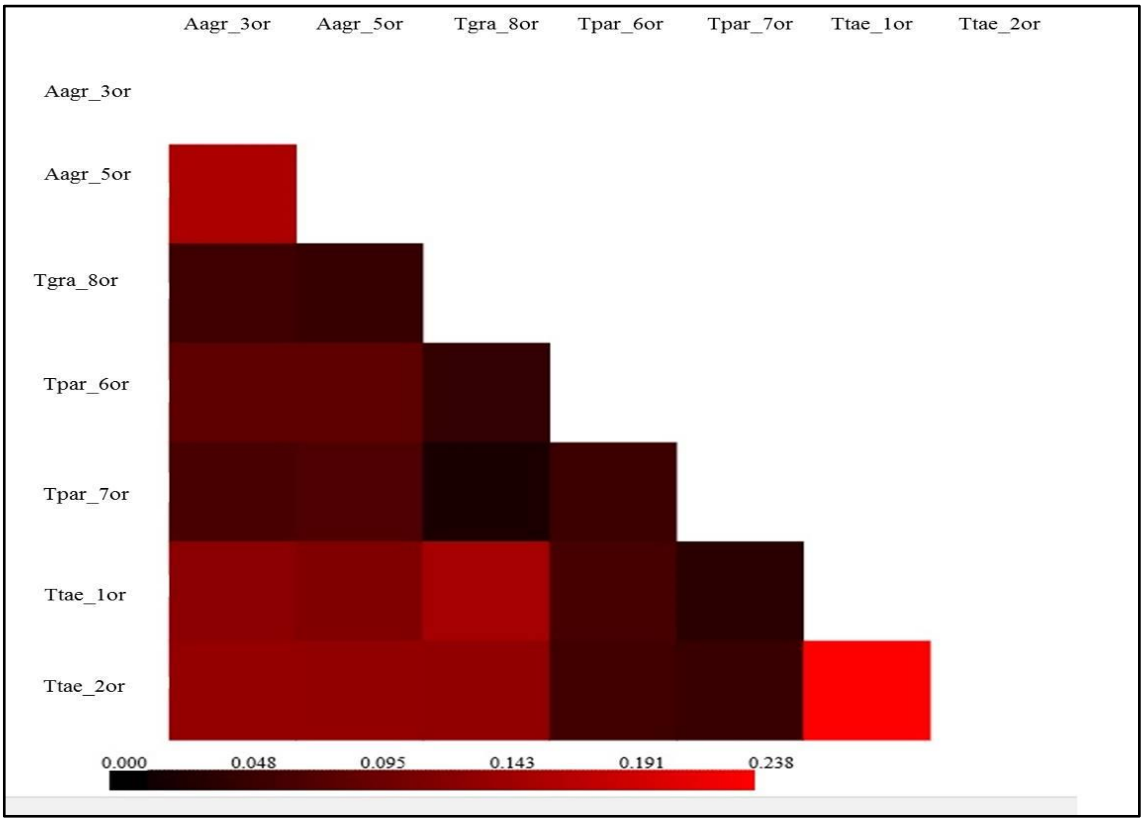

Figure 24a: Heatmap at class level constructed at 0.03 distance level for South African tabanid flies.

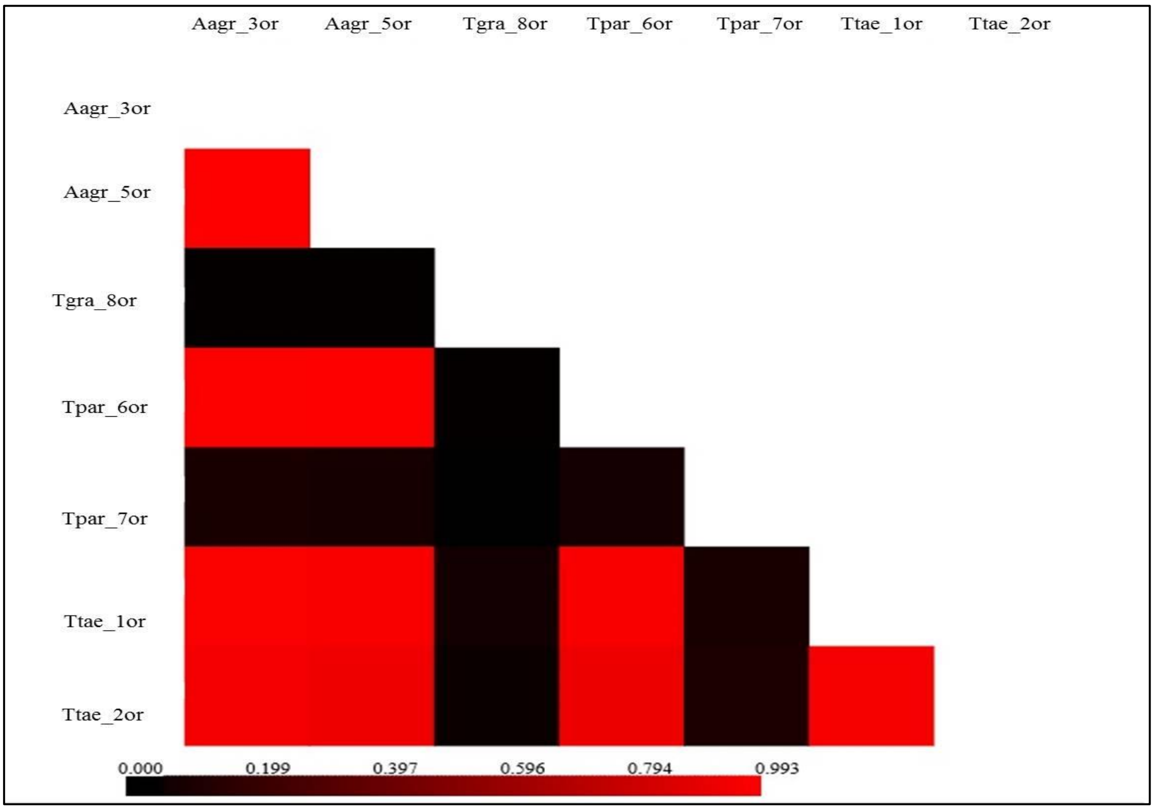

Figure 24b: Heatmap at genus level constructed at 0.03 distance level for South African tabanid flies.

The second part of the *beta* diversity analysis based on Venn diagram was used to determine the shared number of bacterial species within four different sampled species and demonstrate species richness of tabanid flies sampled.

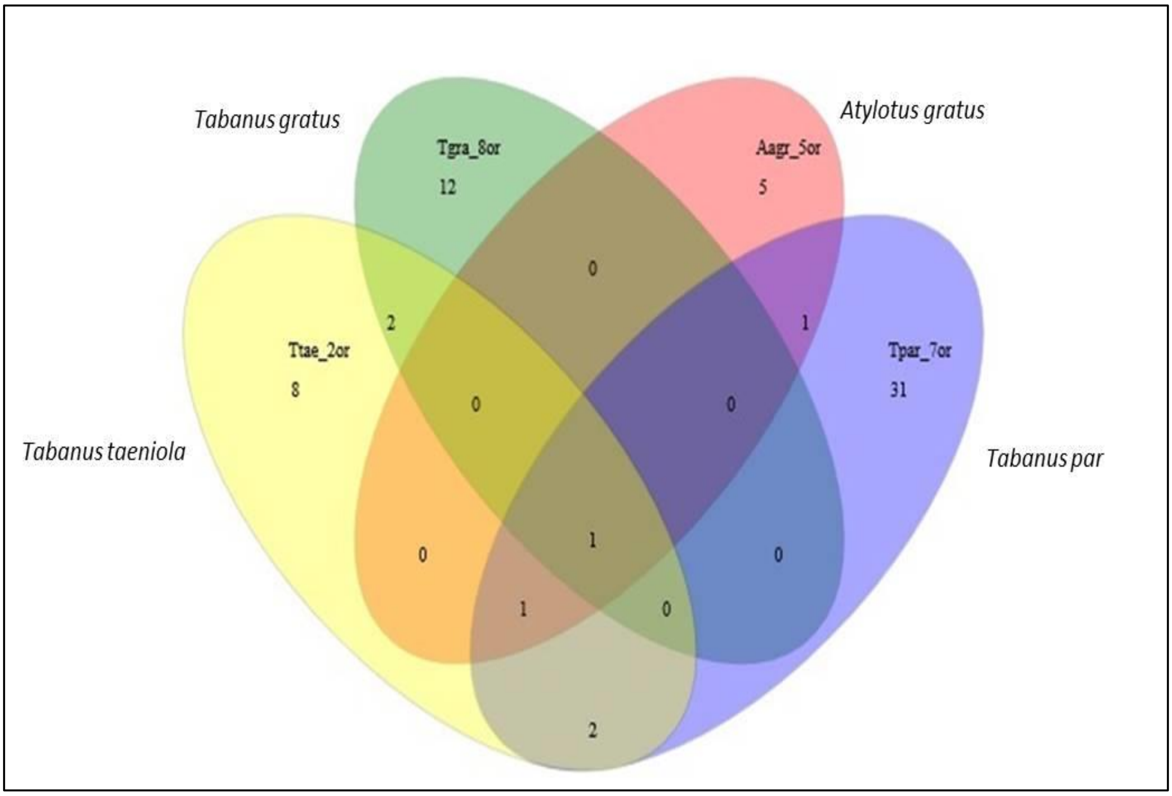

Figure 25: Venn diagram composed of members from *Tabanus taeniola* (Ttae_2or), *T. gratus* (Tgra_8or), *Atylotus agrestis* (Aagr_5or) and *T. par* (Tpar_7or) from South Africa.

In Figure 25, Aagr_5or contained 8 OTUs, Tgar_8or had 15 OTUs, Tpar_7or had 36 OTUs and Ttae_2or contained 14 OTUs. Aagr_5or and Tgra_8or shared only 1 bacterial species. Additionally, Aagr_5or shared 3 species with Tpar_7or and 2 species with Ttae_2or. Tgra_8or shared 4 species with Ttae_2or and only 1 species with Tpar_7or. A total of 4 bacterial species were shared between Tpar_7or and Ttae_2or. There was a poor number of species shared between Tgra_8or, Aagr_5or and Tpar_7or. There was a total richness of 63 species shared in all four groups.

4.3.2.1 Metagenomic analysis of Zambian tabanid flies

Analysis of gut microbes associated with Zambian tabanid flies (n = 12) was composed of 2 524 727 assembled sequences. Sequences were further trimmed and a total of 889 250 good sequences were recovered with 232 699 unique sequences. All sequences were aligned against the reference SILVA bacteria and a total of 882 976 were remaining for analysis with 8 093 unique sequences (Table. 7). A total of 2 285 OTUs per fly species were produced in the final analysis (Appendix IV) and BLASTn similarity match at 97% to 100% were considered significant.

Table 7: Number of sequences from Zambian samples used to produce OTUs

Tabanid fly	Tabanid name	Sample code	Number of sequences assembled	Number of sequences aligned	Total number of OTUs
1	*Tabanus taeniola*	Ttae_O39	127191	38653	2285
2	*Tabanus taeniola*	Ttae_O40	268613	104396	2285
3	*Tabanus taeniola*	Ttae_O41	278045	93136	2285
4	*Tabanus par*	Tpar_O32	176119	56022	2285
5	*Tabanus par*	Tpar_O33	182016	65425	2285
6	*Tabanus par*	Tpar_O34	167825	53080	2285
7	*Atylotus diurnus*	Adiu_O36	379231	156467	2285
8	*Atylotus diurnus*	Adiu_O37	276500	100782	2285
9	*Atylotus diurnus*	Adiu_O48	199336	54816	2285
10	*Tabanus conformis*	Tcon_O42	209085	83279	2285
11	*Tabanus conformis*	Tcon_O43	163741	45499	2285
12	*Tabanus conformis*	Tcon_O44	97025	31417	2285
Total			**2524727**	**882972**	

4.3.2.2 Classification of Zambian tabanid fly OTUs

A total of 12 phyla were recovered from the produced OTUs (Figure 26). The abundant bacterial phyla were Proteobacteria (57.81%), followed by Tenericutes with 22.67% and the least phyla detected included Planctomycetes, Gemmatimonadetes, WS3 (renamed Latescibacteria) as well as Chlamydiae which all had an average of less than ≤1% due to low number of representative members which was less than 20 bacteria species. In addition, a total of 2.28% bacteria (n = 52) were unclassified and not assigned to any taxon beyond the bacteria domain. A summarized table representing the number of phyla detected is given in Appendix IV.

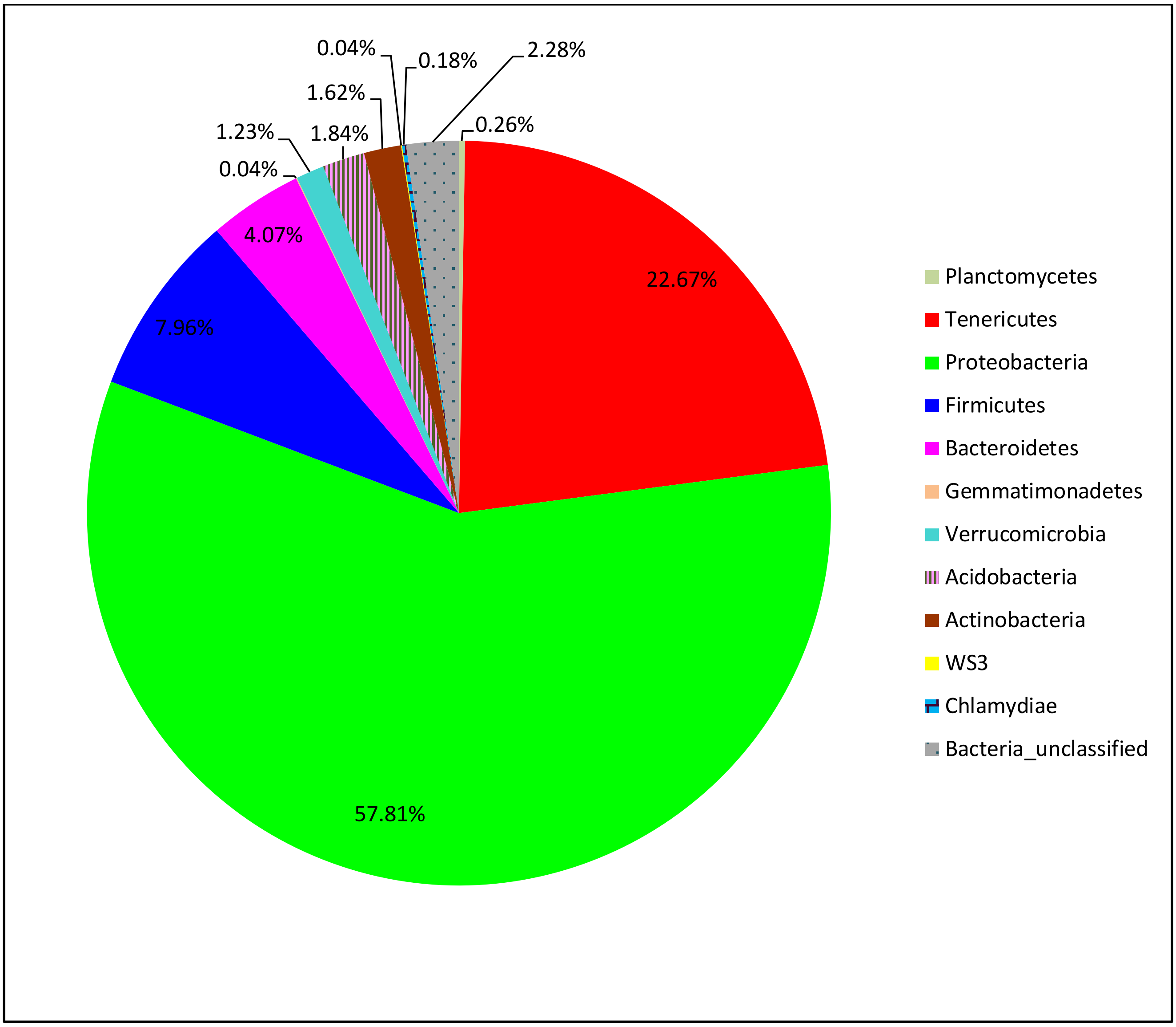

Figure 26: The proportions of bacterial phyla detected from Zambian tabanid flies.

There were a total of 27 bacterial classes with 4 classes being unclassified. The dominant classes included Gammaproteobacteria (52.51%), Mollicutes (22.78%), Bacilli (7.74%) and Betaproteobacteria (3.25%). All remaining classes ranged between 2% and 1%. These included unclassified bacteria, Acidobacteria, Actinobacteria, Bacteroidia, Deltaproteobacteria, Alphaproteobacteria as well as Flavobacteria and Sphingobacteria. Additionally, all the classes with members less than 1% were group together and renamed other (Figure 27). They included Opitutae, Spartobacteria, Erysipelotrichia, Chlamydiae, WS3 (renamed Latescibacteria), Subdivision 3 and 5 from the phylum Verrucomicrobia, Planctomycetacia, Gemmatimonadates, Clostridia, Negativicutes, Verrucomicrobiae as well as unclassified Proteobacteria, Bacteobacteria and Firmicutes.

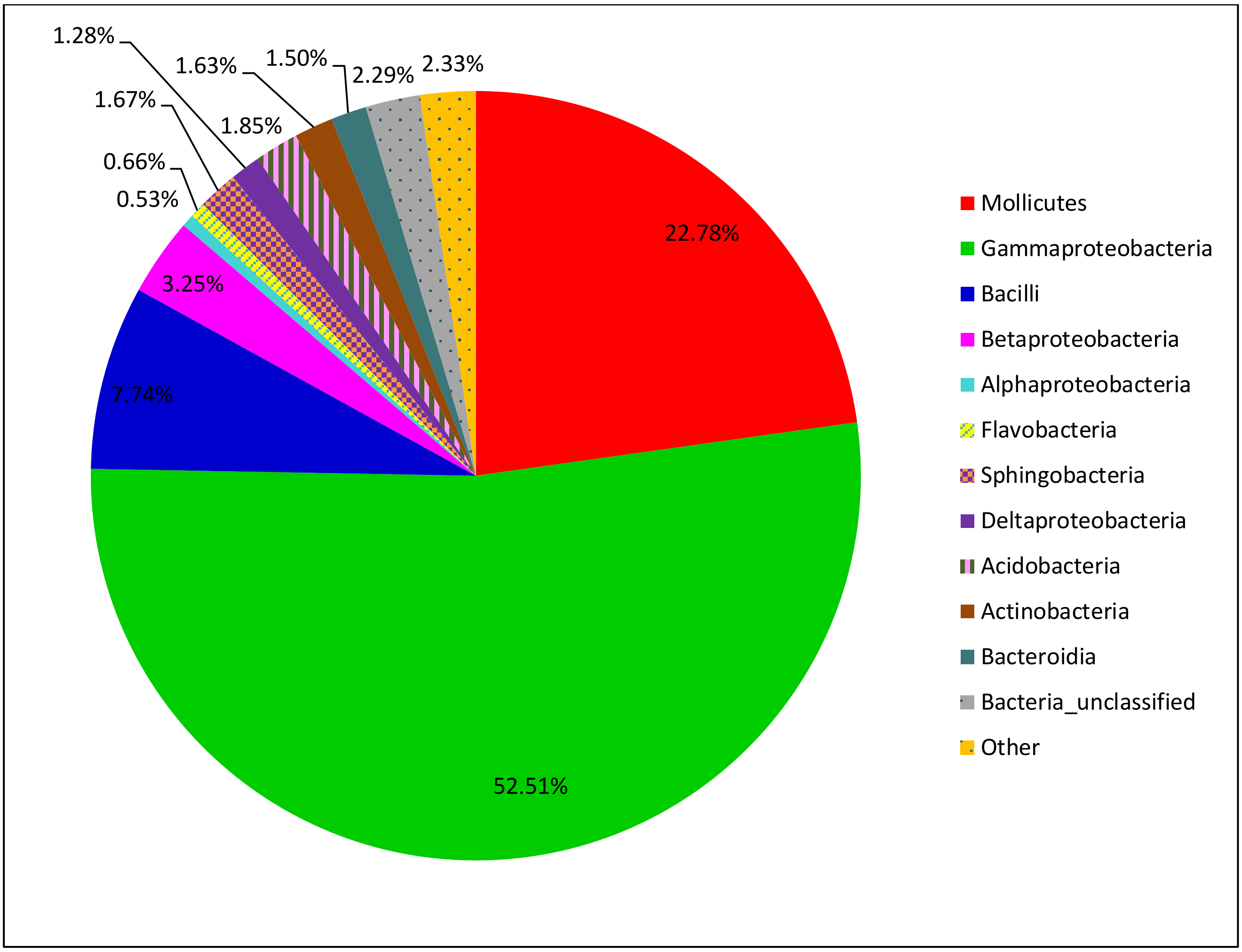

Figure 27: The proportions of bacterial classes detected from Zambian tabanid flies.

A total of 40 bacterial orders were identified. The dominant orders detected included Enterobacteriales (27.45%), Entomoplasmatales (22.50%), Bacillales (7.65%), unclassified Gammaproteobacteria, Oceanospirillales and Vibrionales all at ±5%. Unclassified bacteria below the bacteria domain summed to 2%. The remaining orders all had few representative and ranged between 1% to 2%. These included Burkholderiales, Lactobacillales, Acidobacteria, Sphingobacteriales, Psedomonadales as well as Myxococcales. Additionally, all bacteria orders whose members were less than 20 individuals and contributed ≤1% were all grouped into other and all combined they were 6% of the total composition (Figure. 28). The analyses for family and genus level classifications were based only on the dominant bacteria orders and all the subsequent orders were grouped as other.

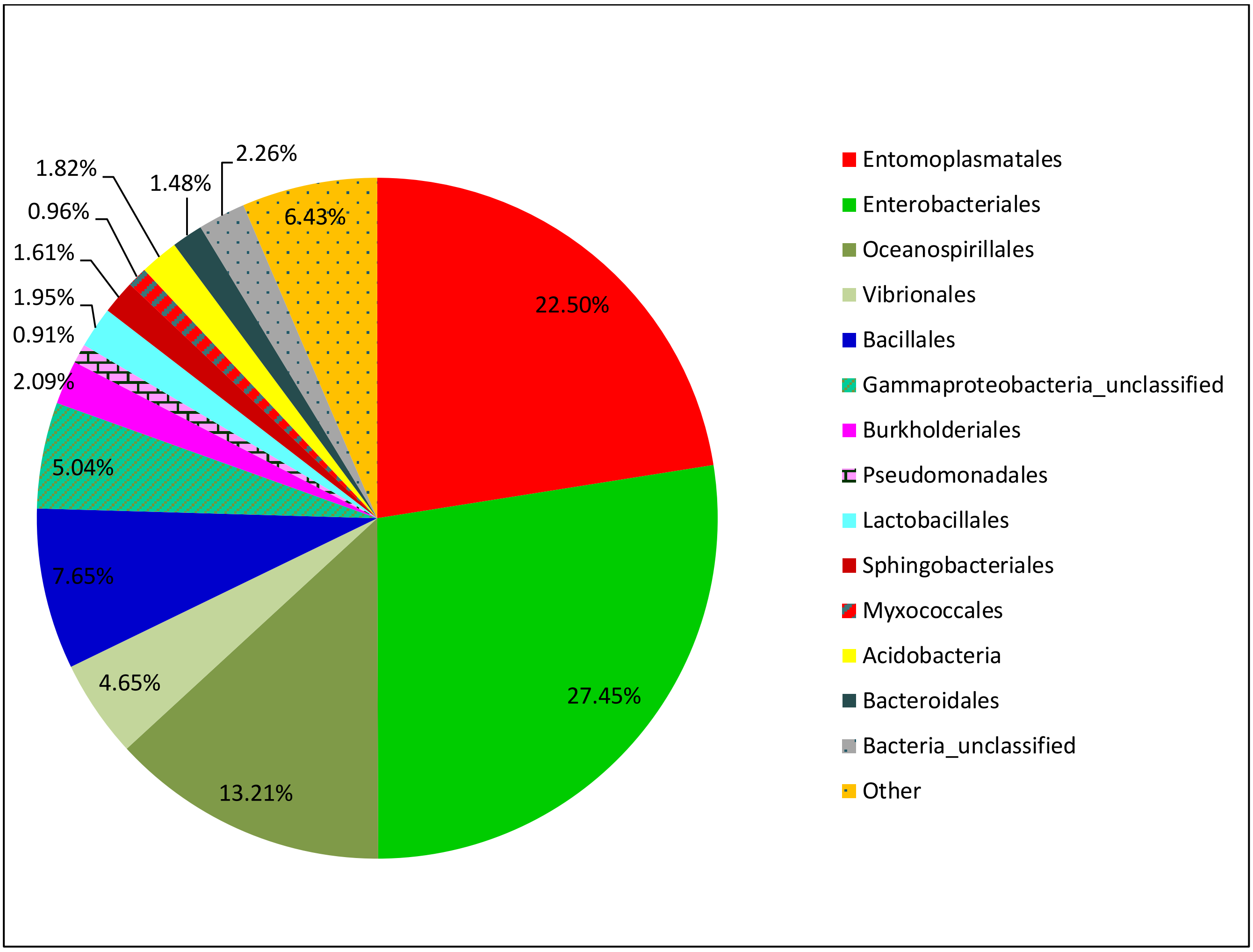

Figure 28: The proportions of bacterial orders detected from Zambian tabanid flies.

Abundant bacterial families identified from the analysed Zambian tabanid flies included Spiroplasmataceae, Enterobacteriaceae, Halomonadaceae, Vibrionaceae, Bacillaceae, and Enterococcaceae (Figure 29). The least detected bacteria families included Comamonadaceae, Moraxellaceae, Pseudomonadaceae, Oxalobacteraceae, Staphylococcaceae, as well as Porphyromonadaceae. All other families which had few representatives (≤10 members) or had no known symbiotic or medical as well as veterinary importance were grouped as other and they included Flavobacteriaceae, Comamonadaceae, Chitinophagaceae, Cystobacteraceae, Oxalobacteraceae, Solirubrobacteracea and Xanthomonadaceae among others. The family Spiroplasmataceae was detected in all sampled flies and it ranged from 0.19% in Tae_O39 to 54.06% in Tcon_O44. The family Enterobacteriaceae was mainly dominant in *T. taeniola* (Ttae_O39) and least dominant in *T. taeniola* (Ttae_O41). Additionally, this family was the second most dominant bacteria family in sampled tabanid flies. The family Halomonadaceae was most dominant in two samples of *Tabanus conformis* (Tcon_O42) followed by *T. par* (Tpar_O34). The family Vibrionaceae was dominant in two species of *T. taeniola* (Ttae_O40 and Ttae_O41). The family Bacillaceae was most dominant in *T. par* (Tpar_O34) followed by *T. conformis* (Tcon_O42).

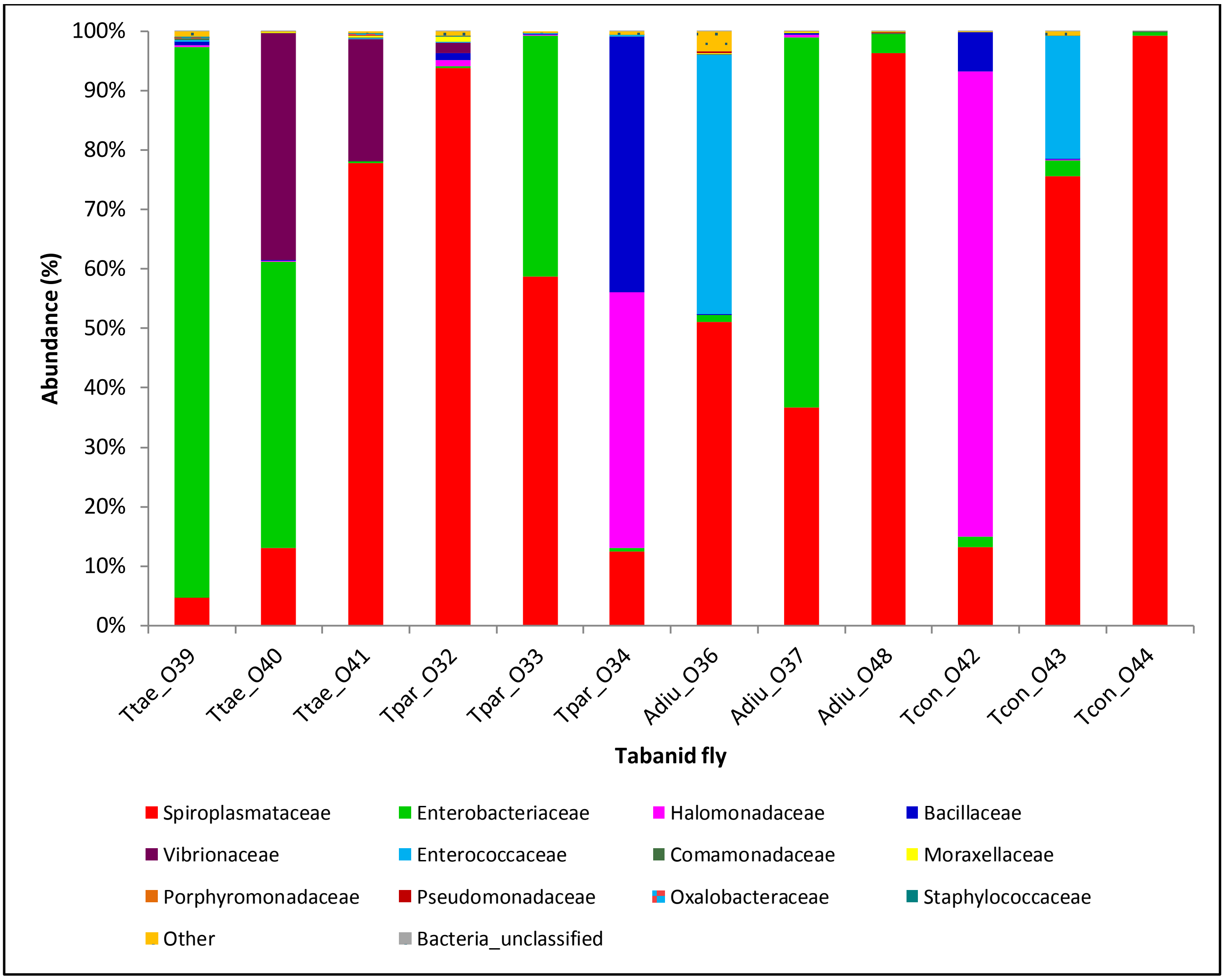

Figure 29: The proportions of bacterial families detected from Zambian tabanid flies.

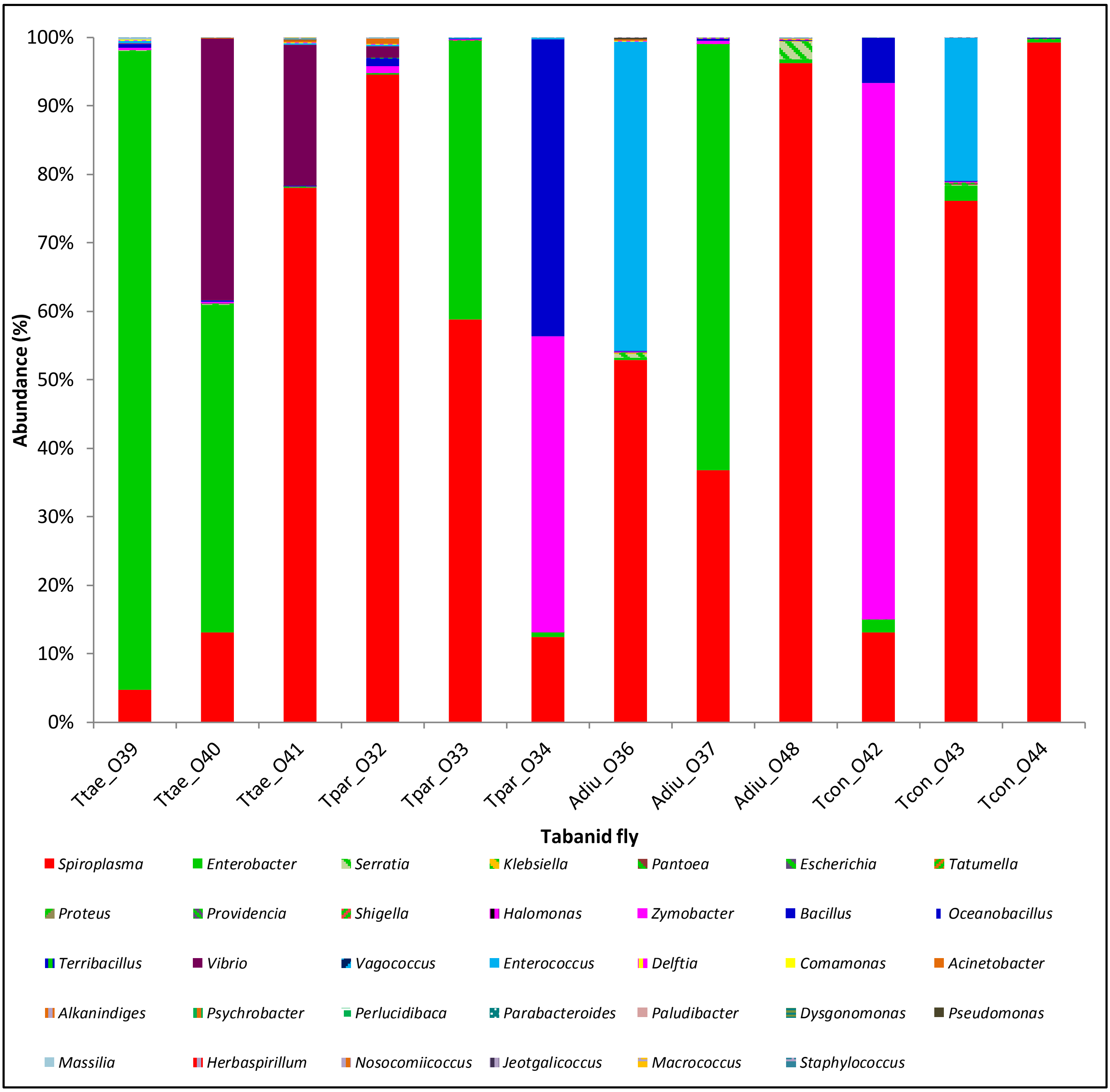

Figure 30: The proportions of bacterial genera detected from Zambian tabanid flies.

Figure 30 shows the summary of the abundant bacterial genera detected from different Zambian tabanid fly species. The most dominant genera detected from all sampled flies included *Spiroplasma*, *Enterobacter*, *Bacillus*, *Zymobacter* and *Vibrio.* These bacteria are known to be symbionts within a wide range of insects and they will be discussed later. The other genera including those of medical and veterinary importance such as *Serratia*, *Klebsiella*, *Shigella*, *Escherichia*, *Proteus* as well as *Staphylococcus* that are known to be harmful to both humans and animals were least detected in most sampled tabanid flies. *Serratia* was the only harmful bacteria dominant in two samples of *Atylotus* *diurnus* (Adiu_O48) followed by Adiu_O36 and this bacteria genus was least detected in other tabanid samples.

4.3.2.3 *Alpha* and *beta* diversity for Zambian tabanid flies

At 0.03 distance level all sequences were maintained at 31 366 sequences at 97% cut-off value. This was done in order to maximize the good sequence coverage for all sequences which was 99% for all sampled flies as observed in table 8 under the coverage column. The number of OTUs ranged between 78 and 196. The inverse Simpson index used to estimate species richness showed that Ttae_O41 had the most species richness of 3.12, followed by Tcon_O43, Tpar_O32 and Tpar_O33 as well as Ttae_O39 with species richness ranging between 2.53 to 2.03. All species of *Atylotus diurnus* had the low species richness as well as other *Tabanus* species with species richness values of ≤ 2.

Table 8: Alpha-diversity indices based on Illumina MiSeq data from Zambian tabanid flies

Species	Sample code	N_{seq}	Coverage	S_{obs}	invSimpson
Tabanus taeniola	Ttae_O39	31366	0.996432	153.34	2.039664
Tabanus taeniola	Ttae_O40	31366	0.997171	105.77	1.916616
Tabanus taeniola	Ttae_O41	31366	0.997429	101.21	3.115941
Tabanus par	Tpar_O32	31366	0.998030	77.79	2.131125
Tabanus par	Tpar_O33	31366	0.997090	110.48	2.035038
Tabanus par	Tpar_O34	31366	0.997250	111.08	1.030481
Atylotus diurnus	Adiu_O36	31366	0.997377	106.93	1.111221
Atylotus diurnus	Adiu_O37	31366	0.996897	112.88	1.288566
Atylotus diurnus	Adiu_O48	31366	0.996664	196.83	1.121334
Tabanus conformis	Tcon_O42	31366	0.996594	135.45	1.844140
Tabanus conformis	Tcon_O43	31366	0.997368	128.09	2.533688
Tabanus conformis	Tcon_O44	31366	0.998248	93.91	1.336387

** N_{seq} = number of sequences; S_{obs} = number of observed OTUs; invSimpson = inverted Simpson's index

Additional analysis of *beta* diversity was conducted whereby two heatmaps, the first for relative abundance at class level and the second for relative abundance at genera level between species. A Venn diagram to determine the shared species richness between all sampled tabanid flies was also calculated. It was clearly shown that there was significantly high relative abundance of bacterial classes at 0.03 distance level among different species of tabanid flies (Figure 31a). Additionally, there was more than 98% sharing between *Tabanus conformis* (Tcon_O43) and *T. conformis* (Tcon_O44).

In Figure 31b it is observed that there was less relative abundance of bacterial genera and low sharing of genera among tabanid species. However, there was some instances where sharing among different tabanid species was fairly significant. *Tabanus taeniola* (Ttae_O32), shared an insufficient number of bacterial genera with all other tabanid species despite its fairly high species richness. Only *T. conformis* (Tcon_O43) and *T. conformis* (Tcon_O44) was shown to have shared quite a large number of genera (≥ 80%) with other tabanid species.

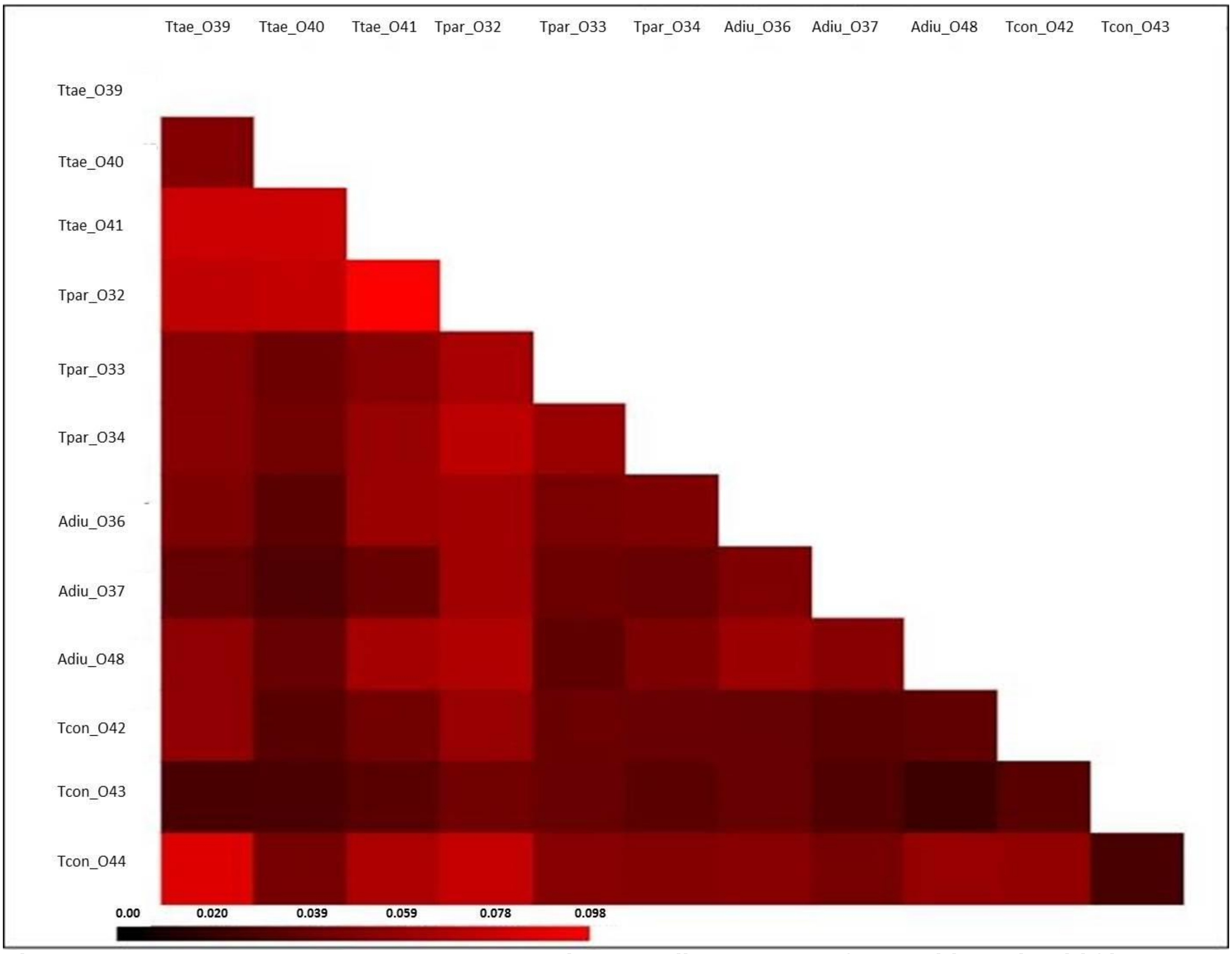

Figure 31a: Heatmap at class level constructed at 0.03 distance level for Zambian tabanid flies.

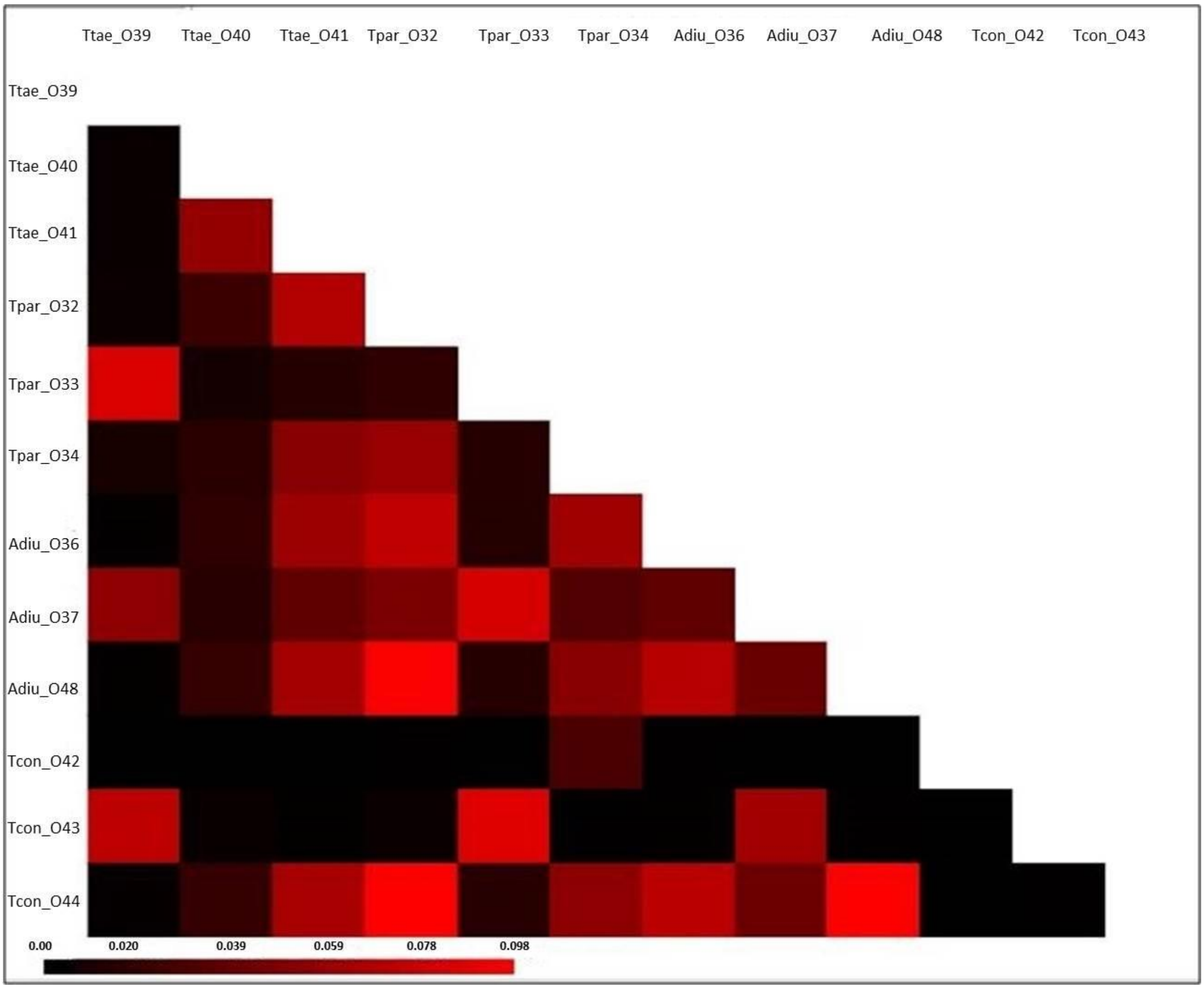

Figure 31b: Heatmap at genus level constructed at 0.03 distance level for Zambian tabanid flies.

Based on the colour intensity in Figures 31a and 31b, the abundance of bacterial classes shared between different tabanid groups is demonstrated and sharing between different groups is apparent despite its low intensities at genus level.

A Venn diagram which was composed of a representative tabanid species from all four genera was conducted. This diagram was used to determine the shared number of bacterial species within four different sampled species.

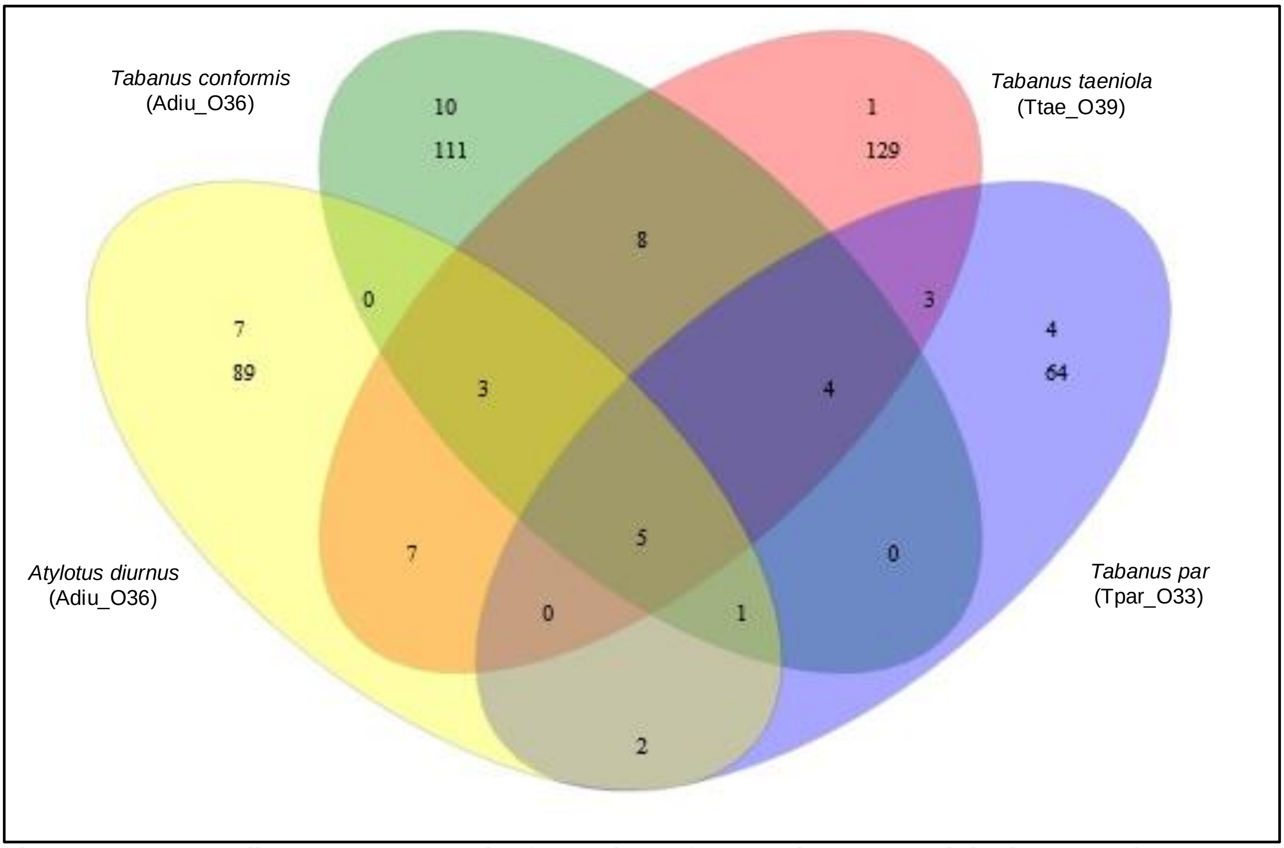

Figure 32: Venn diagram composed of members from *Tabanus taeniola* (Ttae_O39), *T. par* (Tpar_O33), *Atylotus diurnus* (Adiu_O36) and *T. conformis* (Tcon_042) from Zambia.

In Figure 32, Ttae_O39 contained 159 OTUs, group 4 had 79 OTUs, Adiu_O36 had 107 OTUs and Tcon_O42 contained 132 OTUs. Ttae_O39 and Tcon_O44 shared 20 bacterial species. Additionally, Ttae_O39 shared 12 species with Tpar_O33 and 15 species with Adiu_O36. Tcon_042 shared 10 species with Tpar_O33 and 9 species with Adiu_O36. A total of 8 bacterial species were shared between Tpar_O33 and Adiu_O36. There were 5 species shared between Tcon_O42, Ttae_O39 and Tpar_O33. Eight species were shared between groups Ttae_O39, Adiu_O36 and Tcon_O42. Ttae_O39, Tpar_O33 and Adiu_O36 shared 5 species and lastly Tpar_O33, Adiu_O36 and Tcon_O42 shared 6 species. There was a total richness of 426 species shared in the four analysed species.

A summary of bacterial genera of medical and veterinary importance as well as those of symbiotic association detected in the current study is provided in table 9. The association these bacterial genera have with tabanid flies is based on literature of Kikuchi (2009).

Table 9: Bacterial genera of medical, veterinary and environmental importance as well as those involved in symbiotic associations with arthropods

Bacterial genera	Phylum	Family	Medical/Veterinary/Environmental/Symbiotic significance
Spiroplasma	Tenericutes	Spiroplasmataceae	Suspected as gut symbiont of tabanid flies
Enterobacter	Proteobacteria	Enterobacteriaceae	Human, animal and plant pathogens
Serratia	Proteobacteria	Enterobacteriaceae	Human, animal and plant pathogens
Klebsiella	Proteobacteria	Enterobacteriaceae	Human, animal, insect and plant pathogens
Shigella	Proteobacteria	Enterobacteriaceae	Human, animal and plant pathogens
Escherichia	Proteobacteria	Enterobacteriaceae	Human, animal, insect and plant pathogens
Proteus	Proteobacteria	Enterobacteriaceae	Human and animal pathogens
Providencia	Proteobacteria	Enterobacteriaceae	Human, animal, insect and plant pathogens
Acinetobacter	Proteobacteria	Moraxellaceae	Human and animal pathogens
Zymobacter	Proteobacteria	Halomonadaceae	Found in palm plants and plays a role in fermentation
Vibrio	Proteobacteria	Vibrionaceae	Human and animal pathogens
Comamonas	Proteobacteria	Comamonadaceae	Human and animal pathogens
Pseudomonas	Proteobacteria	Pseudomonadaceae	Human and plant pathogens
Brochothrix	Firmicutes	Listeriaceae	Cause meat odour
Bacillus	Firmicutes	Bacillaceae	Human and animal pathogens
Staphylococcus	Firmicutes	Staphylococcaceae	Nosocomial infections in humans
Enterococcus	Firmicutes	Enterococcaceae	Nosocomial infections in humans

4.4 Discussion

The association of gut bacterial communities of field captured *Atylotus agrestis A. diurnus, Tabanus conformis, T. gratus, T. par* and *T. taeniola* is described in this study. South African fly specimens were collected in KwaZulu-Natal Province in uMkhanyakude district and Zambian tabanid flies were collected from Mfuwe in the Eastern Province in Mambwe district. Tabanid flies are known to be biological and or mechanical vectors of several disease causing parasites that infect both domestic and wild animals as well as humans (Zumpt, 1949; Chainey, 1993; Service, 2012; Baldacchino *et al.*, 2014a). However, despite the threats they pose, microbes associated with tabanid flies are not well studied particularly in the African continent. The aims of this study were (i) to determine the microbial composition of different tabanid flies (ii) to identify symbiotic gut bacteria as well as those of medical and veterinary importance. From 11 442 sequences retrieved from South African samples, there was a total of 505 OTUs documented composed of 7 bacterial phyla, 13 bacterial classes and 20 bacterial orders with a total species richness of 63. From 882 976 sequences analysed from Zambia there were 2 285 OTUs produced composed of 12 bacterial phyla, 27 classes and 20 bacterial orders with a total species richness of 426. Whereby the species richness is used in the current study to represent the number of individual bacterial species shared between the compared tabanid flies per sampled country.

The dominant phyla detected from data analyses of both sampled counties included Bacteroidetes, Proteobacteria, Tenericutes and Firmicutes. Zambian samples also had Acidobacteria as well as Actinobacteria. These microbial phyla have been found to be associated with a wide variety of insects such as aphids (Aphidoidea), termites (Isoptera), cockroaches (Blattodea), mosquitos (Culicidae), flesh flies (Sarchophagidae), blow flies (Calliphoridae), fruit flies (Drosophilidae), horn flies (Muscidae), tsetse flies (Glossinidae) as well as in ticks (Ixodoidea) to mention a few (Kikuchi, 2009; Gusmão *et al.,* 2010; Palavesam *et al.*, 2012; Jones *et al.*, 2013; Gupta *et al.*, 2014; Krishnan *et al.,* 2014; Sabree and Moran, 2014; Singh *et al.*, 2014; Qui *et al.*, 2014; Khoo *et al.*, 2016). Bacteria within insects have been found to play a role in either supplementing the insect with nutrients, protection against fungal and viral infections, host insect fitness and competence or temperature regulations (Jones *et al.*, 2013; Gupta *et al.*, 2014; Krishnan *et al.,* 2014; Sabree and Moran, 2014; Khoo *et al.*, 2016;). Additionally, Bacteroidetes, Proteobacteria, Firmicutes and Acidobacteria excluding Tenericutes are known to be associated with other vertebrate animals including humans and it is therefore suspected that these phyla may have some ecological features that enable them to reside within animal hosts making them core microbes that are associated with animals (Jones *et al.*, 2013).

4.4.1 Phylum Proteobacteria

The most abundant bacterial phylum in all tabanid fly samples from both countries was Proteobacteria with 44.38% in South Africa and 57.81% in Zambia. These findings correspond to observations made by Colman *et al.* (2012) and Yun *et al.* (2014) where they assessed different insect orders and found this phylum to be the most dominant from all sampled insect orders. The sampled insect orders were Diptera, Hymenoptera, Coleoptera, Isoptera, Neuroptera and Lepidoptera. Additionally, it has been reported that this phylum accounts for most known primary insect endosymbionts hence its high abundance in the analysed tabanid flies (Jones *et al.,* 2013). The dominant bacterial classes of the phylum Proteobacteria from South African samples included Gammaproteobacteria (37.82%), Betaproteobacteria (1.78%) and unclassified Proteobacteria (4.55%). The dominant classes from Zambian samples included Alphaproteobacteria (0.53%), Betaproteobacteria (3.25%), Deltaproteobacteria (1.27%) and Gammaproteobacteria (52.51%). South African OTUs were dominated by unclassified bacteria and unclassified Proteobacteira as observed in figure 20. As a result, other major bacterial classes such as Alphaproteobacteria and Deltaproteobacteria were not observed from South African OTUs as compared to Zambian OTUs and it is therefore suggested that the missing bacterial classes from the phylum Proteobacteria might be part of the unclassified bacteria.

Focusing on the class Gammaproteobacteria which was the most prevailing in the two countries, the abundant families in South African samples comprised of Enterobacteriaceae which was the most detected among all followed by Moraxellaceae and Pseudomonadaceae. From Zambian samples the abundant families included Enterobacteriaceae, Halomonadaceae, Vibrionaceae, Moraxellaceae as well as Pseudomonadaceae being the least dominant. This class is known to contain bacterial members of medicinal, ecological, and scientific importance which are glycolytic facultative anaerobes that make use of glycolysis and the pentose phosphate pathways to metabolize carbohydrates (Engel and Moran, 2013; Gupta *et al*., 2014). These dominant bacterial families are generally known have pathogenic interactions with their infected host insects and might also be pathogenic to both animals and plants including humans (Sanchez-Contreras and Vlisidou, 2008). Due to high numbers of unclassified bacteria from South African samples, analysis at genus level was only based on few OTUs retrived. The abundant bacterial genera from South African OTUs included *Enterobacter, Serratia*, *Erwinia*, *Klebsiella* and *Escherichia*. *Pantoea* and *Provencia* and *Shimwellia* were also detected but in faily low abundace. For Zambian flies the abundant genera from the produced OTUs included *Enterobacter, Serratia, Klebsiella, Pantoea*, *Escherichia*, *Tatumella*, *Proteus*, *Providencia* and *Shigella.* The abundace of the bacterium *Enterobacter* in all samples from both countries clearly indicates that this bacterium may either have mutualistic or commensalistic associations with tabanid flies.

In the fruit fly (*Drosophila melanogaster*) and the gypsy moth caterpillar (*Lymantria dispar*) these bacterial genera are acquired from decaying fruit or plant leaves and they are known to play a role in the development of the immune system, by negatively affecting the metabolism and mating preference in fruit flies (Engel and Moran, 2013; Douglas, 2015). Within the gypsy moth caterpillar, *Enterobacter* and *Pantoea* are known to increase the susceptibility to toxin by altering the permeability of the midgut epithelial cells (Engel and Moran, 2013) whereas, *Klebsiella oxytoca* produces volatile disulfides in leek moth (*Acrolepiopsis assectella*) which releases kairomones (chemical substances) that attract the parasitoid *Diadromus pulchellus* to the moth host (Dillon and Dillon, 2004). Additionally, in pea aphids (*Acyrthosiphon pisum*) *Pantoea* is highly pathogenic leading to a production of compounds that attract predators (Dillon and Dillon, 2004; Engel and Moran, 2013). It is possible that tabanid flies acquire these bacterial species from the plants as they are also nectar and plant sap feeders or from the natural environment when foraging for hosts or shade.

Despite the negative impact of the above mentioned genera in their host insects, it has been found that *Enterobacter* spp. in *Anopheles* mosquitoes trigger the production of reactive oxygen species (ROS) which inhibit the development of *Plasmodium* ookinete into oocytes and in phlebotomine sand flies (*Lutzomyia longipalpis*) *Leishmania* parasites are sensitive to ROS induced by some members of the gut microbiota (Douglas, 2015). Furthermore, Hrček *et al*. (2016) reported that *Serratia symbiotica* protects its host insects against heat shock and is found at highest frequency in hot environments. In carrion feeding insects such as blow flies (*Lucilia* spp.) it was found that *Providencia* has nutritional benefits by producing several xylanases that help in decomposition of xylan observed at decomposition sites (Singh *et al*., 2014).

Given the pathogenicity of members of the family Enterobacteriaceae and their association with numerous infections in humans, these bacteria are known to be responsible for infections such as conjunctivitis, urinary tract infections, respiratory and systemic infections, wound and bloodstream infections as well as meningitis as summarised in table 9 (Gupta *et al*., 2014). In the current study, they have been found to be limited in abundance except the genus *Enterobacter* from Zambian samples which was fairly dominant in two species of *Tabanus taeniola* (Ttae_O39 and Ttae_040), *T. par* (Tpar_O33) and *Atylotus diurnus* (Adiu_037). As a result it is therefore suspected that these bacterial genera have a mutualistic or parasitic or commensal association with tabanid flies due to that there were low and *Enterobacter* on the other hand may have a mutualistic association with tabanid flies due to its presence in all tested samples of Zambia however the role it plays in these flies is currently unknown and further research is required to address this aspect.

4.4.2 Phylum Tenericutes

The second most abundant phylum from both South African and Zambian samples was Tenericutes which contributed 8.88% from South African samples and 22.67% in Zambian samples. The class Mollicutes with 8.91% from South African samples and 22.78% from Zambian samples was the only class obtained from the phylum Tenericutes. The order Entomoplasmatales was obtained and contributed 8.74% in South African samples and 22.50% in Zambian samples.

Spiroplasma was the only genera found from the family Spiroplasmataceae and this genus was found in all sampled flies from both countries in variable abundance. From South African samples, this genus was most abundant in *Tabanus par* (Tpar_7or) and from Zambian samples *Spiroplasma* was most abundant in *T. conformis* (Tcon_O44) followed by *T. par* (Tpar_O32) as well as *Atylotus diurnus* (Adiu_O48). *Spiroplasma* species are gram-positive bacteria with a small genome size that ranges from 760 to 2 220 kb (Ammar and Hogenhout, 2006; Regassa and Gasparich, 2006). This bacterium is known to be parasitic in plants where it may either reside on plant surfaces, particularly on flowers or within the plant phloem (Ammar and Hogenhout, 2006). However, in arthropods *Spiroplasma* spp. may be found inhabiting the gut as endoparasites or extracellular as intracellular mutualistic symbionts depending on the arthropod species involved as well as the environmental conditions of the host (Ammar and Hogenhout, 2006). It is suggested that *Spiroplasma* spp. may have co-evolved with insects hence their high abundance in their guts (Regassa and Gasparich, 2006). This bacterium has been known to be associated with various insect orders such as Coleoptera, Diptera, Hemiptera, Homoptera, Hymenoptera, Lepidoptera, Odonata as well as with ticks (Regassa and Gasparich, 2006; Henning *et al.*, 2006). In these organisms this bacterium plays different roles for example, in the leafhopper (*Dalbulus maidis*) there is a mutualistic interaction between *Spiroplasma kunkelii* and the leafhopper as it has been found that this bacterium improves the fitness of the insect by enhancing its ability to survive cold temperatures (Ammar and Hogenhout, 2006; Regassa and Gasparich, 2006).

In some instances *Spiroplasma* can be entomopathogenic to its host insect for example, it has been reported that in honey bees (*Apis mellifera*) it has been found that *S. melliferum* and *S. apis* are pathogenic to bees as they can cross the insect gut barrier and reach the hemolymph, where they multiply abundantly and eventually kill the bee host (Ammar and Hogenhout, 2006; Regassa and Gasparich, 2006). Additionally, in the fruit fly (*Drosophila willistoni* and *D. melanogaster*) it has been documented that *S. poulsonii* is responsible for sex ratio disorders where they can kill and eliminate the male progeny of an infected female insect host (Ammar and Hogenhout, 2006; Regassa and Gasparich, 2006). There are situations where this bacterium is an intracellular mutualistic symbiont and does not pose threats to the host insect as observed in Bamboo pseudococcid (*Antonina crawii*) and the pea aphid (*Acyrthosiphon pisum*). It has been shown that injection of an extract from infected pea aphid into uninfected aphids reduced growth, reproduction and longevity of the injected aphids (Ammar and Hogenhout, 2006). Various species of *Spiroplasma* spp. have been extracted from tabanid flies and their phylogeny described however, there is no clear explanation of the role that this bacterium plays in tabanid flies (Henning *et al.*, 2006). It has been reported that the concentration of *Spiroplasma* spp. in arthropod gut is fairly low as it is suggested that they do not replicate in the gut or invade insect cells (Ammar and

Hogenhout, 2006). In the current study this bacterium was abundant and found in all sampled flies. It is therefore suspected that, *Spiroplasma* spp. are commensal or mutualistic symbionts of tabanid flies and not parasitic. However, the exact role it plays in these flies is unknown and requires further investigations.

4.4.3 Phylum Firmicutes

Firmicutes were also abundant in samples from both countries where in South African tabanid flies it contributed 7.30% and 7.96% in Zambian samples. Bacilli were dominant class from this phylum with 6.73% in South African samples and 7.74% in Zambian samples. The abundant orders included Bacillales and Lactobacillales whereby from South African samples they had 6.21% and 1.94% respectively. From Zambian samples they contributed 7.65% for Bacillales and 1.95% for Lactobacillales. From the order Bacillales, Bacillaceae was the only abundant family. In South African samples this family was most dominant in *Tabanus par* (Tpar_7or). Whereas in Zambian samples it was dominant in *T. par* (Tpar_O34) and *T. conformis* (Tcon_O42). *Bacillus, Oceanobacillus, Terribacillus* were the only bacterial genera recovered from this family and only observed in Zambian samples. From the order Lactobacillales, Staphylococcaceae and Enterococcaceae were the most dominant bacterial families retrieved. In South African samples both families were most abundant in *T. par* (Tpar_7or) and in *Atylotus agrestis* (Aagr_5or) only Staphylococcaceae was dominant. In Zambian samples Staphylococcaceae was least abundant and only Enterococcaceae was most abundant mainly in *A. diurnus* (Adiu_O36) and *T. conformis* (Tcon_O43). The most abundant bacterial genera from the family Staphylococcaceae included *Jeotgalicoccus*, *Macrococcus* as well as *Staphylococcus.* Only *Staphylococcus* was observed from South African OTUs and from Zambian OTUs all genera were observed. From the family Enterococcaceae the dominant genera included *Enterococcus* and *Vagococcus* respectively.

Different species of *Bacillus* have been reported in various insects including tabanid flies. However, in tabanid flies and other dipterans (blow flies, house flies, louse flies, stable flies and biting midgets) it has been reported these flies are capable of mechanically transmitting *B. anthracis* which causes anthrax to humans, domestic and wild animals (Zumpt, 1949; Hugh-Jones and Blackburn, 2009; Service, 2012; Baldacchino *et al*., 2014a, b). However, there is no documented information on the role played by this bacterium in these flies. Dillon and Dillon (2004) reported that *Bacillus* and *Enterococcus* species together with *Klebsiella oxytoca* produce volatile chemicals in the leek moth that attract parasitoids. In *Culex pipiens* it has been suggested that *Bacillus* and *Staphylococcus* affect the fertility of the mosquitoes, although the actual mechanism of this occurrence is unknown (Minard *et al*., 2013). Additionally, Harsha *et al.* (2015) documented that two strains of *Bacillus pumilus* (CU1A and CU1B) isolated from the gut of biting midges (Ceratopogonidae) assisted in the digestion of the blood meal and are also linked with oogenesis. The presence of Firmicutes in tabanid flies is only documented in the transmission of *B. anthracis* and its potential effect in the flies is unknown. The same applies to other genera reported in the current study their role in tabanid flies requires further research.

4.4.4 Other significant phyla

Other significant bacterial genera found in this study included *Actinobacter*, *Acinetobacter*, *Delftia*, *Comamonas*, *Holomonas*, *Pseudomonas*, *Vibrio* and *Zymbacter.* These bacteria have different roles in their insect hosts for example; *Delftia* species are known as D-amino acid amidase-producing bacterium and might have a significant role in insect survival (Xei *et al*., 2012). *Vibrio* on the other hand has been found to be responsible for mortalities in fruit flies (Blow *et al*., 2005). In termites it has been reported that *Acidobacteria* is responsible for nitrogen fixation and digestion of cellulose (Engel and Moran, 2013). In blood feeding insects *Comamonas* is suggested to aid in blood digestion (Yun *et al*., 2014). *Pseudomonas* is known to be pathogenic in aphids (Engel and Moran, 2013). However, most of the bacterial genera reported in this study have unknown functions in tabanid flies and the mechanisms involved in their associations requires further investigations.

A similar study was conducted on 400 tabanid flies from Brazil using culture dependent method. In that study the authors were only interested in microorganisms of medicinal importance that pose threats to humans and it was reported that tabanid flies harbour members of the family Enterobacteriaceae such as *Serratia marcescens*, *Salmonella arizonae*, *Escherichia coli* as well as *Staphylococcus aureus* however, in variable abundances (Luz-Alves *et al.*, 2007). Their observations are similar to these reported in the current study. It is not surprising however that different tabanid species harbour different bacterial communities and in variable abundance because factors such as the gut morphology and physicochemical conditions (pH and oxygen availability) in the insect gut, life cycle and duration of metamorphosis as well as metabolism of colonizing bacteria are known to have a significant effect on the assemblage of gut microbes and also determine the role the microbes play in the host insect (Yun *et al.*, 2014). Nonetheless, description of the microbes harboured by insects should ideally be linked to their biological role despite the large variation in population size and composition between individual insects (Dillon and Dillon, 2004).

CHAPTER 5

GENERAL DISCUSSION, CONCLUSIONS AND RECOMMENDATIONS

5.1 Introduction

Major findings from the Chapter 2, 3 and 4 are summarized and the observed short comings addressed in this section. Links of major findings are made in response to the aims of the study and conclusions are presented accordingly. Lastly, recommendations for future research for each section are suggested. The current study aimed at characterizing tabanid flies collected from three countries in southern Africa using both morphological and molecular techniques as well as to determine their role in transmission of haemoparasites. It further sought to determine the microbiota harboured by these flies as well as to identify those of symbiotic association as well as those of medicinal veterinary importance.

5.2.1 Characterization of Lesotho, South Africa and Zambian tabanid flies

The objectives were to (i) identify captured tabanid flies from the sampled countries, (ii) to determine and compare the abundance of the different flies captured and (iii) to determine their phylogenetic position. There were a total of 529 tabanid flies collected whereby, 370 were from South Africa, 157 were from Zambia and only 2 specimens were from Lesotho. From the 529 tabanid flies captured, a total of 5 genera composed of 14 species were identified based on descriptions done by Oldroyd (1952; 1954), Yagi (1964), Veer (1999) and Morita (2008). The genera included *Ancala, Atylotus, Haematopota, Philoliche* and *Tabanus. Tabanus* species were the most dominant species from the entire collection. These findings of *Tabanus* species being the most dominant genera correspond to findings done in other parts of the world including South Africa and Zambia (Okiwelu, 1975; 1976; Barros, 2001; Ahmed *et al.* 2005; Krčmar, 2005; Esterhuizen, 2006). There was also a significant difference observed in the abundance of the flies in the sampled countries. Members of the genera *Chrysops* and *Hybomitra* were not found in the current study. Research conducted by Itina *et al.* (2013) in the Akwa Ibom State of Nigeria found more *Chrysops* species than *Tabanus* in contrast a previous study by Ahmed *et al*. (2005) in Southern Kaduna, Nigeria reported only 18 specimens from *Chrysops.* In studies conducted from South Africa and Zambia it was reported that there was relatively low numbers if not none of *Chrysops* spp (Okiwelu, 1975; 1976; Esterhuizen, 2006). Nonetheless, the lack of these species in the current study does not imply that this genus is absent in the sampled countries.

Temperature, relative humidity, rainfall patterns and vegetation contributed to the low abundance observed in the current study and as a result findings from this study represent a fraction of the actual abundance of these flies in the sampled countries. It has been observed that the use of Malaise traps and canopy traps to be effective in capturing *Chrysops* and other tabanid flies (Barros, 2001; Krčmar, 2005). It was further suggested that traps baited with a combination of both aged horse urine and 1-octen-3-ol or aged horse urine and acetone enhances the effectiveness of traps (Krčmar, 2005). Based on the *cytochrome oxidase 1* (*CO1*) gene, the phylogeny of tabanid flies including those from this study were monophyletic and the genus *Tabanus* was non monophyletic. Additionally, tabanid flies from the Afrotropic region are genetically distinct from those found in the Nearctic and the Neotropical regions as in observations made by Morita *et al.* (2016). From the observations made from the Kruskal–Wallis χ^2 analysis of variance by ranks at a significance of 95%, the null hyphothesis which stated that there was variation in the abundance of tabanid fly populations from the sampled localities due to difference in climate and vegetation in the three countries is therefore accepted.

In conclusion this study demonstrated that there is a high abundance of different tabanid fly species in South Africa and Zambia. However, not much can be said regarding tabanid flies from Lesotho due to the fact that in the current study only 2 specimens were captured during a 3 months sampling period. The *El Nino* phenomenon which occurred between 2015 and 2016 is suspected to have an effect on the presence of dipterans in the sampled countries as it caused widespread draught in Southern Africa. The diversity of the different species in the sampled countries is also documented and it has been tested that the family Tabanidae was found to be monophyletic, furthermore tabanid flies from the Afrotropic region are genetically distinct from those found in the Nearctic and the Neotropical.

5.2.2 Recommendations

Further research is necessary to obtain a comprehensive picture on the relative abundance of tabanid flies in the sampled regions. A combination of odours for bait is suggested as this will enhance the scent released from the traps to attract more flies. Sampling should be conducted seasonally to have an idea of which tabanid species are abundant at which season, and should cover all vegetation types. For phylogenetic analysis more conserved nuclear, mitochondrial or protein coding genes need to be tested as well as other large gene fragments in order to resolve crucial areas of the tabanid tree topology resolution where current morphological and molecular evidence are currently limited should be explored.

5.3.1 Haemoparasites haboured by tabanid flies in Lesotho, South Africa and Zambia

The objectives of this chapter were to detect *Besnoitia besnoiti,* bovine *Babesia* and *Theileria* species as well as *Trypanosoma* species particularly *Trypanosoma b. brucei, T. congolense, T. equiperdum, T. theileri* and *T. vivax* infecting tabanid flies collected in Lesotho, South Africa and Zambia. Samples that tested positive for the tested protozoan parasites were from South Africa and Zambia. None of Lesotho samples tested positive for the above mentioned parasites. South African samples tested positive for only trypanosome parasites which included *Trypanozoon* species, *Trypanosoma congolense*, as well as *T. theileri* parasites. These protozoa parasites were only detected in *Tabanus par* and *T. taeniola* respectively. From Zambian samples *Babesia bovis* was detected from *Atylotus agrestis*, *A. duirnus*, *Tabanus taeniatus*, *T. taeniola*, *T. par* and *T. conformis* respectively. *Besnoitia besnoiti* was detected only in *T. conformis. Theileria parva* was detected only in *T. taeniola*. For trypanosome parasites only *Trypanozoon* was detected from *T. taeniola* and *T. par.* This is the first report of *Besnoitia besnoiti*, *Babesia bigemina*, *Theileria parva* and various trypanosome species from tabanid flies by PCR. Factors such as the biology of the tabanid flies (body size, shape of mouth parts and behaviour), mode of development of the parasites in the insect vector and duration of the survival of the parasite in tabanid flies before possible transmission are known to have an influence in the effectiveness of parasite transmission by tabanid flies (Desquesnes and Dia, 2003a; Desquesnes and Dia, 2003b; Bigalke and Prozesky, 2004). Although in the current study vectorial capacity of these tabanid flies for detected parasites was not conducted, there are reports on possible mechanical transmission of some of the parasites such as *Trypanosoma* species and *Besnoitia* species by tabanid flies (Desquesnes and Dia, 2003a; Desquesnes and Dia, 2003b; Bigalke and Prozesky, 2004; Desquesnes and Dia, 2004; Baldacchino *et al.,* 2013; Baldacchino *et al.,* 2014a; Hornok *et al.,* 2014). There are no reports on transmission of *Babesia* species and *Theileria* species by tabanid flies. Baldacchino *et al*. (2014), states that tabanids are neglected subjects of research but important vectors of disease agents. This is the the first time that the presence of *Babesia* and *Theileria* are reported in tabanid flies.

In conclusion, this study has shown that tabanid flies are possibly carrying or harbouring *Trypanosoma, Besnoitia, Babesia* and *Theileria* species. Further studies on possible transmission of these parasites by tabanid flies in South Africa and Zambia are required as well as sampling the flies in livestock farming areas as only wildlife nature reserves were sampled in the current study. The presence of *Trypanosoma brucei*-like and *T. evansi*-like DNA from South Africa and Zambia respectively needs further confirmation. Control of vectors such as ticks and tsetse flies reduces the prevalence of tick-borne diseases and trypanosomosis respectively, but these diseases will not be eliminated if tabanid flies are not given the attention they deserve.

5.3.2 Recommendations

Further studies on the possible transmission of these parasites by tabanid flies in South Africa and Zambia are required as well as sampling the flies in livestock farming areas as only wildlife nature reserves were sampled in the current study. Additionally, blood samples from host animals such as domestic and wildlife should be collected together with the flies in order to determine the prevalence of these parasites in the sampled areas and in order to estimate the actual impact that these flies have in transmission of pathogens. Deoxyribonucleic acid should be extracted from mouthparts, salivary glands and midgut of the tabanid flies to determine if these parasites can develop within the flies or if they are confined to only the mouthparts.

5.4.1 Microbiota of horse flies (Diptera: Tabanidae) from South Africa and Zambia

The is part of the study was conducted based on objectives which were formulated as follows: (i) to determine gut microbial composition of different tabanid flies collected from South Africa and Zambia using 16S rRNA based metabarcoding on an Illumina MiSeq platform and (ii) to identify symbiotic (commensalistic, mutualistic or parasitic) gut bacteria of tabanids as well as those of medical and veterinary importance.

From both countries the abundant phyla included Bacteroidetes, Proteobacteria, Tenericutes and Firmicutes. Where the families Enterobacteriaceae and Spiroplasmataceae were the most abundant from both countries and it was suggested that members of these families have commensal and mutualistic associations with tabanid flies.

Bacteria of medical and veterinary importance which are known to be pathogenic to both animals and humans which included *Serratia, Klebsiella, Pantoea*, *Escherichia*, *Tatumella*, *Proteus*, *Providencia* and *Shigella* were also detected however in low abundance. The bacterial classes known to be symbiotic, mutualistic or parasitic to invertebrates were detected from the all samples tested. Zambian samples had more sequences produced than South African samples and this is due to the fact that in metagenomic sequence analysis sample processing is the most crucial step.

The quality of DNA extracted should be representative of all cells present in the sample and should be sufficient amounts of high quality DNA in order to maximize the sequencing of microbes from the environmental samples (Thomas *et al.*, 2012). Due to this OTU analysis for South African samples was not conducted and this was also observed in Figure 23b on the heatmap where there was poor sharing at genus level between South African tabanid flies. The hypotheses which stated that, (i) the microbial composition of different tabanid flies will be dominated by similar bacterial phyla, (ii) the bacterial phyla detected were similar to other haematophagous flies and (iii) the tabanid flies also harbour symbiotic bacteria were all accepted due to similar bacterial phyla that were detected in both sampled countries as well as the presence of *Enterobacter* and *Spiroplasma* in high abundance from all samples. The study conducted by Luz-Alves *et al*. (2007) was not able to culture all microbes harboured by tabanid flies from Brazil and as such it is concluded that next generation sequencing is more effective in detecting all microbes within a sample tested provided that there is ample DNA of high quality extracted. Nonetheless, the quality of OTUs produced from Zambian samples was better than those from South African samples as they produced more bacterial genera. Furthermore, due to the uneven distribution of microbes detected in the tabanid flies some of the roles played by these bacteria in the different tabanid flies are currently unknown and whether these flies are capable of transmitting these bacteria to humans and domestic animals is a mystery yet to be solved.

In conclusion, this is the first study which has characterized the gut microbiota harboured by 4 species of field derived tabanid flies, namely *Atylotus diurnus*, *Tabanus* *conformis*, *T. par* and *T. taeniola* in South Africa and Zambia. The characteristics of detected microbes differ considerably, whereby as reported in literature some are of environmental, medical or veterinary importance. The findings obtained in this study open doors for future studies, particularly in identifying candidate microbes that can be used in the control of tabanid flies as well as in determining the actual role played by symbiotic microbes within the flies.

5.4.2 Recommendations

For future research on metagenomic analysis of tabanid flies different DNA extraction methods should be explored in order to extract high quality DNA to produce more sequence reads for analysis. It is also suggested that crucial care be considered when handling the DNA samples for metagenomic library preparation. Additional variable regions should be investigated as in the current study only the V3 – V4 region was investigated. More samples representing different tribes of tabanid flies should be explored to determine if they will harbour similar microbes to these found in the current study. Further analysis on functional genomics and expressed sequence tags (ESTs) should be investigated to determine the role played by these microbes in tabanid flies. Additionally, the possibility of transmission of these microbes by tabanid flies should also be investigated.

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APPENDIX I

Characterization of tabanid flies (Diptera: Tabanidae) in South Africa and Zambia and detection of protozoan parasites they are harbouring

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SUMMARY

Tabanids are haematophagous flies feeding on livestock and wildlife. In the absence of information on the relationship of tabanid flies and protozoan parasites in South Africa and Zambia, the current study was aimed at characterizing tabanid flies collected in these two countries as well as detecting protozoan parasites they are harbouring. A total of 527 tabanid flies were collected whereby 70·2% were from South Africa and 29·8% were from Zambia. Morphological analysis revealed a total of five different genera collected from the sampled areas namely: *Ancala, Atylotus, Haematopota, Philoliche* and *Tabanus*. DNA extracted from South African *Tabanus par* and *Tabanus taeniola* tested positive for the presence of *Trypanosoma congolense* (Savannah) and *Trypanosoma theileri* whilst one member from *T. par* was positive for *Trypanosoma brucei* species. DNA extracted from Zambian tabanid flies tested positive for the presence of *Besnoitia* species at 1·27% (2/157), *Babesia bigemina* 5·73% (9/157), *Theileria parva* 30·11% (30/157) and 9·82% (14/157) for *Trypanosoma evansi*. This study is the first to report on relationship of *Babesia* and *Theileria* parasites with tabanid flies. Further investigations are required to determine the role of tabanids in transmission of the detected protozoan parasites in livestock and wildlife in South Africa and Zambia.

Key words: Horse flies, tabanids, *Babesia bigemina*, *Besnoitia* spp., *Theileria parva*, *Trypanosoma* species.

INTRODUCTION

Tabanids are robust medium-to-large (6–30 mm) biting flies commonly referred to as horse or deer flies (Nevill *et al.* 1994; Service, 2012). They belong to the family Tabanidae which is further divided into four subfamilies, namely Chrysopsinae, Pangoniinae, Scepsidinae and Tabaninae, comprising of more than 4400 species belonging to 114 genera, with a cosmopolitan distribution (Baldacchino *et al.* 2014*a*). However, in Africa only members from the subfamilies Chrysopsinae, Tabaninae, and various species of the genus *Philoliche* from the subfamily Pangoniinae, are of economic, medical and veterinary importance (Nevill *et al.* 1994). In southern Africa there are about 410 species with nine dominant genera (Nevill *et al.* 1994).

The mechanical transmission of various pathogens by tabanid flies has been known for decades (Zumpt, 1949). This mode of transmission may either occur through contamination of mouthparts or regurgitation (Foil and Gorham, 2000; Baldacchino *et al.* 2013). Defecation is also significant as pathogens can be ingested and deposited on food or other surfaces, however if the pathogens do not multiply within the alimentary canal of the insect then this is defined as mechanical transmission (Foil and Gorham, 2000). Tabanid flies are vectors of most disease-causing bacteria and viruses in animals and humans such as *Bacillus anthracis, Listeria monocytogenes, Anaplasma marginale, Coxiella burnetii* and rinderpest virus (Chainey, 1993; Nevill *et al.* 1994; Esterhuizen, 2006; Baldacchino *et al.* 2014*a*; Hornok *et al.* 2014). Protozoan parasites, including

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APPENDIX II

Protozoan parasite sequences

>KX870078_*Trypanosoma brucei* [17-SA] 18S ribosomal RNA gene, partial CDS; internal transcribed spacer 1, 5.8S ribosomal RNA gene

CAAAATCGTACAAGGTAGCTGTAGGCGAACCTGCAGCTGGATCATTTTCTGTTATC
CATTATACAAAAAAGAGCATATTTATGTGCATGTATATTTTGCACAGTATGCAACCA
AAAATATACATATATGT_TTTACTTGTTTGTGTTTCTATATGCCGTTTGACATGGAAA
ATAAGGAATGCTATACATACTTCTGTTATTTTCTATCATGTATGTGGGTTAAAGTGTC
TGTGTTAATATACTTTTTAAGGCATGCTCTACATAATATACAGAAGTATTACCACAAA
GAATACGTATGGAATGCGTATCCCCCTATATATATTTATGTATATATGCTATGTGTTT
ATCAACCCCCCATATTTTTTCTCCCTGTTGACCACCGCCCCCACAACGTGTCGCGG
AAGAAGACTTTTCTTCCTTTTTTTAAGAAAAAAACAAAAAAAA

>KX870079_*Trypanosoma congolense* [32-SA] 18S ribosomal RNA gene, partial CDS; internal transcribed spacer 1, 5.8S ribosomal RNA gene

AAGTCGTAACAGGTTGCTGTTGGTGAACCTGCAGCTGGATCATTTTCCGATGATAA
TGTATATATACATATATGTGTGTGTGTACATACGCGTGTGTGTGTGTAGAGAGAGG
TTGTTGTTTGTGTGTGCGCGTGTGCGGAGGGCCCCCCTCGCGCATGAAAATTATC
CCCCCCCCCCCCCCCCCCGGGGTGGTGTGTTTTGTGTGGTGGAAACCGCGGGGG
GGGGGGTGTTGTTGTTGTACCACCCACTATATAAAAAACCCCCCAAAAAACACGCG
CGTGAAAAAACACCCCCCCCGTGGTTCTCTTTTTTTTGTTTTGTGGGGGAGTTGTTT
ATTGTGGGCGCCCCCCCCGGAGGAAAAAAAGGGGGGGGGAGAAAAAAAAACTA
TTTTTTCCCCCCCCCCCCCATTTTTTGTGTGCGCGCGGTGGCTTTCTTTCTCTCCTT
TTTTCTTCCCCCCATCTTTTTTTTTTCCCTCCTCCCCAGTGTGGAGAGAGAAAAAAA
AAAAGAATGTGTTTTTTTAAAAAGAAAGAGGGGGCAGAGAAAAAAATATGGTGTGT
GTTTGTGTACGTGCGCGTGTGTCTCACCCCCCGCTCTCACAGCGGAGTTGGATGT
ATAATTTGTTTATTTATTTATAGAAAAAAAAAAAAAAA

>KX870080_*Trypanosoma theileri* [B6-SA] 18S ribosomal RNA gene, partial CDS; internal transcribed spacer 1, 5.8S ribosomal RNA gene

CACCCGTCCGTACAGGTTGCTGTTGGTGAACCTGCAGCTGGATCATTTTCCGATGA
GATTATGTATCACACATATTTTTATATGTACCGCGGGGTGGAATAATAATATTATGT
ATATACATATATATATATATTTCTTCCTTCGCACAGATGTATTTACATATGGCAATTTT
GCAATAACAAAAAAAAAACTCATGCCGCTTGACTTTCTCCACATAAAAAATACTATT

AATTATGTGTGTTTGTTGAGAACGGCCCCAACAACGTGTCGCGATGGAAGACTTGG
CTTCCTATTTCGTTGTAGAACGCAACAAAAAAA

>KX870081_*Trypanosoma evansi* [14-ZM] 18S ribosomal RNA gene, partial CDS; internal transcribed spacer 1, 5.8S ribosomal RNA gene
TCTAGGACAAGTCGTAACAGGTAGCTGTAGGTGGACCTGCAGCTGGATCATTTTCT
GTTATCCATTATACAAAAAAGAGCATATTTATGTGCATGTATATATTGCCCAGAATG
CAACCAAAAATATACTTATATGTTTTACTTGTTTGTGTTTCTATATGCCGTTGGACAG
GGGAAAGAAGGAAGGCTACACATACTTCGGTTTTTTTCAATCAGGTAGGTGGGTAA
AATGGTCGGTGTTAATATACTTTTATAGGCTTGCTCTACATAATATACAGAATAAATA
CCACAAAAAATACGTATGGAATGCGAATCTCTCTATATATATTTATGTATATATGCTA
TGTGTATATCAACCCCCCATATTTTTTCCCCCTGGACCCCGCCCCCCCCACCAGGT
GGCGAGGGAGAAGTTGTGTTCTCTTTTTTTTAAAAAAAACACAAAAAAAA

>KX870082_*Trypanosoma evansi* [2-ZM] 18S ribosomal RNA gene, partial CDS; internal transcribed spacer 1, 5.8S ribosomal RNA gene
TCTTGGAGCAAGTCGTACAGGTAGCTGTAGGTGGACCTGCAGCTGGATCATTTTCT
GTTATCCATTATACAAAAAAGAGCATATTTATGTGCATGTATATATTGCACAGTATG
CAACCAAAAATATACATATATGTTTTACATGTATGTGTTTCTATATGCCGTTTGACAT
GGGAGATGAGGGATGCTATACATACTTCTGTTATTTTCTATCATGTATGTGTGTTAG
AGTGTCTGTGTTAATATACTTTTTAATGCATGCTCTACATAATATACAGTTGTTATAC
CACAGAGAATACGTATGGAATGCGTATCTCTCTATATATATTTATGTATATATGCTAT
GTGTGTATATCACCCTCACATATTTTCCCCGTGGACACCACCGCTCCCACAACGTG
TCGCGAGAGAAGATGTGTCTTCCTATTTCTAAGAAAAACACAAAAAA

>KX870083_*Babesia bigemina* [A3-ZM] 18S ribosomal RNA gene, partial CDS; 18S ribosomal RNA gene
CTTTAAAGCCCCACCGTTCCTATTAACCATTACCAAGGCTCAAAACCAACAAAATAG
AACCAAGGTCCTACTCTATTATTCCATGCTGAAGTATTCAAGACAAAAGTCTGCTTG
TAACACTCTAATTTTCTCAAAGTTAAAAAAAAGCCAGCGAAAAGACCCAAAACCAGG
GAAAAAACGCGAGGCTGAAATACAACTACGAGCTTTTTTACTGCAACAAGTTTTATA
TACGCTATTGGAGCTGGAATTACCGCGGCTGCTGGCACCAGACTTGCCCTCCAAT
TGGTACTCTGGTGAGGTTGTACATCACCATCATTCCAATTACAAGACGAAAGCCCT
GTATTGTTATTTCTTGTCACTACCTCCCTGTGTCAAA

>KX870084_Babesia bigemina [C4-ZM] 18S ribosomal RNA gene, partial CDS; 18S ribosomal RNA gene
CATCGGGACTTTCGTCTTGTATTGGATGATGGTGATGTACAACCTCACCAGAGTAC
CAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTATTTCCAGCTCCAATCCGC
GTATATTAAACTTGTTGCAGTTAAAAAGCTCGTAGTTGTATTTCAGCCTCGCGTTTT
TTCCCTGGTTTTGGGTCTTTTCGCTGGCTTTTTTTTTACTTTGAGAAAATTAGAGTGT
TTCAAGCAGACTTTTGTCTTGAATACTTCAGCATGGAATAATAGAGTAGGACCTTGG
TTCTATTTTGTTGGTTTTGAGCCTTGGTATTGGTTAATAGGAACGGTTGGGGGCATT
CGTATTTATCTGTCAGAGGTGAAATTCTTAGA

>KX870085_*Babesia bigemina* [H2-ZM] 18S ribosomal RNA gene, partial CDS; 18S ribosomal RNA gene
CAAAAATATAATTTTTTTTTTCGTCTTGTATTGGATGATGGTGATGTACAACCTCACC
TGGAGTACCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTC
CAATAGCGTATATTAAACTTGTTGCAGTTAAAAAGCTCGTAGTTGTATTTCAGCCTC
GCGTTTTTTCCCTGGTTTTGGGTCTTTTCGCTGGCTTTTTTTTTACTTTGAGAAAATT
ATCGTGTTTCAAGCCAACTTTTGTCTTGAATACTTCAGCATGGAATAATATAGTAGG
ACCTTGGTTCTATTTTGTTGGTTTTGAGCCTTGGTTATGGTTAATAGGAACGGTTGG
GGGCATTCGTATTTTGACTGTCAGAGGTGAGATTCTCAGAT

>KX870086_*Theileria parva* [B2-ZM] 18S ribosomal RNA gene, partial CDS; 18S ribosomal RNA gene
TCATTCGGGGGCTCACGTTCTTGTATTGGATGATGGGAATTTTAAAACCTCTTCCA
GAGTATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGAAATTCCAGCTCCA
AGAGCGTATATTAAAATTGTTGCAGTTAAAAAGCTCGAAGTTGAATTTCTGCTGCAT
CGCCGTGTCCCCTCTGGGCCTCTGCGTGTGTTTTATTTCAAATGGATTTCCCTGTG
TCTGCAGGGCACTTTTTGAAAATAAGAGAGCTCAAAGCCGCTTTTGCCTCTTTAATA
TTGTAGCAAAAAATAAAAACTTGAGACTTTTTTTCTTTTTTTGGGGCAAAGTACCCG
ATAAATGGGAAATATGGGGGCATTTGGGCATTCACATTTCAATGTCAAATGTGAGA
ATCTCAGAGA

Tabanid fly sequences

>KY555737 [*Tabanus par*] [A3-ZM] cytochrome oxidase subunit 1 (COI) gene, partial CDS; mitochondrial

TAAATATATTTTTTTTTTTTTGGGAGATGAGCCGGAAAGTTGGTCTTCATTAAGTATT
TTAATTCGAGCTGAATTAGGACATCCAGGATCATTTTTGGTGATGACCACATTTATA
ATGTTATTGTCACAGCCCGCGCCTTTGTTATTATTTTCTTTATACTATTACCTATTAT
ATTTGGGGGATTTGGAAATTGATTATTTCCTTTATTATTATGAGCTCCTGATATACG
CATTCCCTCGAATAAATAATATAAGTTTTTCATTATTACCCCCCTCTTTGACTCTTCT
ATTAGCTAGTAGTATAGAAGAAAATGGAGCTGGTACTGGATTGAACAGTATACCCC
CCTCTATCTGCAGCAATCGCCCATGGTGGAGGATCAGTTCATTTAGCAATTTTTTCT
TTAATTTAGCAGGAATTTCTTCTATTTTAGGAGCTGTTAATTTTATTACTACTGTTATT
AATATACGATCTACAGGAATTACTTTCGATCGAATACCCTTATTTGTATGTGCTGTA
GTAATTACTGCTATTCTTCTATTATTATCATTACTAGAACTAGCAGGAGCTATTACTA
TACTTTTAACAGACCGAAATTTAAATACTTCATTCTTTGACCCAGCAGGAGGAGGTG
ATCTATTTTATACCAACATTTATTTTGATTTTTTTGGTCACCCAAAATTTAA

>KY555738 [*Tabanus par*] [A2-ZM] cytochrome oxidase subunit 1 (COI) gene, partial CDS; mitochondrial

CCTAATTTTTTTTTTTTTGGGGCATGAGCTGGAATATTTGGTACTTCATTATGTATTT
TATTTCGAGCTGAATTACGGACATCCAGGATCACTAATTGGAGATGACCAAATTTAT
AATGTAATTGTAACAGCACATGCTTTTGTTATAATTTTCTTTATAGTAATACCTATTAT
AATTGGAGGATTTGGAAATTGTTTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGC
ATTTCCTCGAATAAATAATATAAGTTTTTCATTACTCCCCCCTTCACTTACTCTTTTAT
TAGCCAGTAGTATAGTGGAAAATGGAGCTGGAACCGGATGTACAGTTTATCCCCCA
TTATCCGCTGCTATTGCTCATGGAGGAGGATCAGTTGATTTAGCTATTTTTTCCCTT
CATTTAGCTGGAATTTCATCTATTTTAGGAGCTGTTAATTTTATTACTACTGTTATTA
ATATACGATCTACTGGAATTACTTTTGATCGAATACCGTTATTTGTTTGTGCAGTAG
TAATTACTGCTATTTTATTATTATTATCATTACCAGTTTTAGCAGGAGCTATTACTATA
CTTTTAACAGATCGAAATTTAAATACTTCATTTTTTGATCCTGCAGGAGGAGGAGAT
CCAATTTTATATCAACATTTATTTTGTTTTTTTGGTCACCCTGAAGAAACCA

>KY555739 [*Tabanus par*] [A6-ZM] cytochrome oxidase subunit 1 (COI) gene, partial CDS; mitochondrial

CATTTTTATTTTTATTTTTTGGGGCATGAGCTGGATAATTGGTACTTCATTAAGTATT
TTAATTCGAGCTGAATTAGGACATCCAGGATCACTAATTGGAGATGACCAAATTTAT
AATGTAATTGTAACAGCACATGCTTTTGTTATAATTTTCTTTATAGTAATACCTATTAT
AATTGGAGGATTTGGAAATTGTTTAGTTCCTTTAATGTTAGGAGCTCCTGATATAGC
ATTTCCTCGAATAAATAATATAAGTTTTTCATTACTCCCTCCTTCACTTACTCTTTTAT
TAGCCAGTAGTATAGTAGAAAATGGAGCTGGAACCGGATGTACAGTTTATCCCCCA
CTATCCGCTGCTATTGCTCATGGAGGAGGATCAGTTGATTTACTATTTTTTCCCTTC
ATTTTGCTGGAATTTCATCTATTTTTGGAGCTGTTAATTTTATTACTACTGTTATTAAT
ATACAACCTCCTGGAATTATTTTTGATCAATACCTTTATTTGTTTTAGCAGTAG

>KY555740 [*Tabanus par*] [TP14-SA] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial

TTTTCTACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGAGCTG
GAATATTTGGTACTTCATCAAGTATTTGTAATTCGAGCTGAATTGGGCCATCCAGGA
TCATTAATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCACATGCTTTTGTTA
TAATTTTCTTTATAGTAATACCTATTATAATTGGAGGATTTGGAAATTGTTTAGTTCC
CTTAATATTAGGGGCTCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTCA
TTATTACCCCCCTCTCTCACTCTTTTATTAGCCAGTAGTATAGTAGAAAATGGGGCT
GGAACTGGTTGTACAGTATACCCCCCACTTTCTGCTGCTATTGCCCATGGAGGAG
GATCAGTTGATTTAGCTATTTTTTCTCTTCATTTAGCAGGAATTTCTTCTATTTTAGG
AGCTGTAAATTTTATTACCACTGTAATTAATATACGATCTACAGGAATTACATTTGAC
CGAATACCTTTATTTGTTTGTGCAGTAGTAATTACTGCTATTTTATTATTATTATCATT
ACCAGTTTTAGCTGGAGCTATTACTATACTTTTAACAGATCGAAATTTAAATACCTCA
TTTTTTGACCCGGCCGGAGGAGGAGACCCTATTTTATACCAACATTTATTTTGTTTT
TTTGGTCAC

>KY555741 [*Tabanus par*] [A4-ZM] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial

TTTTCTACAAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGTGCT
GGAATAATTGGTACTTCATTAAGTATTTTAATTCGAGCTGAATTGGGCCATCCAGGA
TCATTAATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCACATGCTTTTGTTA
TAATTTTCTTTATAGTAATACCTATTATAATTGGAGGATTTGGAAATTGTTTAGTTCC

TTTAATATTAGGGGCTCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTCA
TTATTACCCCCCTCTCTCACTCTTTTATTAGCCAGTAGTATAGTAGAAAATGGGGCT
GGAACTGGTTGAACAGTATACCCCCCACTTTCTGCTGCTATTGCCCATGGAGGAG
GATCAGTTGATTTAGCTATTTTTTCTCTTCATTTAGCAGGAATTTCTTCTATTTTAGG
AGCTGTAAATTTTATTACCACTGTAATTAATATACGATCTACAGGAATTACATTTGAC
CGAATACCTTTATTTGTTTGTGCAGTAGTAATTACTGCTATTTTATTATTATTATCATT
ACCAGTTTTAGCTGGAGCTATTACTATACTTTTAACAGATCGAAATTTAAATACCTCA
TTTTTTGACCCGGCCGGAGGAGGAGACCCTATTTTATACCAACATTTATTTTGTTTT
TTTGGTCAC

>KY555742 [*Tabanus par*] [TP27-SA] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial
TTTTCCTACCAAATCATATAGATATTTGGAACATTATATTTTTATTTTTGGGGCTTGT
GCTGGAATAATTGGTACTTCATTAAGTATTTTAATTCGAGCTGAATTGGGCCATCCA
GGATCATTAATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCACATGCTTTT
GTTATAATTTTCTTTATAGTAATACCTATTATAATTGGAGGATTTGGAAATTGTTTAG
TTCCCTTAATATTAGGAGCTCCTGATATAGCATTTCCCCGAATAAATAATATAAGTTT
TTGTTTATTACCCCCCTCTCTCACTCTTTTATTAGCCAGTAGTATAGTAGAAAATGG
AGCTGGAACTGGTTCAACAGTATACCCCCCACTTTCTGCTGCTATTGCCCATGGAG
GAGGATCAGTTGATTTAGCTATTTTTTCTCTTCATTTAGCAGGAATTTCTTCTATTTT
AGGAGCTGTAAATTTTATTACCACTGTAATTAATATACGATCTACAGGAATTACATTT
GACCGAATACCTTTATTTGTTTCAGCAGTAGTAATTACTGCTATTTTATTATTATTAT
CATTACCAGTTTTAGCTGGAGCTATTACTATACTTTTAACAGATCGAAATTTAAATAC
CTCATTTTTTGACCCGGCCGGAGGAGGAGACCCTATTTTATATCAACATTTATTTTG
TTTTTTTTGGTCACCCTGTAGT

>KY555743 [*Tabanus par*] [TP39-SA] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial
TTTTTCTACAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCTTGTGCT
GGAATAATTGGTACTTCATTAAGTATTTTAATTCGAGCTGAATTGGGCCATCCAGGA
TCATTAATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCACATGCTTTTGTTA
TAATTTTCTTTATAGTAATACCTATTATAATTGGAGGATTTGGAAATTGTTTAGTTCC
CTTAATATTAGGAGCTCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGT
TTATTACCCCCCTCTCTCACTCTTTTATTAGCCAGTAGTATAGTAGAAAATGGGGCT

GGAACTGGTTGTACAGTATACCCCCCACTTTCTGCTGCTATTGCCCATGGAGGAG
GATCAGTTGATTTAGCTATTTTTTCTCTTCATTTAGCAGGAATTTCTTCTATTTTAGG
AGCTGTAAATTTTATTACCACTGTAATTAATATACGATCTACAGGAATTACATTTGAC
CGAATACCTTTATTTGTTTGTGCAGTAGTAATTACTGCTATTTTATTATTATTATCATT
ACCAGTTTTAGCTGGAGCTATTACTATACTTTTAACAGATCGAAATTTAAATACCTCA
TTTTTTGACCCGGCCGGAGGAGGAGACCCTATTTTATATCAACATTTATTTTGTTTT
TTTGGTCACCCTGAAGTT

>KY555744 [*Tabanus taeniatus*] [J6-ZM] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial
TTTTGGGGCTTGAGCTGGAATAATTGGTACTTCATTAAGTATTTTAATTCGAGCTGT
ATTGGGCCATCCAGGATCATTAATTGGAGATGTCCAAATTTATTATGTAATTGTAAC
AGCACATGCTTTTGTTATAATTTTCTTTATAGTAATACCTATTATAATTGGAGGATTT
GGAAATTGATTAGTTCCCTTAATATTAGGAGCTCCTGTTATAGCATTTCCTCGAATA
AATATTATAAGTTTTTGATTATTACCCCCCTCTCTCACTCTTTTATTAGCCAGTACTA
TAGTAGAAAATGGAGCTGGAACTGGTTGAACAGTATACCCCCCACTTTCTGCTGCT
ATTGCCCATGGAGGAGGATCAGTTGTTTTAGCTATTTTTTCTCTTCATTTAGCAGGA
ATTTCTTCTATTTTAGGAGCTGTAAATTTTATTACCACTGTAATTTATATACGATCTA
CAGGAATTACATTTCGACCGAATACCTTTATTTGTTTGAGCAGTACTATTTACTGCT
ATTTTATTATTATTATCATTACCAGTTTTACCTGGAGCTATTACTATACTTTTATCAGA
TCGAAATTTATATACCTCATTTTTT

>KY555745 [*Atylotus diurnus*] [B2-ZM] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial
TGATGACCAAATTTACAATGTAATTGTAACTGCACATGCTTTTGTTATAATTTTCTTT
ATAGTAATACCTATTATAATTGGGGGATTTGGTAATTGTTTAGTTCCTTTAATATTAG
GAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGTTTACTACCCC
CCTCATTAACCCTTTTATTAGCCAGTAGTATAGTGGAAAATGGGGCCGGAACAGGA
TGTACAGTTTATCCCCCCCTATCTGCTGCAATTGCCCATGGAGGAGGTTCTGTTGA
TTTAGCAATTTTCTCTTTACACCTAGCAGGAATTTCATCTATTTTAGGGGCTGTAAAT
TTTATTACAACAGTAATTAATATACGATCTACAGGAATTACCTTTGATCGAATACCTT
TATTTGTATGCAGCTGTAGTAATTACAGCTATTTTATTATTATTATCTTTACCAGTATT
AGCTGGAGCTATTACTATACTTTTAACAGATCGAAACTTAAATACTTCATTTTTTGTT
CCTGCCGGAGGAGGAGATCCAATTTAACCCACAAAACAAC

>KY555746 [*Atylotus agrestis*] [H1-ZM] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial
AAATATTTTTATTTTTGGGGCATGAGCCGGTATAATTGGTACTTCCTTAAGTATTCTA
ATTCGAGCTGTATTAGGACACCCAGGATCATTAATTGGTGTTCACCAAATTTACAAT
GTAATTGTAACTGCACATGCTTTTGTTATAATTTTCTTTATAGTAATACCTATTATAAT
TGGGGGATTTGGTTATTGATTAGTTCCTTTAATATTAGGAGCCCCTCATATAGCATT
TCCTCGAATAAATTATATAAGTTTTTGATTACTACCTCCCTCATTAACCCTTTTATTA
GCCAGTATTATAGTGGAAAATGGGGCCGGAACAGGATGAACAGTTTATCCTCCCCT
ATCTGCTGCAATTGCCCATGGAGGAGGTTCTGTTCATTTAGCAATTTTCTCTTTACA
CCTAGCAGGAATTTCATCTATTTTAGGGGCTGTAAATTTTATTACAACAGTAATTATT
ATACGATCTACAGGAATTACCTTAGATCGAATACCTTTATTTGTATGAGCTGTAGTA
ATTACAGCTATTTTATTATTATTATCTTTACCAGTATTAGCTGGAGCTATTACTATAC
TTTTAACAGATCGAAACTTAAATACTTCATTTTTTCAT

>KY555747 [*Atylotus agrestis*] [H6-ZM] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial
TTTTCTACAAAATCATAAAGATATTGGTACATTATATTTTATTTTTGGGGCATGGGCC
GGTATAATTGGTACTTCCTTAAGTATTCTAATTCGAGCTGAATTAGGACACCCAGGA
TCATTAATTGGTGATGACCAAATTTACAATGTAATTGTAACTGCACATGCTTTTGTTA
TAATTTTCTTTATAGTAATACCTATTATAATTGGGGGATTTGGTAATTGTTTAGTTCC
TTTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGT
TTACTACCCCCCTCATTAACCCTTTTATTAGCCAGTAGTATAGTGGAAAATGGGGC
CGGAACAGGATGCACAGTTTATCCTCCCCTATCTGCTGCAATTGCCCATGGAGGA
GGTTCTGTTGATTTAGCAATTTTCTCTTTACACCTAGCAGGAATTTCATCTATTTTAG
GGGCTGTAAATTTTATTACAACAGTAATTAATATACGATCTACAGGAATTACCTTTG
ATCGAATGCCTTTATTTGTATGTGCTGTAGTAATTACAGCTATTTTATTATTATTATC
TTTACCAGTATTAGCTGGAGCTATTACTATACTTTTAACAGATCGAAACTTAAATACT
TCATTTTTTGATCCTGCTGGAGGAGGAGATCCAATTTTATACCAACATTTATTCTCA
TTTTTTGGTCACCCTGAAGTTCAA

>KY555748 [*Atylotus agrestis*] [M8-SA] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial

TCTACAAATCATAAAGATATTGGTACATTATATTTTATTTTTGGAGCATGAGCCGGTATATCTTGGTACTTCCTTAAGTATTCTAATTCGAGCTGAATTAGGACACCCAGGATCATTAATTGGTGATGACCAAATTTACAATGTAATTGTAACTGCACATGCTTTTGTTATAATTTTCTTTATAGTAATACCTATTATAATTGGGGGATTTGGTAATTCATTACTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGTTTACTACCCCCCTCATTAACCCTTTTATTAGCCAGTAGTATAGTGGAAAATGGGGCCGGAACAGGAGGAACAGTTTATCCTCCTCTATCTGCTGCAATTGCCCATGGAGGAGGTTCTGTTGATTTAGCAATTTTCTCTTTACACCTAGCAGGAATTTCATCTATTTTAGGAGCTGTAAATTTTATTACAACAGTAATTAATATACGATCTACAGGAATTACCTTTGATCGAATACCTTTATTTGTATGTGCTGTAGTAATTACAGCTATTTTATTATTATTATCTTTACCAGTATTAGCTGGAGCTATTACTATACTTTTAACAGATCGAAACTTAAATACTTCATTTTTTGATCCTGCTGGAGGAGGAGATCCAATTTTATACCAACATTTATTCTCATTTTTTGGTCACCCTGAAAGTT

>KY555749 [*Atylotus diurnus*] [B1-ZM] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial

TACAATGTTATTGTTACTGCACATGCTTTTGTTATTAATTTTCTTTATAGTAATACCTATTATAATTGGGGGATTTGGTAATTGTTTAGTTCCTTTAATATTAGGAGCCCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTCATTACTACCCCCCTCATTAACCCTTTTATTAGCCAGTAGTATAGTGGAAAATGGGGCCGGAACAGGATCAACAGTTTATCCCCCCCTATCTGCTGCAATTGCCCATGGAGGAGGTTCTGTTGATTTAGCAATTTTCTCTTTACACCTAGCAGGAATTTCATCTATTTTAGGGGCTGTAAATTTTATTACAACAGTAATTAATATACGATCTACAGGAATTACCTTTGATCGAATACCTTTATTTGTATGTGCTGTAGTAATTACAGCTATTTTATTATTATTATCTTTACCAGTATTAGCTGGAGCTATTACTATACTT

>KY555750 [*Atylotus diurnus*] [B5-ZM] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial

GGTACATTATATTTTATTTTTGGGGCATGAGCCGGTATTATTGGTACTTCCTTTAGTATTCTTATTCGAGCTGAATTACGGACACCCAGGATCATTAATTGGTGATGACCAAATTTACAATGTAATTGTAACTGCACATGCTTTTGTTATAATTTTCTTTATAGTAATACCTATTATAATTGGGGGATTTGGTAATTGTTTAGTTCCTTTAATATTAGGAGCCCCTGATA

TAGCATTTCCTCGAATAAATAATATAAGTTTTTGTTTACTACCCCCCTCATTAACCCT
TTTATTAGCCAGTAGTATAGTGGAAAATGGGGCCGGAACAGGAGGAACAGTTTATC
CTCCTCTATCTGCTGCAATTGCCCATGGAGGAGGTTCTGTTGATTTAGCAATTTTCT
CTTTACACCTAGCAGGAATTTCATCTATTTTAGGAGCTGTAAATTTTATTACAACAGT
AATTAATATACGATCTACAGGAATTACCTTTGATCGAATACCTTTATTTGTAAGAGCT
GTAGTAATTACAGCTATTTTATTATTATTATCTTTACCAGTATTAGCTGGAGCTATTA
CTATACTTTTAACAGATCGAAACTTAAATACTTCATTTTTTGATCCTGCTGGAGGAG
GAGATCCAATTTTATACCAACATTTATTCTGTTTTTTTGGTCACCC

>KY555751 [*Tabanus gratus*] [CB2-SA] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial
TTGGAACATTATATTTTATTTTTGGGGCATGAGCTGGAATAATTGGTACTTCATTAA
GTATTTTAATTCGAGCGAATTAGGACATCCAGGACCATTAATTGGAGATGTCCAAAT
TTATAATGTAATTGTAACAGCACATGCTTTTGTTATAATTTTCTTTATAGTAATACCTA
TTATAATTGGAGGATTTGGAAATTGTTTAGTTCCTTTAATATTAGGAGCCCCTGCTA
TAGCATTTCCTCGAATAAAAAATATAAGTTTTTGTTTACTTCCCCCTTCACTTACTCT
TTTATTAGCCAGTAGTATAGTAGAAAATGGAGCCGGAACTGGAGGAACAGTTTATC
CACCACTATCTGCTGCTATTGCCCATGGAGGAGGATCAGTTGATTTAGCTATTTTTT
CTCTCCATTTAGCTGGAATTTCATCTATTTTAGGGGCTGTTAATTTTATTACTACTGT
TATTAATATACGATCTACTGGAATTACCTTTGACCGAATACCTTTATTTGTTTCAGCA
GTAGTAATTACTGCTATTTTATTATTATTATCATTACCAGTTTTAGCAGGAGCTATTA
CTATACTTTTAACAGATCGAAATTTAAATACTTCATTTTTTGATCCTGCGGGAGGAG
GAGATCCAATTTTATATCAACATTTATTTTCATTTTTTGGTCACCTTGGAAGTT

>KY555752 [*Haematopota longa*] [E1-ZM] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial
CCTTTTATTTTTTTTTTGGAGCATGAGCTGGAATAATTGGAACCTCATTAAGTATTTT
AATTCGAGCTGCATTAGGACATCCAGGATCTTTAATTGGTGTTGCCCCAAATTTATA
TTGTTATTGTATCTGCACATGCATTTGTATTTATTTTCTTTAAAGTTATACCCATTATT
ATTGGTGGATTTGGAAATTGATAAGTTCCATGAATATTTGGAGCTCCTGTTATTGCA
TTCCCACGAAAAAAAAATATATGTTTTTGACTTTTACCTCCATCATTTACTCTTTTATT
TGCAAGTACCTATAGTAGAAAATGGAGCTGGAACTGGTTCAACAGTTTACCCACCA
TTATCAGCTGCAATTGCTCATGGGGGAGGATCAGTAGATTTAGCAATTTTTTCTTTA
CACCTTGCAGGAATTTCTTCAATTTTAGGGGCTGTAAATTTTATTACTACTGTAATTA

ATATACGATCAACAGGAATTACTTTTGATCGAATACCTTTATTTGTATCAGCTGTAGT
AATTACAGCTATTCTATTATTGTTATCTTTACCAGTATTAGCCGGTGCCATTACTATA
CTTTTAACAGATCGAAATTTAAATACTTCTTTTTTTGATCCTGCTGGAGGAGGAGAC
CCTATTTTATATCAACATTTATTTTCTTTTTTTGGTCTCCCTCAAGTTTACAAT

>KY555753 [*Haematopota longa*] [E3-ZM] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial
ACATTATATTTTATTTTTTGGAGCATGTGCTGGACAATTGGAACCTCATTATGTATTT
TCATTCGAGCTGAATTACGGACATCCAGGATCTTTAATTGGTGATGACCAAATTTAT
AATGTAATTGTAACTGCACATGCATTTGTAATAATTTTCTTTATAGTTATACCCATTA
TAATTGGTGGATTTGGAAATTGGTTAGTTCCATTAATATTAGGAGCTCCTGATATAG
CATTCCCACGAATAAATAATATAAGTTTTTGTCTTTTACCTCCATCATTAACTCTTTT
ATTAGCAAGTAGTATAGTAGAAAATGGAGCTGGAACTGGCTCAACAGTTTACCCAC
CATTATCAGCTGCAATTGCTCATGGAGGAGGATCAGTAGATTTAGCAATTTTTTCTT
TACACCTTGCAGGAATTTCTTCAATTTTAGGGGCTGTAAATTTTATTACTACTGTAAT
TAATATACGATCAACAGGAATTACTTTTGATCGAATACCTTTATTTGTATTAGCTGTA
GTAATTACAGCTATTCTATTATTGTTATCTTTACCAGTATTAGCCGGTGCCATTACTA
TACTTTTAACAGATCGAAATTTAAATACTTCTTTTTTTGATCCTGCTGGAGGAGGAG
ACCCTATTTTATATCAACATTTATTTCGATTTTTTTGGTCACCCTGGAAGTT

>KY555754 [*Tabanus laverani*] [M3-SA] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial
TCTACAAAATCATAAAGATATTGGAACATTATATTTTATTTTTGGGGCATCAGCTGG
AATAATTGGTACTTCATTAAGTATTTTAATTCGAGCTGAATTAGGACATCCAGGATC
ATTAATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCACATGCTTTTGTTATA
ATTTTCTTTATAGTAATACCTATTATAATTGGAGGATTTGGAAATTCATTAGTTCCTT
TAATATTAGGAGCTCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTGTTT
ACTTCCCCCTTCACTTACTCTTTTATTAGCCAGTAGTATAGTAGAAAATGGAGCTGG
AACTGGATGTACAGTTTACCCACCACTATCTGCTGCTATTGCCCATGGAGGAGGAT
CAGTTGATTTAGCTATTTTTTCTCTCCATTTAGCTGGAATTTCATCTATTTTAGGGGC
TGTTAATTTTATTACTACTGTAATTAATATACGATCTACTGGAATTACCTTTGACCGA
ATACCTCTATTTGTTTGTGCAGTAGTAATTACTGCTATTTTATTATTATTATCATTACC
AGTTTTAGCAGGAGCTATTACTATACTTTTAACAGATCGAAATTTAAATACTTCATTT

TTTGATCCTGCGGGAGGAGGAGATCCAATTTTATACCAACATTTATTTTGTTTTTTT
GGTCACCCTGAAGTT

>KY555755 [*Tabanus taeniola*] [B4-SA] cytochrome oxidase 1 (COI) gene, partial CDS; mitochondrial
TTTCTACAAATCAAAAAGATATTGGAACATTATATTTTATTTTTGGGGCATGAGCTG
GAATAATTGGTACTTCATTAAGTATTTTAATTCGAGCTGCCAATTAGGACATCCAGG
ATCACTAATTGGAGATGACCAAATTTATAATGTAATTGTAACAGCACATGCTTTTGTT
ATAATTTTCTTTATAGTAATACCTATTATAATTGGAGGATTTGGAAATTGGTTATTTC
CTTTAATGTTAGGAGCTCCTGATATAGCATTTCCTCGAATAAATAATATAAGTTTTTG
TTTACTCCCTCCTTCACTTACTCTTTTATTAGCCAGTAGTATAGTGGAAAATGGAGC
TGGAACCGGAAGAACAGTTTATCCCCCATTATCCGCTGCTATTGCTCATGGAGGAG
GATCAGTTGATTTAGCTATTTTTTCCCTTCATTTAGCTGGAATTTCATCTATTTTAGG
AGCTGTTAATTTTATTACTACTGTTATTAATATACGATCTACTGGAATTACTTTTGAT
CGAATACCGTTATTTGTTTGGGCAGTAGTAATTACTGCTATTTTATTATTATTATCAT
TACCAGTTTTAGCAGGAGCTATTACTATACTTTTAACAGATCGAAATTTAAATACTTC
ATTTTTTGATCCTGCAGGAGGAGGAGATCCAATTTTATATCAACATTTATTTTGTTTT
TTTGGTCACCCT

APPENDIX III

Appendix III: OTUs produced from South African tabanid flies

OTU	Size	Phylum	Class	Order	Family	Genus
Otu001	7648	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu002	2076	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu003	381	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu004	253	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu005	184	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu006	60	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*
Otu007	60	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu008	34	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu009	27	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu010	18	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu011	16	Firmicutes	Bacilli	Bacillales	Listeriaceae	*Brochothrix*
Otu012	16	Firmicutes	Bacilli	Bacillales	Bacillales_Incertae_Sedis_XII	*Exiguobacterium*
Otu013	14	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu014	14	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu015	11	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Psychrobacter*
Otu016	11	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu017	10	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Staphylococcus*
Otu018	10	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Staphylococcus*
Otu019	10	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu020	9	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	*Aerococcus*
Otu021	9	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Erwinia*
Otu022	8	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Jeotgalicoccus*
Otu023	6	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Sphingobacterium*
Otu024	6	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Staphylococcus*
Otu025	5	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu026	5	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XI	*Peptoniphilus*

Otu027	5	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu028	4	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu029	4	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu030	4	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu031	4	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	
Otu032	4	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu033	4	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu034	3	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu035	3	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu036	3	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu037	3	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu038	3	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Stenotrophomonas*
Otu039	3	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu040	3	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu041	3	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu042	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu043	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu044	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu045	2	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu046	2	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu047	2	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu048	2	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu049	2	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Comamonas*
Otu050	2	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	
Otu051	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu052	2	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu053	2	TM7	TM7_class_incertae_sedis	TM7_order_incertae_sedis	TM7_family_incertae_sedis	*TM7_genus_incertae_*
Otu054	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu055	2	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	*Alcaligenes*
Otu056	2	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Staphylococcus*

Otu057	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu058	2	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Comamonas*
Otu059	2	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu060	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu061	2	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu062	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu063	2	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Sphingobacterium*
Otu064	2	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu065	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu066	1	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Stenotrophomonas*
Otu067	1	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	*Streptococcus*
Otu068	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu069	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu070	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu071	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu072	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu073	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu074	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu075	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu076	1	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	
Otu077	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu078	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu079	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu080	1	Firmicutes	Bacilli	Bacillales	Listeriaceae	*Brochothrix*
Otu081	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu082	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu083	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu084	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu085	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu086	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	

Otu087	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu088	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu089	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu090	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu091	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu092	1	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Jeotgalicoccus*
Otu093	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu094	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu095	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu096	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu097	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu098	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu099	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu100	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu101	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu102	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu103	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu104	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu105	1	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Mucilaginibacter*
Otu106	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu107	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu108	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu109	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu110	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	
Otu111	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu112	1	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Sphingobacterium*
Otu113	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu114	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu115	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu116	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	

Otu117	1	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	
Otu118	1	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	*Pisciglobus*
Otu119	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu120	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu121	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu122	1	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	
Otu123	1	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	*Facklamia*
Otu124	1	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Staphylococcus*
Otu125	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu126	1	Firmicutes	Bacilli	Bacillales	Bacillales_unclassified	
Otu127	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu128	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu129	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu130	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu131	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu132	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu133	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu134	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu135	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu136	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu137	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu138	1	Firmicutes	Bacilli	Bacillales	Bacillales_unclassified	
Otu139	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu140	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu141	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu142	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu143	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu144	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu145	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu146	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	

Otu147	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu148	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu149	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu150	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu151	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu152	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu153	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu154	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales_unclassified	
Otu155	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu156	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu157	1	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriales"_unclassified	
Otu158	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu159	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu160	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu161	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu162	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu163	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu164	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu165	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu166	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu167	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu168	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu169	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu170	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu171	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu172	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu173	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu174	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu175	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu176	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	

Otu177	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu178	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu179	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu180	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu181	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu182	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu183	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu184	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu185	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu186	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu187	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu188	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu189	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu190	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu191	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu192	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu193	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu194	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu195	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu196	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu197	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu198	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu199	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu200	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu201	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu202	1	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Staphylococcus*
Otu203	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu204	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu205	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu206	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	

Otu207	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu208	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu209	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu210	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu211	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu212	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu213	1	Firmicutes	Bacilli	Bacillales	Bacillales_unclassified	
Otu214	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu215	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*
Otu216	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu217	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu218	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu219	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu220	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu221	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu222	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu223	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu224	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu225	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu226	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu227	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu228	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu229	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu230	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu231	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu232	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu233	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu234	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu235	1	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	
Otu236	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	

Otu237	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu238	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu239	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified
Otu240	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu241	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu242	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae
Otu243	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu244	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified
Otu245	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu246	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae
Otu247	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu248	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu249	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu250	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu251	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu252	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu253	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae
Otu254	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu255	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified
Otu256	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified
Otu257	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu258	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified
Otu259	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu260	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu261	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified
Otu262	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu263	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu264	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae
Otu265	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu266	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae

Otu267	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu268	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu269	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu270	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu271	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu272	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu273	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu274	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu275	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu276	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu277	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu278	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu279	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu280	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu281	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu282	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu283	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu284	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu285	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu286	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu287	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	
Otu288	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu289	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu290	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shimwellia*
Otu291	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu292	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu293	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu294	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu295	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu296	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	

Otu297	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified
Otu298	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu299	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu300	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae
Otu301	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu302	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu303	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu304	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu305	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu306	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu307	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu308	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae
Otu309	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified
Otu310	1	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae
Otu311	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae
Otu312	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu313	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified
Otu314	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu315	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu316	1	Firmicutes	Bacilli	Bacillales	Bacillales_unclassified
Otu317	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu318	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified
Otu319	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae
Otu320	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu321	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu322	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu323	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Otu324	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu325	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*
Otu326	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified

Otu327	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu328	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu329	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu330	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu331	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu332	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu333	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu334	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu335	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu336	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*
Otu337	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu338	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu339	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu340	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu341	1	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Enterococcus*
Otu342	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu343	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu344	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu345	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu346	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu347	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu348	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu349	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu350	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu351	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu352	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu353	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu354	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu355	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu356	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	

Otu357	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu358	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu359	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu360	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu361	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu362	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu363	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu364	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu365	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu366	1	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	*Leuconostoc*
Otu367	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu368	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu369	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu370	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu371	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu372	1	Proteobacteria	Proteobacteria"_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu373	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu374	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu375	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu376	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu377	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu378	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu379	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu380	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu381	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu382	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu383	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu384	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu385	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu386	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	

Otu387	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu388	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu389	1	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	*Opitutus*
Otu390	1	Firmicutes	Bacilli	Bacilli_unclassified	Bacilli_unclassified	
Otu391	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu392	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu393	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu394	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu395	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu396	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu397	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu398	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu399	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	
Otu400	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu401	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu402	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu403	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu404	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu405	1	Firmicutes	Bacilli	Bacilli_unclassified	Bacilli_unclassified	
Otu406	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu407	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Delftia*
Otu408	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu409	1	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Flavobacterium*
Otu410	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu411	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu412	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu413	1	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	
Otu414	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu415	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu416	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	

Otu417	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu418	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu419	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu420	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu421	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu422	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu423	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu424	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu425	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu426	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu427	1	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Enterococcus*
Otu428	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu429	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu430	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu431	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu432	1	Firmicutes	Bacilli	Bacillales	Bacillales_unclassified	
Otu433	1	Firmicutes	Bacilli	Bacillales	Bacillales_unclassified	
Otu434	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu435	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu436	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu437	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu438	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu439	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu440	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu441	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu442	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu443	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu444	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu445	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu446	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	

Otu447	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu448	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu449	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu450	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu451	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu452	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu453	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu454	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu455	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu456	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu457	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu458	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu459	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu460	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu461	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu462	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu463	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu464	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu465	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu466	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu467	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu468	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu469	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu470	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu471	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu472	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu473	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu474	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu475	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu476	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*

Otu477	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu478	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu479	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales_incertae_sedis	*Aquabacterium*
Otu480	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu481	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu482	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu483	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
Otu484	1	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Vagococcus*
Otu485	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu486	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu487	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu488	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu489	1	Firmicutes	Bacilli	Bacillales	Listeriaceae	*Brochothrix*
Otu490	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu491	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu492	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	*Exiguobacterium*
Otu493	1	Firmicutes	Bacilli	Bacillales	Bacillales_Incertae_Sedis_XII	
Otu494	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu495	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu496	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu497	1	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	
Otu498	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu499	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu500	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu501	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclassified*	
Otu502	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu503	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu504	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu505	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	

APPENDIX IV

Appendix IV: OTUs produced from Zambian tabanid flies

OTU	Size	Phylum	Class	Order	Family	Genus
Otu0001	303189	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0002	226917	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu0003	175588	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0004	71298	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0005	41545	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0006	36439	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0007	11997	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Enterococcus*
Otu0008	5319	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0009	1166	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0010	850	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0011	762	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0012	644	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0013	584	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0014	450	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu0015	248	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Delftia*
Otu0016	235	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0017	200	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu0018	184	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0019	165	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu0020	139	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0021	129	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0022	110	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu0023	103	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Stenotrophomonas*
Otu0024	101	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*
Otu0025	101	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	*Massilia*
Otu0026	94	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*

Otu0027	92	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Stenotrophomonas*
Otu0028	90	Firmicutes	Bacilli	Bacillales	Planococcaceae	*Lysinibacillus*
Otu0029	89	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	*Massilia*
Otu0030	79	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Staphylococcus*
Otu0031	70	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0032	63	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	*Acetobacter*
Otu0033	63	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0034	60	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0035	52	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Stenotrophomonas*
Otu0036	35	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Enterococcus*
Otu0037	34	Firmicutes	Bacilli	Bacillales	Planococcaceae	*Lysinibacillus*
Otu0038	34	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Flavobacterium*
Otu0039	33	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Terribacillus*
Otu0040	32	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Salinicoccus*
Otu0041	28	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Flavobacterium*
Otu0042	28	Firmicutes	Bacilli	Bacillales	Bacillales_unclassified	
Otu0043	28	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*
Otu0044	27	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	*Carnobacterium*
Otu0045	26	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	*Herbaspirillum*
Otu0046	24	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu0047	23	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0048	22	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Tatumella*
Otu0049	21	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu0050	21	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Comamonas*
Otu0051	21	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	*Marinobacter*
Otu0052	20	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0053	19	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0054	18	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Stenotrophomonas*
Otu0055	18	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu0056	17	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales_incertae_sedis	

Otu0057	17	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0058	17	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0059	16	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0060	16	Firmicutes	Bacilli	Bacillales	Planococcaceae	*Planococcaceae_incertae_sed*
Otu0061	15	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*
Otu0062	14	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0063	14	Firmicutes	Bacilli	Bacillales	Bacillales_unclassified	
Otu0064	13	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu0065	13	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0066	12	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Paludibacter*
Otu0067	12	Firmicutes	Bacilli	Bacillales	Planococcaceae	*Lysinibacillus*
Otu0068	12	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Nosocomiicoccus*
Otu0069	12	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0070	12	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Jeotgalicoccus*
Otu0071	11	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Comamonas*
Otu0072	11	Firmicutes	Bacilli	Bacillales	Planococcaceae	*Planococcus*
Otu0073	11	Proteobacteria	Gammaproteobacteria	Alteromonadales	Shewanellaceae	*Shewanella*
Otu0074	11	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0075	11	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Paludibacter*
Otu0076	10	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Flavisolibacter*
Otu0077	10	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	
Otu0078	10	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0079	9	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	*Opitutus*
Otu0080	9	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0081	9	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*
Otu0082	9	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu0083	8	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0084	8	Verrucomicrobia	Spartobacteria	Spartobacteria_order_incertae_sedis	Spartobacteria_family_incertae_sedis	*Spartobacteria_genera_incerta*
Otu0085	8	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu0086	8	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	*Azohydromonas*

Otu0087	8	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu0088	7	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu0089	7	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu0090	7	Verrucomicrobia	Spartobacteria	Spartobacteria_order_incertae_sedis	Spartobacteria_family_incertae_sedis	*Spartobacteria_genera_incerta*
Otu0091	7	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0092	7	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0093	7	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Flavisolibacter*
Otu0094	7	Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	*Aeromonas*
Otu0095	7	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu0096	7	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0097	7	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	*Acetobacter*
Otu0098	7	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Flavisolibacter*
Otu0099	7	Firmicutes	Bacilli	Bacillales	Planococcaceae	*Lysinibacillus*
Otu0100	6	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu0101	6	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Alkanindiges*
Otu0102	6	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	
Otu0103	6	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu0104	6	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Wautersiella*
Otu0105	6	Proteobacteria	Deltaproteobacteria	Deltaproteobacteria_unclassified	Deltaproteobacteria_unclassified	
Otu0106	6	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0107	6	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu0108	6	Verrucomicrobia	Spartobacteria	Spartobacteria_order_incertae_sedis	Spartobacteria_family_incertae_sedis	*Spartobacteria_genera_incerta*
Otu0109	6	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu0110	6	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	*Anaeromyxobacter*
Otu0111	6	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu0112	6	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	*Massilia*
Otu0113	6	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	*Steroidobacter*
Otu0114	6	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Comamonas*
Otu0115	6	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Psychrobacter*
Otu0116	6	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	*Alistipes*

Otu0117	6	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Paludibacter*
Otu0118	6	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Paludibacter*
Otu0119	6	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu0120	6	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu0121	5	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Flavisolibacter*
Otu0122	5	Firmicutes	Bacilli	Bacillales	Bacillaceae_2	
Otu0123	5	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	*Bacteroides*
Otu0124	5	Actinobacteria	Actinobacteria	Rubrobacterales	Rubrobacteraceae	*Rubrobacter*
Otu0125	5	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0126	5	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0127	5	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobacterales_unclassified	
Otu0128	5	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu0129	5	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	*Trichococcus*
Otu0130	5	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu0131	5	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu0132	5	Verrucomicrobia	Spartobacteria	Spartobacteria_order_incertae_sedis	Spartobacteria_family_incertae_sedis	*Spartobacteria_genera_incerta*
Otu0133	5	Chlamydiae	Chlamydiae	Chlamydiales	Parachlamydiaceae	*Parachlamydia*
Otu0134	5	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	*Acetobacter*
Otu0135	5	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0136	5	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0137	5	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Jeotgalicoccus*
Otu0138	5	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0139	5	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*
Otu0140	5	Proteobacteria	Deltaproteobacteria	Myxococcales	Kofleriaceae	*Kofleria*
Otu0141	5	Firmicutes	Bacilli	Bacillales	Bacillaceae	*Bacillus*
Otu0142	5	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales_incertae_sedis	*Tepidimonas*
Otu0143	5	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*
Otu0144	5	WS3	WS3_class_incertae_sedis	WS3_order_incertae_sedis	WS3_family_incertae_sedis	*WS3_genus_incertae_sedis*
Otu0145	5	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu0146	4	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*

Otu0147	4	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu0148	4	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*
Otu0149	4	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Pedobacter*
Otu0150	4	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu0151	4	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu0152	4	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	*Massilia*
Otu0153	4	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Pseudorhodoferax*
Otu0154	4	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Cloacibacterium*
Otu0155	4	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0156	4	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu0157	4	Proteobacteria	Gammaproteobacteria	Alteromonadales	Shewanellaceae	*Shewanella*
Otu0158	4	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobacteraceae	*Solirubrobacter*
Otu0159	4	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	*Opitutus*
Otu0160	4	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	*Bacteroides*
Otu0161	4	Firmicutes	Bacilli	Bacillales	Bacillaceae_2	*Oceanobacillus*
Otu0162	4	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	*Massilia*
Otu0163	4	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	*Streptococcus*
Otu0164	4	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0165	4	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu0166	4	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	*Macrococcus*
Otu0167	4	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu0168	4	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	
Otu0169	4	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	*Lactobacillus*
Otu0170	4	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*
Otu0171	4	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	*Tumebacillus*
Otu0172	4	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobacterales_unclassified	
Otu0173	4	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu0174	4	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0175	4	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	*Desemzia*
Otu0176	4	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*

Otu0177	4	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	*Atopostipes*
Otu0178	4	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	*Neisseria*
Otu0179	4	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu0180	4	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Flavisolibacter*
Otu0181	4	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	
Otu0182	3	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0183	3	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*
Otu0184	3	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales_unclassified	
Otu0185	3	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	
Otu0186	3	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Paludibacter*
Otu0187	3	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0188	3	Acidobacteria	Acidobacteria_Gp25	Acidobacteria_Gp25_order_incertae_sedis	Acidobacteria_Gp25_family_incertae_sedis	*Gp25*
Otu0189	3	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu0190	3	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu0191	3	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu0192	3	Firmicutes	Bacilli	Bacillales	Bacillaceae_2	*Oceanobacillus*
Otu0193	3	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0194	3	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	
Otu0195	3	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu0196	3	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0197	3	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Vagococcus*
Otu0198	3	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	*Bacteroides*
Otu0199	3	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Pedobacter*
Otu0200	3	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	*Tumebacillus*
Otu0201	3	Firmicutes	Bacilli	Bacillales	Bacillales_unclassified	
Otu0202	3	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0203	3	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu0204	3	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	*Aerococcus*
Otu0205	3	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales_unclassified	
Otu0206	3	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	*Bacteroides*

Otu0207	3	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	*Atopococcus*
Otu0208	3	Bacteroidetes	Bacteroidetes"_unclassified	Bacteroidetes"_unclassified	Bacteroidetes"_unclassified	
Otu0209	3	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Flavisolibacter*
Otu0210	3	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu0211	3	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	
Otu0212	3	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu0213	3	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	
Otu0214	3	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0215	3	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0216	3	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	*Gemmatimonas*
Otu0217	3	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	
Otu0218	3	Verrucomicrobia	Subdivision3	Subdivision3_order_incertae_sedis	Subdivision3_family_incertae_sedis	*3_genus_incertae_sedis*
Otu0219	3	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0220	3	Firmicutes	Bacilli	Bacillales	Bacillales_unclassified	
Otu0221	3	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0222	3	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Parabacteroides*
Otu0223	3	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu0224	3	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Flavisolibacter*
Otu0225	3	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu0226	3	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu0227	3	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Flavisolibacter*
Otu0228	3	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0229	3	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	*Acetobacter*
Otu0230	3	Verrucomicrobia	Spartobacteria	Spartobacteria_order_incertae_sedis	Spartobacteria_family_incertae_sedis	*Spartobacteria_genera_incerta*
Otu0231	3	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	*Pusillimonas*
Otu0232	3	Chlamydiae	Chlamydiae	Chlamydiales	Chlamydiales_unclassified	
Otu0233	3	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetales_unclassified	
Otu0234	3	Verrucomicrobia	Spartobacteria	Spartobacteria_order_incertae_sedis	Spartobacteria_family_incertae_sedis	*Spartobacteria_genera_incerta*
Otu0235	3	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Flavobacterium*
Otu0236	3	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*

Otu0237	3	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Mucilaginibacter*
Otu0238	3	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*
Otu0239	3	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu0240	3	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu0241	3	Firmicutes	Bacilli	Bacillales	Bacillaceae_2	*Paucisalibacillus*
Otu0242	3	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu0243	3	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Chryseobacterium*
Otu0244	3	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Mucilaginibacter*
Otu0245	3	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Luteimonas*
Otu0246	3	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0247	3	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Flavobacterium*
Otu0248	3	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu0249	3	Firmicutes	Bacilli	Bacillales	Bacillales_Incertae_Sedis_XII	*Exiguobacterium*
Otu0250	3	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0251	3	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	*Cohnella*
Otu0252	3	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0253	3	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	*Opitutus*
Otu0254	3	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Sphingobacterium*
Otu0255	3	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Stenotrophomonas*
Otu0256	3	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Chryseobacterium*
Otu0257	3	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Mucilaginibacter*
Otu0258	3	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	*Anaeromyxobacter*
Otu0259	3	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0260	2	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	*Conexibacter*
Otu0261	2	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0262	2	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	*Conexibacter*
Otu0263	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0264	2	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	*Acetobacter*
Otu0265	2	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu0266	2	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	*Legionella*

Otu0267	2	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Flavisolibacter*
Otu0268	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0269	2	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	*Lactobacillus*
Otu0270	2	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0271	2	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu0272	2	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Sphingobacterium*
Otu0273	2	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Parabacteroides*
Otu0274	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0275	2	Verrucomicrobia	Spartobacteria	Spartobacteria_order_incertae_sedis	Spartobacteria_family_incertae_sedis	*Spartobacteria_genera_incerta*
Otu0276	2	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0277	2	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	*Tumebacillus*
Otu0278	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0279	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0280	2	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu0281	2	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	
Otu0282	2	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	*Methylophilus*
Otu0283	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0284	2	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	*Paenibacillus*
Otu0285	2	Verrucomicrobia	Subdivision3	Subdivision3_order_incertae_sedis	Subdivision3_family_incertae_sedis	*3_genus_incertae_sedis*
Otu0286	2	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu0287	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu0288	2	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	*Paenibacillus*
Otu0289	2	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	*Bacteroides*
Otu0290	2	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0291	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0292	2	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu0293	2	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Lysobacter*
Otu0294	2	Firmicutes	Bacilli	Bacillales	Bacillaceae_2	*Gracilibacillus*
Otu0295	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0296	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	

Otu0297	2	Verrucomicrobia	Subdivision3	Subdivision3_order_incertae_sedis	Subdivision3_family_incertae_sedis	*3_genus_incertae_sedis*
Otu0298	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0299	2	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0300	2	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0301	2	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Segetibacter*
Otu0302	2	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	*Methylophilus*
Otu0303	2	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Comamonas*
Otu0304	2	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Flavobacterium*
Otu0305	2	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu0306	2	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu0307	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0308	2	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0309	2	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu0310	2	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Segetibacter*
Otu0311	2	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Terrimonas*
Otu0312	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0313	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0314	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0315	2	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	*Opitutus*
Otu0316	2	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu0317	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0318	2	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Terrimonas*
Otu0319	2	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobacterales_unclassified	
Otu0320	2	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	*Opitutus*
Otu0321	2	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu0322	2	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Segetibacter*
Otu0323	2	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0324	2	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Segetibacter*
Otu0325	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0326	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*

Otu0327	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0328	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0329	2	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	*Anaeromyxobacter*
Otu0330	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0331	2	Bacteroidetes	Bacteroidetes"_unclassified	Bacteroidetes"_unclassified	Bacteroidetes"_unclassified	
Otu0332	2	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0333	2	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu0334	2	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*
Otu0335	2	Actinobacteria	Actinobacteria	Rubrobacterales	Rubrobacteraceae	*Rubrobacter*
Otu0336	2	Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae_1	*Desmospora*
Otu0337	2	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0338	2	Verrucomicrobia	Opitutae	Puniceicoccales	Puniceicoccaceae	*Pelagicoccus*
Otu0339	2	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Filimonas*
Otu0340	2	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobacteraceae	*Solirubrobacter*
Otu0341	2	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobacterales_unclassified	
Otu0342	2	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*
Otu0343	2	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Filimonas*
Otu0344	2	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0345	2	Acidobacteria	Acidobacteria_Gp7	Acidobacteria_Gp7_order_incertae_sedis	Acidobacteria_Gp7_family_incertae_sedis	*Gp7*
Otu0346	2	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0347	2	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Parabacteroides*
Otu0348	2	Firmicutes	Bacilli	Bacillales	Bacillales_unclassified	
Otu0349	2	Verrucomicrobia	Opitutae	Opitutae_unclassified	Opitutae_unclassified	
Otu0350	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu0351	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0352	2	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu0353	2	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Chryseobacterium*
Otu0354	2	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae	*Peredibacter*
Otu0355	2	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	*Planctomyces*
Otu0356	2	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Enhydrobacter*

Otu0357	2	Proteobacteria	Gammaproteobacteria	*Gammaproteobacteria_unclassified*		
Otu0358	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0359	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0360	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0361	2	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	*Facklamia*
Otu0362	2	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	*Bacteroides*
Otu0363	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0364	2	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Parabacteroides*
Otu0365	2	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Pedobacter*
Otu0366	2	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Sphingobacterium*
Otu0367	2	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu0368	2	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu0369	2	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0370	2	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	*Paenibacillus*
Otu0371	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0372	2	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0373	2	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu0374	2	Verrucomicrobia	Subdivision3	Subdivision3_order_incertae_sedis	Subdivision3_family_incertae_sedis	*3_genus_incertae_sedis*
Otu0375	2	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0376	2	Proteobacteria	Proteobacteria_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu0377	2	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0378	2	Firmicutes	Bacilli	Bacillales	Bacillaceae_2	*Ornithinibacillus*
Otu0379	2	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	*Alistipes*
Otu0380	2	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	*Massilia*
Otu0381	2	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	
Otu0382	2	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	*Paenibacillus*
Otu0383	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu0384	2	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu0385	2	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	
Otu0386	2	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*

Otu0387	2	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	*Planctomyces*
Otu0388	2	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	*Conexibacter*
Otu0389	2	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0390	2	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Acidovorax*
Otu0391	2	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	*Acetobacter*
Otu0392	2	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0393	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu0394	1	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Enterococcus*
Otu0395	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0396	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0397	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0398	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0399	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0400	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0401	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0402	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu0403	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0404	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0405	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0406	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0407	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0408	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0409	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu0410	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0411	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0412	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0413	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0414	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0415	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0416	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Tatumella*

Otu0417	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0418	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0419	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0420	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0421	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0422	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0423	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0424	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0425	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0426	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0427	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0428	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu0429	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu0430	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu0431	1	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Enterococcus*
Otu0432	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0433	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0434	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0435	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0436	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0437	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0438	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0439	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0440	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0441	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0442	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0443	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0444	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0445	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0446	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	

Otu0447	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0448	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0449	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0450	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0451	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0452	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0453	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0454	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0455	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0456	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0457	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0458	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0459	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0460	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0461	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0462	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0463	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0464	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0465	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0466	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0467	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0468	1	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu0469	1	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	*Paenibacillus*
Otu0470	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0471	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0472	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0473	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0474	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0475	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0476	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*

Otu0477	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0478	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0479	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0480	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0481	1	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales"_unclassified	
Otu0482	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0483	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0484	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0485	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0486	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0487	1	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	*Planctomyces*
Otu0488	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0489	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0490	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0491	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0492	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0493	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0494	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0495	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0496	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0497	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0498	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0499	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0500	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0501	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0502	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0503	1	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	*Planctomyces*
Otu0504	1	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Lysobacter*
Otu0505	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0506	1	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	*Nocardioides*

Otu0507	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0508	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0509	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0510	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0511	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0512	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0513	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0514	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0515	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0516	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0517	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0518	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0519	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0520	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0521	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0522	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0523	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0524	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0525	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0526	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0527	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0528	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0529	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0530	1	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae	
Otu0531	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0532	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0533	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0534	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0535	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0536	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*

Otu0537	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0538	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0539	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0540	1	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales"_unclassified	
Otu0541	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0542	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0543	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0544	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0545	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0546	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0547	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0548	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu0549	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0550	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0551	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0552	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu0553	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0554	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0555	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0556	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0557	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0558	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0559	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0560	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0561	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0562	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0563	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0564	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0565	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0566	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*

Otu0567	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0568	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0569	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0570	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu0571	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu0572	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu0573	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu0574	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu0575	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0576	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0577	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0578	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0579	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0580	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0581	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0582	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0583	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0584	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0585	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0586	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0587	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0588	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0589	1	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	*Acetobacter*
Otu0590	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0591	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0592	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0593	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0594	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0595	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0596	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*

Otu0597	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0598	1	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Enterococcus*
Otu0599	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0600	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0601	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0602	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0603	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0604	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0605	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0606	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0607	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0608	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0609	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0610	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0611	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0612	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0613	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0614	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0615	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0616	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0617	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0618	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0619	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0620	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0621	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0622	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0623	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0624	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0625	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0626	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*

Otu0627	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0628	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0629	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0630	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu0631	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu0632	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu0633	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0634	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0635	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0636	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0637	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0638	1	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	*Acetobacter*
Otu0639	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0640	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0641	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0642	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0643	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0644	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0645	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0646	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0647	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0648	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0649	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0650	1	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Enterococcus*
Otu0651	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0652	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0653	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0654	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu0655	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0656	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*

Otu0657	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu0658	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu0659	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu0660	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu0661	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0662	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0663	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0664	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0665	1	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Enterococcus*
Otu0666	1	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetales_unclassified	
Otu0667	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0668	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0669	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0670	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0671	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0672	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0673	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0674	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0675	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0676	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0677	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0678	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0679	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0680	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0681	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0682	1	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Sphingobacterium*
Otu0683	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0684	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0685	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0686	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*

Otu0687	1	Proteobacteria	Proteobacteria_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu0688	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0689	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0690	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0691	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0692	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0693	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0694	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0695	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0696	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0697	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu0698	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0699	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0700	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0701	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0702	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0703	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0704	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0705	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu0706	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmatales_unclassified	
Otu0707	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0708	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0709	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0710	1	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Flavisolibacter*
Otu0711	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0712	1	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Enterococcus*
Otu0713	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0714	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0715	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0716	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*

Otu0717	1	Proteobacteria	Proteobacteria_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu0718	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0719	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0720	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0721	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0722	1	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0723	1	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Enterococcus*
Otu0724	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0725	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0726	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0727	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0728	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0729	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0730	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0731	1	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	*Acetobacter*
Otu0732	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0733	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0734	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0735	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0736	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0737	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0738	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0739	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0740	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0741	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0742	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0743	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0744	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0745	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0746	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	

Otu0747	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0748	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0749	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0750	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0751	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0752	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0753	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0754	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0755	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0756	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0757	1	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Parabacteroides*
Otu0758	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0759	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0760	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0761	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0762	1	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetales_unclassified	
Otu0763	1	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetales_unclassified	
Otu0764	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0765	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0766	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0767	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0768	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0769	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0770	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0771	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0772	1	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	
Otu0773	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0774	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0775	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0776	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*

Otu0777	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0778	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0779	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0780	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0781	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0782	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0783	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0784	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0785	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0786	1	Chlamydiae	Chlamydiae	Chlamydiales	Parachlamydiaceae	*Parachlamydia*
Otu0787	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0788	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0789	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0790	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0791	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0792	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0793	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0794	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0795	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0796	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0797	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0798	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0799	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0800	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0801	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0802	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0803	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0804	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0805	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0806	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	

Otu0807	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0808	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0809	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0810	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0811	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0812	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0813	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0814	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0815	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0816	1	Firmicutes	Negativicutes	Selenomonadales	Selenomonadales_unclassified	
Otu0817	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0818	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0819	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0820	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0821	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0822	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0823	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0824	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0825	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0826	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0827	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0828	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0829	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0830	1	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	*Clostridium_XVIII*
Otu0831	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0832	1	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	*Streptococcus*
Otu0833	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0834	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0835	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0836	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*

Otu0837	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0838	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0839	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0840	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0841	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0842	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0843	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0844	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0845	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0846	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0847	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0848	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0849	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0850	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0851	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0852	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0853	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0854	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0855	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0856	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0857	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0858	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0859	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0860	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0861	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0862	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0863	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0864	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0865	1	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu0866	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*

Otu0867	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0868	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0869	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0870	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0871	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0872	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0873	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0874	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0875	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0876	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0877	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0878	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0879	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0880	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0881	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0882	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0883	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0884	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0885	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0886	1	Firmicutes	Bacilli	Bacillales	Bacillales_unclassified	
Otu0887	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0888	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0889	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0890	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0891	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0892	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu0893	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0894	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0895	1	Firmicutes	Bacilli	Bacillales	Bacillales_unclassified	
Otu0896	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	

Otu0897	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu0898	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0899	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0900	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0901	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0902	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0903	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu0904	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0905	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0906	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0907	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0908	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0909	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0910	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0911	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0912	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0913	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0914	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0915	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0916	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0917	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0918	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0919	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0920	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0921	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	
Otu0922	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu0923	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0924	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu0925	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0926	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	

Otu0927	1	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0928	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0929	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0930	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0931	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0932	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0933	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0934	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0935	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu0936	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0937	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*
Otu0938	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0939	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0940	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0941	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0942	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0943	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0944	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0945	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0946	1	Bacteroidetes	Bacteroidetes"_unclassified	Bacteroidetes"_unclassified	Bacteroidetes"_unclassified	
Otu0947	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0948	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0949	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0950	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0951	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0952	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0953	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0954	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0955	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0956	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*

Otu0957	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0958	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0959	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0960	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0961	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0962	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0963	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0964	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0965	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu0966	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0967	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0968	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0969	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Psychrobacter*
Otu0970	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0971	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0972	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0973	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0974	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0975	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu0976	1	Bacteroidetes	Sphingobacteria	Shingobacteriales	Larkinella	*Cytophagaceae*
Otu0977	1	Proteobacteria	Proteobacteria_unclassified	Proteobacteria_unclassified	Proteobacteria_unclassified	
Otu0978	1	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	*Opitutus*
Otu0979	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0980	1	Bacteroidetes	Bacteroidetes"_unclassified	Bacteroidetes"_unclassified	Bacteroidetes"_unclassified	
Otu0981	1	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu0982	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0983	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu0984	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0985	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0986	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*

Otu0987	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0988	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0989	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0990	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu0991	1	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu0992	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0993	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu0994	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu0995	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0996	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu0997	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu0998	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu0999	1	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Flavisolibacter*
Otu1000	1	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu1001	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1002	1	Proteobacteria	Proteobacteria_unclassified	Proteobacteria_unclassified	Proteobacteria_unclassified	
Otu1003	1	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu1004	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1005	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1006	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1007	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1008	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1009	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1010	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1011	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1012	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1013	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1014	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1015	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1016	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*

Otu1017	1	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Parabacteroides*
Otu1018	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1019	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1020	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1021	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1022	1	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu1023	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1024	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1025	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1026	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1027	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1028	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1029	1	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu1030	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Comamonas*
Otu1031	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Comamonas*
Otu1032	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1033	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1034	1	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu1035	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1036	1	Verrucomicrobia	Subdivision3	Subdivision3_order_incertae_sedis	Subdivision3_family_incertae_sedis	*3_genus_incertae_sedis*
Otu1037	1	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	
Otu1038	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1039	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1040	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1041	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1042	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1043	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1044	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1045	1	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetales_unclassified	
Otu1046	1	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*

Otu1047	1	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetales_unclassified	
Otu1048	1	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu1049	1	Verrucomicrobia	Spartobacteria	Spartobacteria_order_incertae_sedis	Spartobacteria_family_incertae_sedis	*Spartobacteria_genera_incerta*
Otu1050	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1051	1	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	*Cohnella*
Otu1052	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1053	1	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu1054	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*
Otu1055	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1056	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1057	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1058	1	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Niastella*
Otu1059	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1060	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1061	1	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobacterales_unclassified	
Otu1062	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1063	1	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Flavisolibacter*
Otu1064	1	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	
Otu1065	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1066	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1067	1	Acidobacteria	Acidobacteria_Gp7	Acidobacteria_Gp7_order_incertae_sedis	Acidobacteria_Gp7_family_incertae_sedis	*Gp7*
Otu1068	1	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	*Steroidobacter*
Otu1069	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1070	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1071	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1072	1	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Lysobacter*
Otu1073	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1074	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1075	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1076	1	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	*Singulisphaera*

Otu1077	1	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu1078	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1079	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1080	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1081	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1082	1	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Dysgonomonas*
Otu1083	1	Verrucomicrobia	Spartobacteria	Spartobacteria_order_incertae_sedis	Spartobacteria_family_incertae_sedis	*Spartobacteria_genera_incerta*
Otu1084	1	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	*Leuconostoc*
Otu1085	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1086	1	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu1087	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1088	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1089	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1090	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1091	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1092	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1093	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1094	1	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Parabacteroides*
Otu1095	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1096	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1097	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1098	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1099	1	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	*Alistipes*
Otu1100	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1101	1	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	*Alistipes*
Otu1102	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1103	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1104	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1105	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1106	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*

Otu1107	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1108	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1109	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1110	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1111	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1112	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1113	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1114	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1115	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1116	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1117	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1118	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1119	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1120	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1121	1	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu1122	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1123	1	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	*Acetobacter*
Otu1124	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1125	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1126	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1127	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1128	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1129	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1130	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1131	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1132	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1133	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1134	1	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	*Alistipes*
Otu1135	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1136	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*

Otu1137	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1138	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1139	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1140	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1141	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1142	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1143	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1144	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1145	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1146	1	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
Otu1147	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1148	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1149	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1150	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1151	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1152	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1153	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1154	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1155	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1156	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1157	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1158	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1159	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1160	1	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Chryseobacterium*
Otu1161	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1162	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1163	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1164	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1165	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1166	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*

Otu1167	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1168	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1169	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1170	1	Proteobacteria	Proteobacteria_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu1171	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1172	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1173	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1174	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1175	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1176	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1177	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1178	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1179	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1180	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1181	1	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Parabacteroides*
Otu1182	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Morganella*
Otu1183	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1184	1	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	*Bacteroidaceae*
Otu1185	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1186	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1187	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1188	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1189	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1190	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1191	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1192	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1193	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1194	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1195	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1196	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*

Otu1197	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1198	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1199	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1200	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1201	1	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Parabacteroides*
Otu1202	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1203	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1204	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	
Otu1205	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1206	1	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	*Alistipes*
Otu1207	1	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Vibrio*
Otu1208	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1209	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu1210	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1211	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1212	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1213	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1214	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1215	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1216	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1217	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1218	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1219	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1220	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1221	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1222	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1223	1	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	*Hydrogenophilus*
Otu1224	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1225	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1226	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*

Otu1227	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1228	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1229	1	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu1230	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1231	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1232	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1233	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1234	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1235	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1236	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1237	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1238	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1239	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1240	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu1241	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1242	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1243	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1244	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1245	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1246	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1247	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1248	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1249	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1250	1	Bacteroidetes	Bacteroidetes"_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified	
Otu1251	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1252	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1253	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1254	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1255	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1256	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*

Otu1257	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1258	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1259	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1260	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1261	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1262	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1263	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1264	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1265	1	Bacteroidetes	Bacteroidetes"_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified	
Otu1266	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1267	1	Verrucomicrobia	Subdivision3	Subdivision3_order_incertae_sedis	Subdivision3_family_incertae_sedis	*3_genus_incertae_sedis*
Otu1268	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1269	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1270	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1271	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1272	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1273	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1274	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1275	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1276	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1277	1	Proteobacteria	Proteobacteria_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu1278	1	Proteobacteria	Proteobacteria_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu1279	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1280	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1281	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1282	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1283	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1284	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1285	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1286	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*

Otu1287	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1288	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1289	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1290	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1291	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1292	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1293	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1294	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1295	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1296	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1297	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1298	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1299	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1300	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1301	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1302	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1303	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1304	1	Proteobacteria	Proteobacteria_unclassified	Proteobacteria_unclassified	Proteobacteria_unclassified	
Otu1305	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1306	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1307	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1308	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1309	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1310	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1311	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1312	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1313	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1314	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1315	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1316	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*

Otu1317	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1318	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1319	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1320	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1321	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1322	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1323	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1324	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1325	1	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Sphingobacterium*
Otu1326	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1327	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1328	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1329	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1330	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1331	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1332	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	*Massilia*
Otu1333	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1334	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1335	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1336	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1337	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1338	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1339	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria	Gammaproteobacteria	
Otu1340	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1341	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1342	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1343	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1344	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1345	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1346	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*

Otu1347	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1348	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1349	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1350	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1351	1	Proteobacteria	Betaproteobacteria	Betaproteobacteria_unclassified	Betaproteobacteria_unclassified	
Otu1352	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1353	1	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	*Acetobacter*
Otu1354	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1355	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1356	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_2	*Oceanobacillus*
Otu1357	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_2	*Oceanobacillus*
Otu1358	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1359	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1360	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1361	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1362	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1363	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1364	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1365	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1366	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1367	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1368	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1369	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1370	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1371	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1372	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1373	1	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu1374	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1375	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1376	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*

Otu1377	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1378	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1379	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1380	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1381	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1382	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1383	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1384	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1385	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1386	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1387	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1388	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1389	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1390	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1391	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1392	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1393	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1394	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1395	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1396	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1397	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1398	1	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Enterococcus*
Otu1399	1	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	*Enterococcus*
Otu1400	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1401	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1402	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1403	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1404	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1405	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1406	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*

Otu1407	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1408	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1409	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Delftia*
Otu1410	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1411	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1412	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1413	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1414	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1415	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1416	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1417	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1418	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1419	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1420	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1421	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1422	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1423	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1424	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1425	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1426	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1427	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1428	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1429	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1430	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1431	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1432	1	Firmicutes	Bacilli	Bacillales	Planococcaceae	*Kurthia*
Otu1433	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1434	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1435	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1436	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*

Otu1437	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1438	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1439	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1440	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	*Massilia*
Otu1441	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1442	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1443	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1444	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1445	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1446	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1447	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1448	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1449	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1450	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1451	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1452	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1453	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1454	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1455	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1456	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1457	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1458	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1459	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1460	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1461	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1462	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1463	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1464	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1465	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1466	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*

Otu1467	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1468	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1469	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1470	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1471	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1472	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1473	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1474	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1475	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1476	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1477	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1478	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1479	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1480	1	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Sphingobacterium*
Otu1481	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1482	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1483	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1484	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1485	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1486	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1487	1	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Segetibacter*
Otu1488	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1489	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1490	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1491	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1492	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1493	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1494	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1495	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1496	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*

Otu1497	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	*Massilia*
Otu1498	1	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Flavobacterium*
Otu1499	1	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Flavobacterium*
Otu1500	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1501	1	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu1502	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1503	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Comamonas*
Otu1504	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1505	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1506	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1507	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1508	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1509	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1510	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1511	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1512	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1513	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1514	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1515	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu1516	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1517	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1518	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1519	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1520	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1521	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1522	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1523	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1524	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1525	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1526	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*

Otu1527	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1528	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1529	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1530	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1531	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1532	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1533	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1534	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1535	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1536	1	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	*Flavisolibacter*
Otu1537	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1538	1	Proteobacteria	Proteobacteria_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu1539	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1540	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1541	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1542	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1543	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1544	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1545	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	*Lactobacillus*
Otu1546	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1547	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1548	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1549	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1550	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1551	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1552	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Delftia*
Otu1553	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Delftia*
Otu1554	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1555	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1556	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*

Otu1557	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1558	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1559	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1560	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1561	1	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	*Anaeromyxobacter*
Otu1562	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1563	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1564	1	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Flavobacterium*
Otu1565	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1566	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1567	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1568	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1569	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1570	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1571	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1572	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1573	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1574	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1575	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1576	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1577	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1578	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1579	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1580	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1581	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1582	1	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu1583	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1584	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1585	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1586	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*

Otu1587	1	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu1588	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1589	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1590	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1591	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1592	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1593	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu1594	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1595	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1596	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1597	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1598	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1599	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1600	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1601	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1602	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1603	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1604	1	Proteobacteria	Proteobacteria_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu1605	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1606	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1607	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1608	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1609	1	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	
Otu1610	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1611	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1612	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1613	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1614	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1615	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1616	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*

Otu1617	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1618	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1619	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1620	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1621	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Leclercia*
Otu1622	1	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu1623	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1624	1	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	*Acetobacter*
Otu1625	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1626	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1627	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1628	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1629	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1630	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1631	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1632	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1633	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1634	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1635	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1636	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1637	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1638	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1639	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1640	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1641	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1642	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1643	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1644	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1645	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1646	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*

Otu1647	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1648	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1649	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1650	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1651	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1652	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1653	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1654	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1655	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1656	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1657	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1658	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1659	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1660	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1661	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1662	1	Acidobacteria	Acidobacteria_Gp7	Acidobacteria_Gp7_order_incertae_sedis	Acidobacteria_Gp7_family_incertae_sedis	*Gp7*
Otu1663	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1664	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1665	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1666	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1667	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1668	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1669	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1670	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1671	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1672	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1673	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1674	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1675	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1676	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*

Otu1677	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Pantoea*
Otu1678	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1679	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu1680	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1681	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1682	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1683	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1684	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1685	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1686	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1687	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1688	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1689	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1690	1	Verrucomicrobia	Spartobacteria	Spartobacteria_order_incertae_sedis	Spartobacteria_family_incertae_sedis	*Spartobacteria_genera_incerta*
Otu1691	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1692	1	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobacteraceae	*Solirubrobacter*
Otu1693	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu1694	1	Acidobacteria	Acidobacteria_Gp6	Acidobacteria_Gp6_order_incertae_sedis	Acidobacteria_Gp6_family_incertae_sedis	*Gp6*
Otu1695	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1696	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1697	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1698	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1699	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1700	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1701	1	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu1702	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1703	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1704	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1705	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1706	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*

Otu1707	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1708	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1709	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1710	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1711	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1712	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1713	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1714	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1715	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1716	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1717	1	Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	*Planctomyces*
Otu1718	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1719	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1720	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1721	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1722	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1723	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1724	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1725	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1726	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1727	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1728	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1729	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu1730	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1731	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1732	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1733	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1734	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1735	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1736	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*

Otu1737	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1738	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1739	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1740	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1741	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu1742	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1743	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1744	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1745	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1746	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1747	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu1748	1	Verrucomicrobia	Spartobacteria	Spartobacteria_order_incertae_sedis	Spartobacteria_family_incertae_sedis	*Spartobacteria_genera_incerta*
Otu1749	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1750	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1751	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1752	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1753	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1754	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1755	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1756	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1757	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1758	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1759	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1760	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1761	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1762	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1763	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu1764	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1765	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1766	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*

Otu1767	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1768	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1769	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1770	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1771	1	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	*Atopococcus*
Otu1772	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1773	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1774	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1775	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1776	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1777	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1778	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1779	1	Acidobacteria	Acidobacteria_Gp4	Acidobacteria_Gp4_order_incertae_sedis	Acidobacteria_Gp4_family_incertae_sedis	*Gp4*
Otu1780	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1781	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1782	1	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	*Alistipes*
Otu1783	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1784	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1785	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1786	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1787	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1788	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1789	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1790	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1791	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1792	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1793	1	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Sphingobacterium*
Otu1794	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	*Lactobacillus*
Otu1795	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1796	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*

Otu1797	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1798	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1799	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1800	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1801	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1802	1	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	*Parabacteroides*
Otu1803	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1804	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1805	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1806	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu1807	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1808	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1809	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1810	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1811	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1812	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1813	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1814	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1815	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1816	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1817	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1818	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1819	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1820	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1821	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Hydrogenophaga*
Otu1822	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1823	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1824	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1825	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1826	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*

Otu1827	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1828	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1829	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1830	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1831	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1832	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1833	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1834	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Hydrogenophaga*
Otu1835	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1836	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1837	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1838	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1839	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1840	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1841	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1842	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1843	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1844	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1845	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1846	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1847	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1848	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1849	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1850	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Acinetobacter*
Otu1851	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1852	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1853	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1854	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1855	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1856	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*

Otu1857	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1858	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1859	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1860	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1861	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1862	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1863	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1864	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1865	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1866	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1867	1	Proteobacteria	Deltaproteobacteria	Deltaproteobacteria_unclassified	Deltaproteobacteria_unclassified	
Otu1868	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1869	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1870	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1871	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1872	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1873	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu1874	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1875	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1876	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1877	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1878	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1879	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1880	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1881	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1882	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1883	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1884	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1885	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1886	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*

Otu1887	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1888	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1889	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu1890	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1891	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1892	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1893	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1894	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1895	1	Acidobacteria	Acidobacteria_Gp10	Acidobacteria_Gp10_order_incertae_sedis	Acidobacteria_Gp10_family_incertae_sedis	*Gp10*
Otu1896	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1897	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1898	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1899	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1900	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1901	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1902	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu1903	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1904	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1905	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1906	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1907	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1908	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1909	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1910	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1911	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1912	1	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	*Paenibacillus*
Otu1913	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1914	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1915	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1916	1	Verrucomicrobia	Subdivision5	Subdivision5_order_incertae_sedis	Subdivision5_family_incertae_sedis	*5_genus_incertae_sedis*

Otu1917	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1918	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1919	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1920	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu1921	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu1922	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu1923	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1924	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1925	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1926	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1927	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1928	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1929	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1930	1	Firmicutes	Negativicutes	Selenomonadales	Acidaminococcaceae	*Phascolarctobacterium*
Otu1931	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1932	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1933	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1934	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1935	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1936	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu1937	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1938	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1939	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1940	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1941	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1942	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1943	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1944	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	*Azohydromonas*
Otu1945	1	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	*Myxococcus*
Otu1946	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*

Otu1947	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1948	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1949	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1950	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1951	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu1952	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1953	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu1954	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1955	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1956	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1957	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1958	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1959	1	Actinobacteria	Actinobacteria	Thermoleophilales	Thermoleophilaceae	*Thermoleophilum*
Otu1960	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1961	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1962	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1963	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1964	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1965	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1966	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1967	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1968	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1969	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1970	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1971	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1972	1	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	*Bacillus*
Otu1973	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1974	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1975	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1976	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*

Otu1977	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1978	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1979	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1980	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1981	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1982	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1983	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu1984	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1985	1	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetales_unclassified	
Otu1986	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1987	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1988	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*
Otu1989	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu1990	1	Verrucomicrobia	Subdivision5	Subdivision5_order_incertae_sedis	Subdivision5_family_incertae_sedis	*5_genus_incertae_sedis*
Otu1991	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1992	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1993	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1994	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1995	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1996	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1997	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1998	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu1999	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2000	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2001	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2002	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2003	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu2004	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2005	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2006	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*

Otu2007	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2008	1	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	*Sphingobacterium*
Otu2009	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2010	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2011	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2012	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2013	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2014	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2015	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2016	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2017	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2018	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2019	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2020	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2021	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2022	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2023	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2024	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2025	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2026	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2027	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu2028	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2029	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu2030	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2031	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2032	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2033	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2034	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu2035	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2036	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*

Otu2037	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2038	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2039	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2040	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu2041	1	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Lysobacter*
Otu2042	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu2043	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2044	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2045	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2046	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2047	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2048	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2049	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu2050	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2051	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	*Hylemonella*
Otu2052	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2053	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2054	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2055	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2056	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2057	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2058	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2059	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2060	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2061	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2062	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2063	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2064	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2065	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2066	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*

Otu2067	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2068	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2069	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2070	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2071	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu2072	1	Chlamydiae	Chlamydiae	Chlamydiales	Parachlamydiaceae	*Parachlamydia*
Otu2073	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu2074	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2075	1	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	*Paenibacillus*
Otu2076	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2077	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2078	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*
Otu2079	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2080	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2081	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2082	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2083	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2084	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2085	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2086	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2087	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2088	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2089	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2090	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2091	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2092	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2093	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu2094	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2095	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2096	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*

Otu2097	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2098	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2099	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2100	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2101	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2102	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2103	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2104	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2105	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2106	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	*Pseudomonas*
Otu2107	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2108	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2109	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2110	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	*Lactobacillus*
Otu2111	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2112	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2113	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2114	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2115	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Proteus*
Otu2116	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2117	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2118	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2119	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2120	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2121	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2122	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2123	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2124	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2125	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2126	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*

Otu2127	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2128	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2129	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2130	1	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_unclassified	Gammaproteobacteria_unclassified	*Gammaproteobacteria_unclass*
Otu2131	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2132	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2133	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu2134	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2135	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2136	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2137	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2138	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2139	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2140	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2141	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2142	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	*Lactobacillus*
Otu2143	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2144	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2145	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2146	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2147	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2148	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2149	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2150	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2151	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2152	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2153	1	Proteobacteria	Proteobacteria_unclassified	Proteobacteria"_unclassified	Proteobacteria"_unclassified	
Otu2154	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2155	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2156	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*

Otu2157	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2158	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2159	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2160	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2161	1	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	*Prosthecobacter*
Otu2162	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2163	1	Firmicutes	Bacilli	Bacillales	Planococcaceae	*Lysinibacillus*
Otu2164	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2165	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2166	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2167	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2168	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu2169	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2170	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2171	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2172	1	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	*Lactobacillus*
Otu2173	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2174	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2175	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2176	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Zymobacter*
Otu2177	1	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	*Halomonas*
Otu2178	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2179	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2180	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2181	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu2182	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2183	1	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	*Azoarcus*
Otu2184	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu2185	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2186	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Perlucidibaca*

Otu2187	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2188	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2189	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2190	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2191	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2192	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2193	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2194	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2195	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2196	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2197	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2198	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2199	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2200	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2201	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2202	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2203	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2204	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2205	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2206	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2207	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2208	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2209	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2210	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2211	1	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	*Alishewanella*
Otu2212	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2213	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2214	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia*
Otu2215	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2216	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*

Otu2217	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2218	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2219	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2220	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2221	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2222	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2223	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2224	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2225	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2226	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2227	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2228	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2229	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2230	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2231	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2232	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2233	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2234	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2235	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu2236	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2237	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2238	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2239	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2240	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu2241	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu2242	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2243	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2244	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2245	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2246	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*

Otu2247	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Enterobacter*
Otu2248	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2249	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2250	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2251	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2252	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu2253	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu2254	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2255	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2256	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu2257	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2258	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu2259	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Providencia*
Otu2260	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2261	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2262	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2263	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Shigella*
Otu2264	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2265	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2266	1	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	
Otu2267	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2268	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2269	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2270	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2271	1	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	*Entomoplasma*
Otu2272	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2273	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2274	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2275	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2276	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*

Otu2277	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Escherichia*
Otu2278	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2279	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2280	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2281	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2282	1	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	*Spiroplasma*
Otu2283	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Klebsiella*
Otu2284	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*
Otu2285	1	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	*Serratia*