DETERMINATION OF ILLEGAL BUSH-MEAT AVAILABILITY IN RANDOMLY SELECTED BUTCHERIES IN NAIROBI AND ITS ENVIRONS USING CYTOCHROME B MITOCHONDRIAL DNA MARKER

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DECLARATION

This thesis is my original work and has not been presented for any degree award in any other university or any other award.

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DEDICATION

This work is dedicated to my loving wife Neema for her moral and financial support and my two lovely children Tatyanna and Christian.

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LIST OF ABBREVIATIONS AND ACRONYMS

ALFPs	Amplified Fragment Length Polymorphism
BLAST	Basic Local Alignment Search Tool
CO I	Cytochrome Oxidase I
Cyt-*b*	Cytochrome *b*
DNA	Deoxyribonucleic Acid
ELISA	Enzyme linked Immunosorbent Assay
EDTA	Ethylenediaminetetraacetic Acid
HIV	Human Immunodeficiency Virus
Kg	Kilograms
MTDNA	Mitochondrial DNA
PCR	Polymerase Chain Reaction
PCR-RFLP	Polymerase Chain Reaction-Restriction Fragment Length Polymorphism
RAPD	Random Amplified Polymorphic DNA
TAE	Tris Acetate EDTA
UV	Ultraviolet

ABSTRACT

Kenya’s invaluable wildlife is under threat from wildlife crime, which has been on the increase in the recent past. With up to 70% of wildlife living outside protected areas either seasonally or permanently, protecting them from poaching has continued to be a great challenge. In the year 2012, KWS reported recovery of 7515kg of bush-meat in Kenya. Currently, prosecuting wildlife offenders, especially in bush-meat cases, has become nearly impossible due to the fact that poachers use highly sophisticated methods. They slaughter cleanly and de-bone the poached animal, taking only the red meat. The processed bush-meat product becomes difficult to distinguish from livestock meat based on near similar morphological features. Immunological methods such as ELISA and ouchterlony have been used in bush-meat identification but they have some limitations. Recent advances in DNA-typing enable bush-meat to be identified beyond reasonable doubt and yield results that are admissible in court for purposes of prosecution. This study aimed at evaluating the putative occurrence and prevalence of bush-meat in butcheries within Nairobi and its environs. A simple randomized survey was carried out in which 138 meat samples of approximately 250 g were purchased from various butcheries. The DNA was extracted from these samples using the high pure PCR template preparation Kit (Roche, Germany) following the manufacturer’s protocol and a partial region of the mitochondrial DNA was amplified using Mcb398 and Mcb869 markers. The resulting PCR products were sequenced on the big Dye terminator sequencing platform. The contigs were assembled and BLAST searches conducted against the Genbank database. The results revealed that no bush-meat was present in the sampled markets and that 86.96% of the purchased meat originated from cattle (*Bos taurus),* 10.87% from goat (*Capra hircus)* and 2.17% from Sheep (*Ovis aries)*. Curiously, in 11.6% of the purchased samples, the meat was identified wrongly by the traders. Phylogenetic analysis using maximum likelihood method based on 32 haplotypes posted three clades corresponding to *Bos taurus*, *Capra hircus* and *Ovis aries*; an affirmation of blast results. This study therefore did not detect any overt bush-meat trade in the areas sampled within Nairobi and its environs.

CHAPTER ONE

INTRODUCTION

1.1 Background Information

The creation and the use of a globally available DNA sequences database from a standardized gene region has been extensively proposed as an invaluable tool for the identification of species, genetic diversity assessments, discovery of new species and the surveillance of illegal and legal trade in wildlife species (Eaton *et al*., 2009; Olayemi *et al*., 2011;). In light of this development numerous studies have been undertaken with the use of mitochondrial DNA markers such as the Cytochrome Oxidase sub unit 1 (COX1) and the Cytochrome *b* (Cyt-*b*) regions to delineate samples down to the species level (Eaton *et al*., 2009). For instance, Yan *et al*., (2005) applied cytochrome *b* gene to identify Chinese alligators (*Alligator sinensis*) from partially cooked and fresh meat found in Chinese markets while Marko *et al*., (2004) used the same marker to determine that 77% of fish sold labeled as Red Snapper were actually from other species.

The mitochondrial genes are also considered very useful for phylogenetic work (Esposti *et al*., 1993; Farias *et al*., 2001), because they contain both slowly and rapidly evolving codon positions, as well as more conservative and more variable domains (Farias *et al*., 2001). Cytochrome *b* as a molecular marker is a potentially useful and easy to implement tool for bush-meat identification because of three main reasons. First, its rate of evolution is comparable with those of the other mitochondrial genes such as COX1, though Cyt-*b* might be even more informative due to its larger product size. Second, Cyt-*b* gene genuine “universal” primers are available (Kocher *et al*., 1989; Irwin *et al*., 1991). Finally, it is the most widely represented of the mitochondrial genes in nucleotide databases (Olayemi *et al*., 2011). Various immunological methods have also been used in bush meat identification. Ayaz *et al*., 2005, successfully used ELISA method to report that meat products in Turkish markets were adulterated. Ouchterlony method has also been used to distinguish between domestic and bush-meat (Free, 2004). The general limitations with this method include giving false positives between closely related species and unreliability when working with heat degraded samples of temperatures upto 70^0c (Kangethe *et al.*, 1986).

In Africa, forests are generally called “the bush” and as such meat from wild animals derived from it is referred to as “bush-meat”. The term bush-meat therefore applies to all wildlife species used as edible meat for example, elephants, duikers, bush pig, gorilla, elands among others, some of which are threatened or endangered. Over the decades, research has clearly shown that wildlife hunting in tropical forest in Central and West Africa presents a major threat to biodiversity (Daniels, 2010). The savannah of East Africa has also witnessed widespread bush-meat trade (Ndibalema and Songorwa, 2008). Coupled to this trade is the significant risk posed to public health through transmission of zoonotic infections such as Ebola, HIV and other diseases (Daniels, 2010).

It is therefore important to know the species hunted and possibly design a management system for conservation and for mitigating possible transmission pathways for the emerging zoonotic infections.

Several factors have fuelled trade in bush-meat such as increase in human population straining the limited resources, poverty, food insecurity, religious rituals, and the increased access to the previously inaccessible wildlife habitats due to the opening up of remote regions (Wilkie and Carpenter, 1999; Refisch, 2004; Redmond *et al.*, 2006). Increase in demand for bush-meat has seen former locally based subsistence bush-meat economies become global making bush-meat a significant export product traded at regional and international scales (Eaton *et al.*, 2009), with an estimated worth of more than US$5 billion annually (Baker, 2008). This has also seen an evolution of the wildlife harvesting techniques to more sophisticated levels such as use of long-range guns to maximize their yield. In 2001, the International Union for Conservation of Nature disclosed the severity of the impact of bush-meat trade on the species extinction rates (Tieguhong and Zwolinski, 2009; Daniels, 2010). In Kenya, drought, escalating poverty, population increase, prevailing food shortages and global financial crisis, has led to a rise in the bush-meat trade (Iregi and Kariuki, 2009).

This study examined the application of the cytochrome *b* marker based on mammalian universal primers in the identification of species from already processed animal samples in the form of tissue that can’t be ascribed to any order through its now absent morphological features. The study involved meat samples purchased from meat retailers within Nairobi and its environs. The results were indicative of the strength of the use of DNA-typing in the identification of species regardless of the nature of the samples being used and therefore provide a means for an easier tool for the prosecution of future bush-meat related cases in Kenya and the region, since these prosecutions are presently largely reliant on the use of morphological features for the identification of animal. However, once the animals are processed (dehorned, skinned, smoked, burnt, cut into small pieces), identification of their meat requires a more intrusive approach. As such, molecular assisted identification ensures positive identification of exhibits and forms the basis of wildlife conservancy. It is applicable in monitoring the success of initiatives against bush-meat trade. The study also works in providing formidable evidence against suspects and thus ensuring convictions which should act as a deterrent to other would be perpetrators (Ogden *et al*., 2009; Deguilloux *et al*., 2003; Bhaskar and Khan, 2011; Gupta *et al*., 2014).

1.2 Problem Statement and Justification

Currently in Kenya, loss of wildlife due to poaching is on the rise. Such wildlife ends up in our markets as bush-meat to the unsuspecting consumers with recovered quantities ranging from 2676kgs in the year 2003 to 75155kgs in the year 2010 as reported by KWS. This trade in bush-meat poses serious health risk to both the hunter and consumer who may end up contracting zoonotic diseases because such meat is not inspected by public health officers. Additionally, the indiscriminate trapping of wildlife for example, use of snare ends up killing non-targeted animals. Others are orphaned and end up dying if not rescued. Prosecution based on morphological identification of the animal has proved futile because poachers have come up with clever ways of making such meat unidentifiable through techniques such as deboning, skinning, smoking or cutting into small pieces. As such a more intrusive approach is required. Furthermore, various immunological methods such as Ouchterlony immunodiffusion and ELISA that have been used in species identification show various limitations especially in identifying high heat degraded samples or those from closely related species. As such molecular assisted identification will ensure positive identification of bush meat resulting into prosecution and convictions. This would have a deterrent effect against bush meat trade thereby enhancing wildlife conservancy. This study demonstrates the reliability of molecular exploration of cytochrome *b* marker in the identification of confiscated meat samples.

1.3 Research Questions

i. What is the prevalence of bush-meat trade in Nairobi and its environs?

ii. What are the common species sold as meat in Nairobi and its environs?

iii. What is the phylogenetic relationship of different meat species sold in Nairobi and its environs?

1.4 Hypotheses

i. The prevalence of bush-meat sales in Nairobi area is zero (0) %

ii. There is no single species commonly sold as bush-meat in Nairobi and its environs

iii. There is no phylogenetic relationship between the species sold as meat in Nairobi and its environs

1.5 Objectives

1.5.1 General Objective

To determine using Cytochrome *b* mitochondrial DNA markers whether butcheries in Nairobi and its environs are the outlet of illegal bush-meat.

1.5.2 Specific Objectives

i. Determine the type of meat sold in butcheries within Nairobi and its environs.

ii. Determine the molecular identity of species whose meat is sold in Nairobi and its environs.

iii. Determine the phylogenetic relationship of species sold as meat within Nairobi and its environs.

CHAPTER TWO

LITERATURE REVIEW

2.1 Bush-Meat Trade

From time immemorial in sub-Saharan Africa, equatorial rainforest Africa, Asia, Latin America and the developing world in general, bush-meat has been consumed in rural societies as the main and much valued source of proteins (Kümpel *et al.*, 2007) and a contributor to local economies with high variations across different countries (Asibey, 1977). Bush-meat hunting was sustainable for many decades (Connolly, 2004; Cowlishaw *et al.*, 2005). However, the recent population growth and increase in bush-meat trade has made wildlife harvesting unsustainable. According to the bush-meat crisis task force in west and central Africa, over 24 million people live in forest region, majority of who rely on wild meat as a primary source of animal protein. This has occasioned millions of metric tons of wildlife being killed for food annually (Brown and Davies, 2007).

In rural households of Central Africa, bush-meat consumption accounts for about 100 % of animal proteins (Vliet van, 2011), whereas in Tanzania, consumption amongst the communities living around the Serengeti National Park ranges from 10.95 to 32.4 kg/ capita/ year. In West Africa, bush-meat accounts for up to 75 % of animal protein in rural communities in Ghana and up to 20% in Nigeria and between 80-90 % in Liberia (Vliet van, 2011). In the Congo basin, consumption of bush-meat amongst the rural communities ranges between 14.6 - 97.6 kg/ capita/ year (Starkey, 2004). Bush-meat consumption in urban areas is not well documented as it occurs in hidden markets where it is not a staple food as opposed to rural communities. In Kenya, bush-meat trade has also been reported (Free, 2004) at a prevalence rate of 25% in the sampled area. Additionally, in the year 2012, KWS also tabled a report on bush-meat recoveries as shown in table 2.1

Table 2.1: Bush-meat recoveries by KWS personnel in Kenya from 2003-2010

Source: KWS Symposium on "challenges gaps and ongoing interventions in combating bush-meat in Kenya 2012"

YEAR	QUANTITIES IN KGs
2003	2676.9
2004	536
2005	8324
2006	6955
2007	19431
2008	14370.125
2009	22903.75
2010	75155

2.2 Species Targeted for Bush-meat

Several studies conducted in various localities world over have revealed that a wide variety of animals are hunted for bush-meat based on availability. This ranges from insects, rodents and birds to small and medium sized antelopes like duikers, gazelles and impalas to big game like zebras, giraffe, eland and buffaloes (Plate 2.1) (Ndibalema and

Songorwa, 2008).In west Africa, several primates hunted for bush-meat include monkeys, chimpanzees (Plate 2.1) (Willcox and Nambu, 2007), baboons, colobus (Connolly, 2004; Chapman *et al*., 2006;) and the endangered mountain gorilla (Grevengoed, 2001). In the Congo basin, majority of the catch is represented by blue tail porcupine and blue and red duikers (Kümpel *et al*., 2010; Nasi *et al*., 2011). Small antelopes have been targeted for subsistence and trade in the Tsavo Conservancy Area in Kenya (Iregi and Kariuki, 2009)

Plate 2.1: An assortment of wildlife harvested and sold in Asijere market in Nigeria (Source: Bush-meat task force in west and central Africa, 2000).

2. 3 Bush-meat Hunting Tools and Methods

Poachers have sophisticated bush-meat hunting over the ages through the use of rifles and short guns to target larger animals and arboreal species (Kümpel, 2006; Coad, 2008; Van Vliet *et al*., 2008). Dogs have also been used to trail, locate and corner the prey (Noss *et* *al.*, 2004) for subsistence and to support local or rural economies. Use of traps and wire snare (Plate 2.2) is frequent and prominent in Africa because the material is cheap, durable and strong enough to capture large animals (Swank and Teer, 1989; Noss, 1998; Nasi *et al.*, 2011) .

Plate 2.2: Buffalo captured with a foot snare. Source: (Kenya Wildlife Services, Veterinary and Capture Department).

In Kenya, wire snares, jack lighting/ lamping/ night torching, spears, bows and arrows, dogs and pit traps are the preferred methods (Iregi and Kariuki, 2009). In 2007, about 500 wire snares and several foot thumbs were removed from Maasai Mara game reserve (Plate 2.3). A Kenya bush-meat symposium 2012 report at KWS headquarters revealed that out of the 301 people arrested in the David Sheldon Wildlife Trust and KWS joint patrols in 2011 in the Tsavo ecosystem, 90 of them were bush-meat poachers. Also 6,134 snares were lifted and 67 shooting platforms destroyed.

Plate 2.3: Wire snares and foot thumbs collected from various conservancy in Kenya by KWS warders.

Source: (Kenya wildlife services, veterinary and capture department).

2. 4 Drivers of Bush-meat Trade

A myriad of factors has contributed to the upsurge of bush-meat trade in sub – Saharan Africa. For most rural African communities, bush-meat is abundant and inexpensive or ‘free’ compared to meat from domestic animals (Connolly, 2004). Bush-meat trade prevalence appears to be high (Lindsey *et al*., 2011b) under conditions of economic and political instability (De Merode and Cowlishaw, 2006). The 2007/2008 post-election violence in Kenya saw an increase in bush-meat trade as a result of displacement of people from their homes and farm lands (Iregi and Kariuki, 2009), whereas in Tanzania, bush-meat trade rose significantly due to influx of refugees from neighbouring Burundi, The Democratic Republic of Congo (DRC) and Rwanda. Further in the DRC, consumption of bush-meat from protected species increased during civil war (De Merode and Cowlishaw, 2006).

High poverty levels in rural Africa has also contributed to bush-meat trade with hunters selling their catch as a form of subsistence to augment the families meager income (Ndibalema and Songorwa, 2007; Lindsey *et al.*, 2011a). In Central Africa, one third of the population is undernourished and hunting contributes between 30 % and 80 % of dietary proteins of forest dwellers (Wilkie and Carpenter, 1999).

Increased accessibility to forest has also contributed directly to increase in bush-meat trade (Laurance *et al.*, 2006). Concessions given by governments and local authorities to logging and mining companies have opened up the once remote forests (Wilkie and Carpenter, 1999) to poachers.

Cultural proclivity has also contributed to the rise of bush-meat trade in Sub-Saharan Africa. Most communities favour bush-meat over domestic meat and with frequent usage and familiarity, preference develops (Schenck *et al.*, 2006). Beliefs that consumption of bush-meat such as primates in West Africa makes one strong and vigorous cannot be understated. Other commercial, foreign interest and local communities have turned to bush-meat for development of medicinal products and performing rituals or religious rights. (Wilkie and Carpenter, 1999).

Population increase has led to a high number of people depending on bush-meat and other income opportunities from the trade (Bowen-Jones *et al*., 2002; Milner-Gulland and Bennett, 2003; Swensson and Study, 2005).

2.5 Impacts of Bush-meat Trade

Various studies world over now contend that bush-meat hunting is unsustainable and warned of dire ecological consequences and disruption of national economies dependent on wildlife biodiversity. Ecological, health and socio-economic impacts of bush-meat trade have been studied extensively

2.5.1 Ecological Impact of Bush-meat Trade

Conservation biologists argue that bush-meat trade fuelled by illegal hunting has increased drastically and is a major threat to Africa's rich biodiversity (Kaiser, 2003; Walsh *et al.*, 2003; Whitfield, 2003). Extinction of species in some localities such as the red colobus monkey; an inhabitant of rainforests in Ghana and Cote d'lvore (Oates *et al*., 2000) and massive depopulation of slow reproducers such as primates and large mammals (Cowlishaw *et al.*, 2005) have been documented. Additionally, the dwindling numbers of large species in the markets is an indicator of their over exploitation (Bennett *et al*., 2002) as bush-meat.

Zoologist contend that bush-meat hunting resulted in a conspicuous drop of apes' populations (Walsh *et al*., 2003) and is likely to lead to extinction of many species if not checked (Bowen-Jones *et al*., 2002; Swensson and Study, 2005). Not only are the animal populations endangered, but also the forests due to disruption of important ecological connections with animals. For instance, decline in populations of key seed dispersers such the primates that play a critical role in tropical forest disturbs the ecosystem (Chapman, 1995), such as in the dispersion of icecream bean tree by spider monkey through faeces (Moore, 2001). Disruptions of such ecological connections have lead conservation biologists to make dire predictions of ‘empty forest syndrome’ (Bennett *et al.*, 2002; Nasi *et al*., 2011).

2.5.2 Health Impact of Bush-meat Trade

Bush-meat trade has led to emergence of zoonotic diseases throwing the public health order in serious risk with about 75 % of new diseases that have affected humans in the last 10 years being caused by pathogens originating from domestic or wildlife or their products (Apetrei *et al*., 2005; Wolfe *et al*., 2005). This is because such illegal bush-meat is not subjected to inspection by public health officers (Free, 2004).

Deadly viral diseases which affect and continue to wipe out human populations have been linked to bush-meat trade. Outbreaks of Ebola, a hemorrhagic fever disease in Democratic Republic of Congo from 1976 to 1979 involved victims who reportedly handled carcasses of gorilla or chimpanzee (Subramanian, 2012) or had physical contact with those who handled these carcasses (Free, 2004). Epidemiological evidence also suggests that HIV arose from Simian Immunodeficiency Virus (SIV) through butchering of bush-meat (Gao *et al*., 1999; Refisch, 2004) whereas in central Africa, there was an increase in T-lymphotropic viruses among bush-meat hunters due to exposure to blood and body fluids from infected non-human primates during hunting and butchering. In

Botswana, the consumption of buffalo meat was linked to zoonotic threat of brucellosis (Alexander *et al.*, 2012).

Other zoonotic diseases resulting from bush-meat hunting and trade are foot and mouth diseases, Lasa Fever, monkey pox and anthrax (Bailey and Africa, 2009).

2.5.3 Socio-economic Impacts of Bush-meat Trade

Wildlife populations continue to decline in most African countries (Caro and Scholte, 2007) and bush-meat hunting is the key contributor to this in Kenya and Zambia (Okello and Kiringe, 2004). Ecotourism operations which require higher densities of wildlife are very sensitive to bush-meat hunting (Wilkie and Carpenter, 1999) as witnessed in the Makuleke concession of Kruger National Park where ecotourism operators incurred huge losses for the first six years as wildlife recovered from previously high levels of bush-meat hunting (Lindsey *et al.*, 2013).

Bush-meat hunting has also reduced the viability of wildlife-based land use in many concessions where trophy hunting has become financially unviable reducing income by between 18.8 to 92.3% depending on the country (Lindsey *et al.*, 2013). For example, trophy income hunting reduced by 96 % in Mozambique (Coutada 9 area), 67 % in Tanzania (Burigi and Biharamulo game reserves) and by US$ 1.1 million per year in Zimbabwe (Save` Valley Conservancy) (Lindsey *et al.*, 2011b; Lindsey and Bento, 2012) due to illegal bush-meat hunting. Social consequences include loss of wildlife heritage for future generations and loss of tourism-based employment.

Illegal bush-meat which is sold as domestic meat to unsuspecting customers also amounts to economic fraud as customers do not get their money’s worth. It also poses both cultural and religious implications for example to Muslims who do not consume both wild and domestic pig

2. 6 Identification of Bush-meat Species

2.6.1 Morphological Method

Identification of species is a standard practice in biological science. For a long time, wildlife identification has solely depended on morphological and anatomical features. However, identification of processed bush-meat (dried, smoked and minced) presents considerable challenge and is accepted only in limited cases as evidence (“Wildlife Crime : Wildlife Crime :,” 2005). This has therefore necessitated exploration of other methods of species identification such as serology and molecular based assays.

2.6.2 Immunological Method

Techniques relying on protein electrophoresis (Kim and Shelef, 1986; Skarpeid *et al*., 1998), immunoassays (Hsieh *et al*., 1998) and liquid chromatography (Ashoor *et al*., 1987) have been used to identify bush-meat successfully. In the past, KWS has used the immunodiffusion technique which involves the analysis of antibodies successfully to detect the presence of certain species in mixed samples such as in ground samples. However, these immunological methods have major limitations in that they are less useful on heat degraded samples at temperatures of 70ºC and inadequate recovery from degraded or very minute samples such as blood stains and closely related species (Swart and Wilks, 1982).

2.6.3 Molecular Identification of Species

Molecular markers are a group of assays that detect variations in sequences between two or more individuals. These markers could be protein based (isoenzymes) or DNA based. With protein based markers, the variation is in the amino acid sequence that leads to different electrophoretic motility of the two alleles, while with DNA based markers, the variation is in the nucleotide sequence of coding or non-coding regions of the genome which can be detected using several techniques. (Pereira., *et al* 2008)

In the recent past, use of genetic analysis in species identification has greatly revolutionized wildlife DNA forensics. In cases of poaching, DNA analysis has been used to positively identify confiscated trace evidence either from the suspect or in the field (Gupta *et al*., 2014) or where the product in question has lost morphological characteristics for example after processing (Deguilloux *et al*., 2003). It has also helped enhance law enforcement and conservation by helping in reaching a consensus during an investigation of cases concerning bush-meat trade (Ogden *et al*., 2009). This method has also been used to identify animals whose body parts had been burnt beyond recognition (Bhaskar and Khan, 2011). The success of species identification using molecular tools is based on isolation and analysis of DNA markers that show variations amongst species. Such markers should be conserved within the species. Such DNA based molecular markers include:

2.6.3.1 Restriction Fragment Length Polymorphism (RFLPs)

RFLPs are electrophoretic comparisons of the size of restriction fragments derived from genomic DNA (Lockley and Bardsley, 2000). Fragments are derived from digestion of genomic DNA with endonucleases which can recognise and cut DNA wherever a specific short sequence occurs. The resultant DNA fragments which vary in length can then be analysed by electrophoresis or by hybridization with labelled DNA probes and detected by autoradiography (Semagn *et al*., 2006).

Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) has also been used in identification of different species (Akasaki *et al*., 2006). PCR-RFLP technique was used to identify ten different animal species namely, chicken, wild duck, dog, pig, cat, bear, deer, baboon, cow and raccoon (Nakaki *et al*., 1999).

This method involves the analysis of DNA fragment profiles which are obtained by digesting PCR amplicons using endonucleases. These are then sorted by gel electrophoresis to obtain patterns which can be used to discriminate species based on pattern similarities or lack of it. However, this method is not seen completely effective due to the possible variation of patterns depending on the conditions of gel electrophoresis. Therefore, variable and inconclusive results are often observed. In addition, gel electrophoresis requires use of hazardous reagents which are not convenient for long time use (Dooley *et al*., 2005). Due to these drawbacks of PCR-RFLP, cytochrome *b* gene sequencing was opted for use in species identification.

2.6.3.2 Amplified Fragment Length Polymorphism (AFLPs)

These markers are similar to RFLPs but restriction digestion is done on PCR products. Restriction endonucleases such as Msel and EcoR1 are used to digest the DNA before amplification. The subsequent restriction site is then used as a primer binding site for amplification using PCR. The amplified fragments are then analysed using denaturing Polyacrylamide gel electrophoresis which generates fingerprints to be compared as polymorphism (Mueller and Wolfenbarger, 1999). Analysis is done by electrophoretic separation of amplicons on a gel matrix, followed by visualization of the band (Semagn et al., 2006).

2.6.3.3 Randomly Amplified Polymorphic DNA (RAPDs)

RAPDs use approximately 10-12 bp arbitrary primers to amplify fragments of DNA from total DNA. The segments of DNA that are amplified are random. No knowledge of the DNA sequence for the targeted gene is required as the primers bind randomly along the sequence. This method is popular for comparing the DNA of biological systems that have not been studied extensively before. This technique has limitation in the use of degraded samples because it relies on large intact DNA samples. It also has problems with reproducibility and are difficult to discern during electrophoresis. RAPD technique has been used to identify different species of meat from beef, buffalo, mule, donkey, kangaroo, ostrich and goat (Martinez and Malmheden, 1998) whereas Koh *et al.*, (1998) used RAPD to generate fingerprint patterns that were species specific in the identification of pig, horse, buffalo, dog, cat and rabbit.

2.6.3.4 DNA Barcoding

DNA barcoding has become a promising tool for rapid and accurate identification of various taxa and it has been used to reveal unrecognized species in several animal groups. It employs sequence diversity, in short, standardized gene regions to aid species identification and discovery in large assemblages of life (Hebert *et al*., 2003b). It has been proposed that DNA barcoding (Tautz *et al*., 2003) plays a central and mandatory role in both taxonomy and identification (Teletchea *et al*., 2008). However, a different school of thought has argued against it because it could replace the concept of taxonomy that has been used for over two centuries to aid in species identification (Will and Rubinoff, 2004). Moreover, the use of barcoding which employs DNA sequences as taxons or barcodes is the best option (Hebert *et al*., 2003b) in species identification.

2.6.3.5 Mitochondrial DNA Genes

Mitochondrial DNA (mtDNA) gene regions (Figure 2.1) are currently the markers of choice for species identification because they show variation between species but are generally conserved within species (Ogden *et al*., 2009). The most commonly used genes for animal identification are mitochondrial cytochrome *b* (cty *b*) (Pearson *et al*., 2000) cytochrome c oxidase subunit I (COI) genes (Hebert *et al*., 2004) and are recommended in analysis of old, trace or degraded samples (Prusak *et al*., 2005). Mitochondrial DNA are also valuable for the construction of evolutionary relationships (phylogenetics) among populations (Avise, 1986; Moritz *et al*., 1987).

Moreover, mtDNA is of higher stability and occurs in a much higher number of copies than nuclear DNA (Prusak *et al*., 2005; Chen *et al*., 2012). It has also been successfully used in studies of molecular evolution (Irwin *et al*., 1991). The preferred markers are those that flank mitochondrial gene loci and include cytochrome oxidase I (COI) (Hebert *et al*., 2003a) and cytochrome *b*. These markers are popular because their mutation rate roughly coincides with the rate of species evolution (Parson *et al*., 2000). Other markers are those for the 16S and 12S regions. 12s rRNA is highly conserved and has been used to understand the genetic diversity of higher levels such as phyla, while 16s rRNA is often used for studies at middle categorical levels such as families or genera (Gerber *et al*., 2001). Constructed phylogenetic trees are also able to discern evolutionary relationships between test samples and reference sequence from each possible species (Verma and Singh, 2003) and hence can be used in species identification.

Cytochrome *b* of mtDNA has been found to be a powerful indicator for identifying the species (Prusak *et al*., 2005). It is one of the best known gene of the 10 genes involved in mitochondrial oxidative phosphorylation system (Hatefi, 1985) and has been used to address many phylogenetic questions (Su *et al*., 1999). It has also been used successfully to identify bush-meat (Olayemi *et al*., 2011) as well as in studies of molecular evolution (Irwin *et al*., 1991).

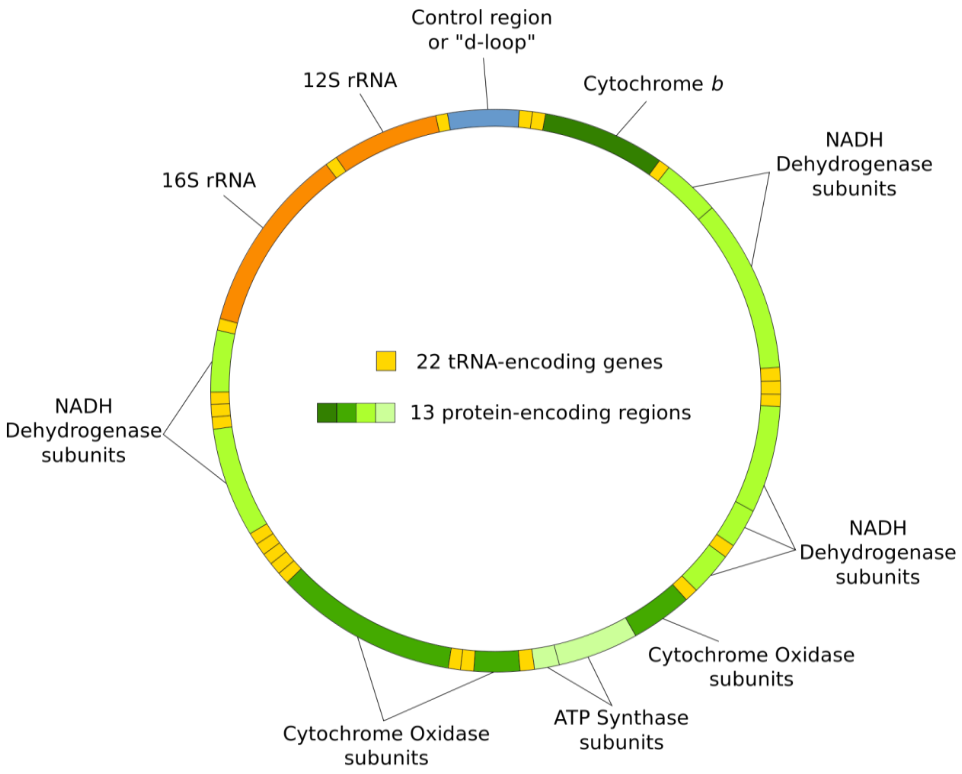


Figure 2.1: Structure of mitochondrial DNA. (Adapted from Moraes et al., 2002)

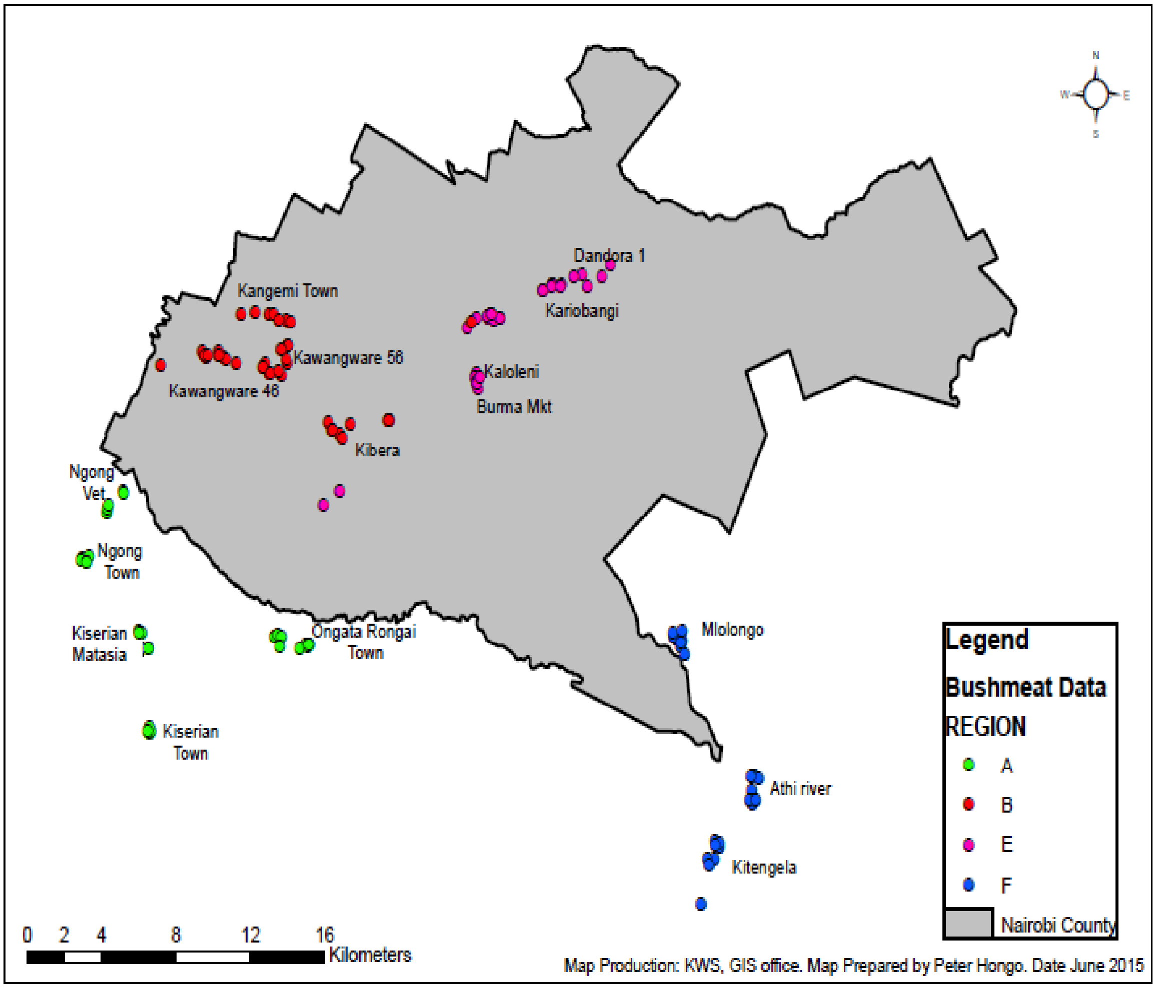
CHAPTER THREE

MATERIALS AND METHODS

3.1 Study Area

The study was carried out in Nairobi and its environs. Nairobi occupies 696 square kilometers with estimated population of about 3 million according to the 2009 Census (KNBS, n.d.).It houses Nairobi National Park, which is a potential target for poachers and has good transport connectivity with neighbouring towns and international via Jomo Kenyatta International Airport.

The meat samples were purchased randomly from various butcheries within Nairobi and its environs (Figure 3.2) specifically from the following areas: Ongata Rongai, Ngong and Kiserian (area A), Dagoreti, Kawangware, Kangemi and Kibera (area B), Burma Market, Dandora, Kariobangi Mlango Kubwa and Huruma (area E), Mlolongo, Kitengela, and Athi River (area F). The specific coordinates of the collection sites were mapped using Global Positioning Systems (GPS) (Figure 3.1). All the molecular analysis studies were performed in the Forensic and Genetics Laboratory at the Kenya Wildlife (KWS) Headquarters, in Nairobi.



Map Production: KWS, GIS office. Map Prepared by Peter Hongo. Date June 2015

Figure 3.1: Map of Nairobi showing the locations of meat sample collection for molecular characterization

3.2 Sample Collection

Simply random sampling was applied when selecting sampling butcheries in each study area with a sampling interval of one kilometre. One hundred and thirty-eight (138) meat samples were purchased. The putative identities, name and the location from which the samples were purchased are listed in table 3.1 with details shown in appendix 2. The samples were temporarily stored in cooler boxes during transportation to the laboratory where they were stored in -80^{o}C freezers.

Table 3.1: Types of meat samples collected from various butcheries in different sampling sites in Nairobi and its environs for molecular characterization

Sampling Site	**Number of Samples Collected and Putative species**	
	Beef (Cattle)	**Chevon (goat)**
AREA A		
Kiserian	9	1
Ngong	9	1
Ongata Rongai	7	3
AREA B		
Dagoreti	11	-
Kawangware	10	-
Kibera	10	-
Kangemi	10	-
AREA E		
Burma market	8	-
Dandora	7	2
Kariobangi	10	-
Mlango Kubwa	10	-
Kaloleni	1	-
Huruma	2	-
AREA F		
Mlolongo	5	3
Athi River	9	1
Kitengela	9	-
Total	**127**	**11**

3.3 DNA Extraction

Meat samples were thawed at room temperature for two hours. Genomic DNA was extracted using the High Pure PCR Template Preparation Kit (Roche, Germany) according to the manufacturer's instructions. A 30 mg portion of each meat sample was excised and put into sterile micro-centrifuge tubes. Sequentially, 200µl of tissue lysis buffer and 40 µl of proteinase K were added into each sample and mixed thoroughly. The mixtures were then incubated for 16hrs at 55°C to completely digest the sample.

The liquid portion of the lysate was transferred into the eppendorf tubes and 200µl of aliquot Binding Buffer added into each and mixed thoroughly. The mixtures were then incubated for 10 minutes at 70°C. One hundred microliters aliquots of isopropanol was then added into each eppendorf tube and mixed well. The liquid sample were then transferred into the upper buffer reservoir of the High Pure filter tubes fitted into the collection tubes and centrifuged at 13000rpm and the flow through discarded.

To wash and elute the DNA, the high pure filter tubes were assembled with a new collection tubes and 500µl aliquots of removal buffer added to the upper reservoir of each high pure filter tubes and centrifuged for 1 minute at 13000rpm and the flow through discarded.

Sequentially, the high pure filter tubes were transferred onto new collection tubes, 500µl aliquots of Wash Buffer added to the upper reservoir of each high pure filter tubes and then centrifuged at 13000rpm for 1 minute and the flow through discarded. This procedure was repeated twice. The High Pure filter tube dry assembly centrifuged for 10seconds at full speed to completely remove residual buffer.

DNA was then eluted by transferring the high pure filter tubes into a sterile 1.5ml micro-centrifuge tubes and 150µl aliquots of pre-warmed elution Buffer (at 70°C) added to the upper reservoir of the Filter Tubes and centrifuged at 13000rpm for 1 minute. The eluted DNA were stored at -80^{o}C.

3.4 DNA amplification

The mitochondrial cytochrome *b* gene was amplified by polymerase chain reaction (PCR) using universal primers (Mcb398 Forward-Mcb869 Reverse) shown in table 3.2 targeting a 500bp fragment (Verma and Singh, 2003). PCR was done in a total volume of 25µl containing 12.5µl of a 2X Hot Start Taq Mix (Qiagen, Cat No 203443) 1µl of 0.1µM of each primer, 4 µl of the template DNA and topped up with sterile PCR water. Amplification was carried out on a 96 well Veriti thermo cycler (Applied Bio systems) under the following cycling parameters: 15 min activation at 95°C, 35 cycles of 1 min denaturation at 95°C, 1 min primer annealing at 51°C, and a final 10 min extension at 72°C (Verma and Singh, 2003).

Table 3.2: Primers used to amplify cytochrome b gene in a bush meat identification study in butcheries in Nairobi and its environs.

Primer Name	Primer Sequence (5'-3')	PCR Product size
Mcb398 Forward	TACCATGAGGACAAATATCATTCTG`	500bp
Mcb869 Reverse	CCTCCTAGTTTGTTAGGGATTGATCG`	

Both positive and negatives controls were instituted to make sure that the results obtained were authentic. A negative PCR reaction containing water and PCR master mix only was run in each batch of PCR reaction. This showed that no laboratory condition was affecting the results. Positive controls using known gerenuk (gazelle) sample were also run in each batch of the PCR reaction which validated the workability of my primers.

3.5 Gel electrophoresis of PCR Products

PCR products were visualized through gel electrophoresis using a 1.5% agarose gel stained with Ethidium bromide. The gel was prepared by dissolving one gram of agarose powder in 100ml of 1x TAE buffer. The mixture was then heated to dissolve the agarose and allowed to cool on an electrophoresis casting tray with combs inserted to form wells. 4μl of the PCR product was mixed with 1μl of loading dye and added into the wells. A molecular weight ladder was introduced to the first well to give indication of the size of amplified product. The rest of the samples were loaded to the other wells and ran at 100 volts for 1 hour. The gel was then visualised under UV light for bands. Positive PCR products were properly labelled and preserved for purification.

3.6 Purification of PCR products

PCR products showing the expected fragment size on agarose gel analysis were purified by enzymatic treatment using exonuclease I and shrimp alkaline phosphatase (PCR Product Presequencing Kit, Amersham).

3.7 DNA Sequencing

All DNA sequencing was carried out by direct cycle sequencing on both strands of purified PCR DNA products from PCR amplification. Sequencing reactions were performed using ABI PRISM DigDye Terminator v3.1 cycle sequencing kit and analyzed on an ABI310 DNA sequencer (Applied Biosystems, CA).

3.8 Data Analysis

Contigs from the forward and reverse sequences were assembled using Genious 7.1.2 software to generate consensus sequences (Appendix 1). The consensus sequences were then cleaned and used to conduct a nucleotide search on Basic Local Alignment Search Tool (BLASTn) against GenBank database provided online at NCBI (Altschul *et al*., 1990). This gave the specific names as described by their genetic sequences. The blast search parameters used were as follows: Program: BlastN, word size: 28, Expect threshold value: 10, Hit list size: 100, match/ mismatch score: 1,-2, gap costs: 0, 2.5 and low complexity filter on. The sequences were aligned using ClustalW software (Thompson *et al*.,1994), as implemented on Mega 6 (Koichiro *et al*., 2013) software.

To construct the phylogenetic tree, all the 138 consensus sequences that were generated in this study were then collapsed on an online DNA collapse (http://users birc.au.dk/biopv/php/fabox/dnacollapser.php#) and yielded 32 distinct haplotypes (Appendix 3) following removal of identical sequences and redundancies. The generated haplotypes together with six representative sequences from NCBI database (http://www.ncbi.nlm.nih.gov/nucleotide/) (Appendix 3) were used to construct the phylogenetic tree using MEGA 6 software. The evolutionary relationship was determined using maximum likelihood method with 1000 replicates (Felsenstein, 1985; Tamura and Nei, 1993) to determine branch support values. Sequences retrieved from GenBank databases were: *Ovis aries* (D84205), *Capra hircus* (KP662716) and (JX286551) and *Bos taurus* (KJ789953) and (EU177836), and *Xenopus laevis* (AY819740). *Xenopus laevis*

C*ytb* gene was used as an outgroup to help resolve the evolutionary relatedness among the sequences under this study.

CHAPTER FOUR

RESULTS

4.1 DNA Extraction and PCR

All the PCR products visualized on 1.5% agarose gel showed that DNA was successfully extracted and amplified as shown in Figure 4.1. The size of the amplified DNA was in the range of 480-500bp.

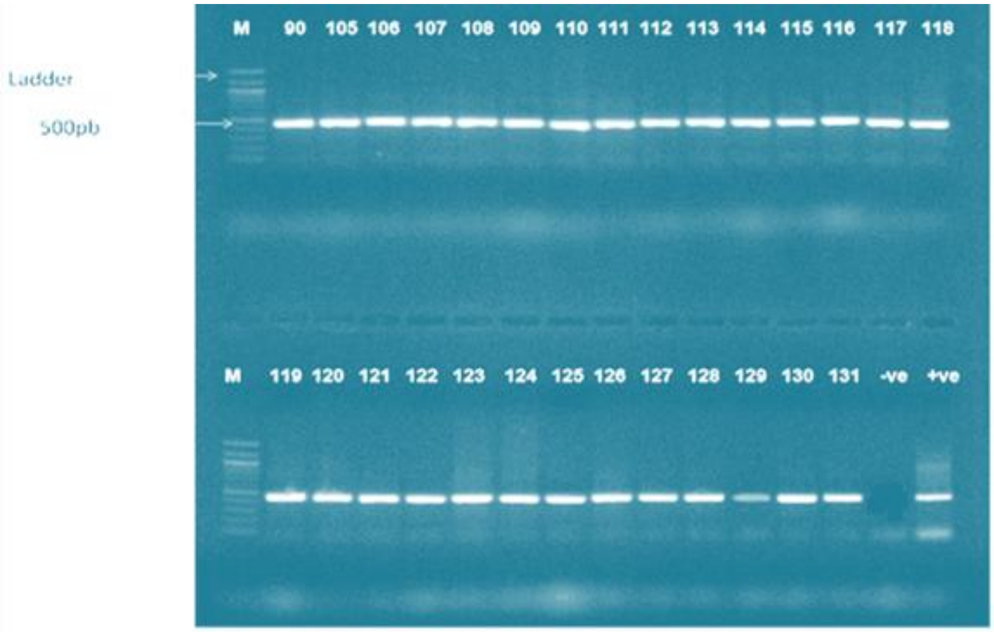


Figure 4.1: Representative gel image for a bush-meat study in Nairobi and its environs for samples 90-131 illustrating amplification of the expected bands.

4.2 Sequence Analyses

BLAST searches confirmed the species identity of the samples. As summarized in Table 4.1 and detailed in appendix 2, 120 (86.96%) of the analyzed samples were found to have >99% similarity to *Bos taurus* (Cattle = Beef), 15 (10.87%) of the analyzed samples had

>99% similarity to *Capra hircus* (Goat = Chevon) while 3 (2.17%) of the samples had >99% similarity to *Ovis aries* (Sheep = Mutton). The frequencies of molecular species identity on the collected samples are represented in Figure 4.2.

Table 4.1: Summary of putative and confirmed species originating from meat samples in Nairobi butcheries.

	Cattle	Goat	Sheep	Total
Putative species	125	13	0	138
BLAST(Confirmed) species	120	15	3	138

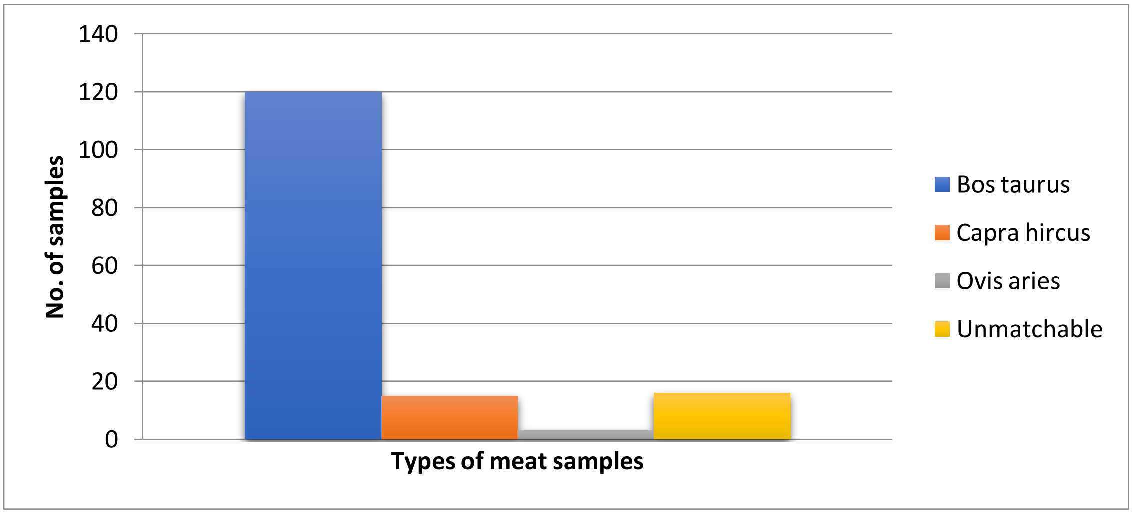


Figure 4.2: Frequency representation of meat samples identified using the BLAST program in a bush meat study in Nairobi and its environs.

Most of the samples corresponded to their respective putative species identity upon sequence analysis. However, 16 (11.59%) of the samples showed a mismatch with their respective putative species identity during sample collection. These are scenarios where a sample was acquired from a meat retailer/butcher as beef (from Cattle: *Bos taurus*) or Chevon (from Goat: *Capra hircus)* only for its generated sequences to indicate otherwise as summarized in table 4.2 below. None of the collected samples was identified as bush-meat.

Table 4.2: Detailed account showing inter-species substitution of meat samples in Nairobi butcheries

Putative species	**BLAST(Confirmed) species**	**Total**
Cattle	(Goat)	9
Cattle	(Sheep)	2
Goat	(Sheep)	1
Goat	(Cattle)	4

4.3 Phylogenetic analysis

Similarity searching mapped the haplotypes to homologous mitochondrial cytochrome b gene from ovine, caprine and bovine species. The percentage of replicate trees in which the species clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein, 1985).Three clades corresponding to *Ovis aries* , *Capri hircus* and *Bos taurus* were observed with a minimum bootstrap support value of 51 (Figure 4.3). The first clade was composed of samples 10,20,19,30,28,70,48 and 47 that clustered together with the *Capra hircus* GenBank reference sequences (KP662716 and JX286551) while the second clade was composed of samples 97 and 40 which clustered together with *Ovis aries* GenBank reference sequence (D84205). The major clade in the tree topology was composed of 22 samples

(17,105,129,76,9,66,88,57,22,127,59,136,44,49,18,135,91,101,23,37,62 and 34), which clustered with the *Bos Taurus* GenBank reference sequences (EU177836 and KJ789953).

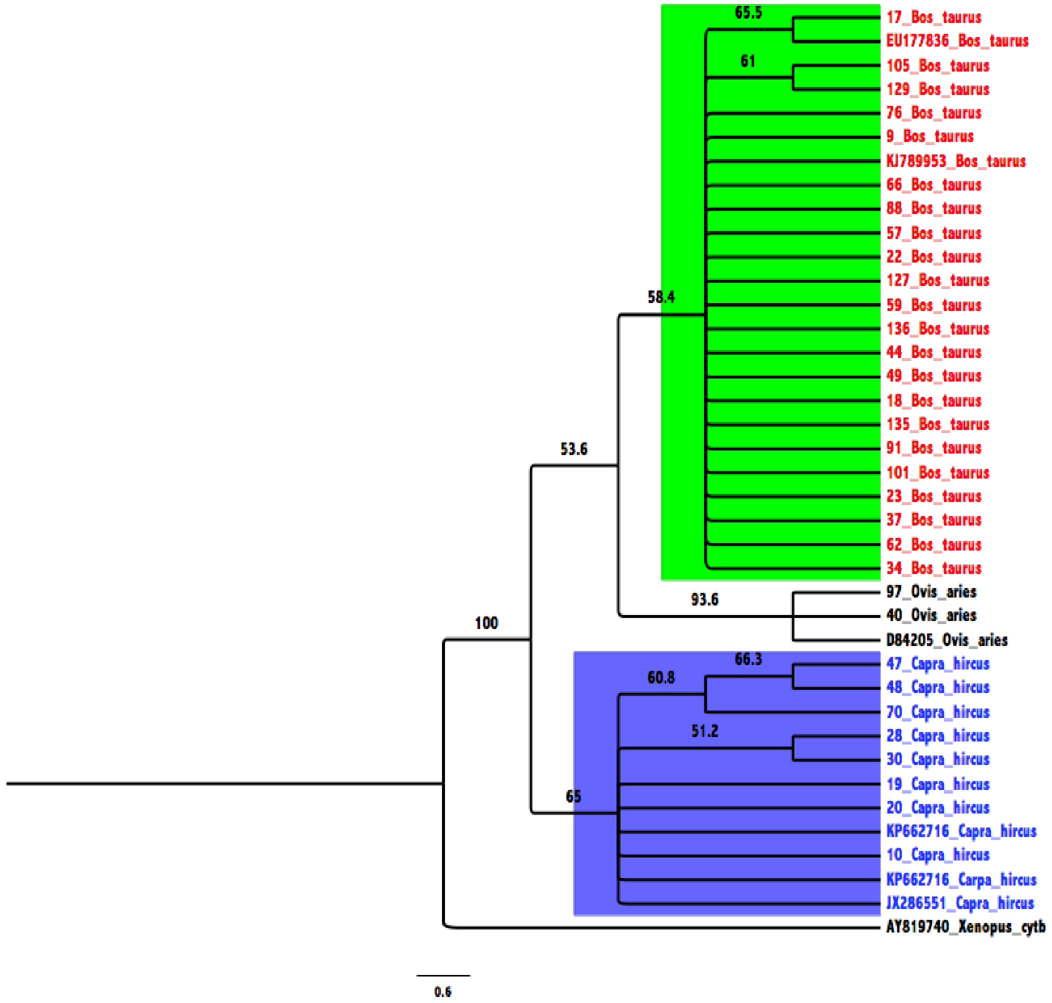


Figure 4.3: Phylogenetic tree showing distinct clustering of haplotypes representing three distinct species of meat samples in Nairobi butcheries

CHAPTER FIVE

DISCUSSION, CONCLUSIONS AND RECOMMENDATIONS

5.1 DISCUSSION

Results from this study revealed that none of the sampled butcheries in Nairobi and its environs were bush-meat outlets during the time of sampling since none of the sampled 138 stalls tested positive for any wildlife products. All the analyzed samples were from domestic animals namely; cattle, goat, and sheep as revealed by sequencing data. Sutton, (2008) also documented lack of bush-meat in his study. The results therefore supported the study hypothesis that the prevalence of bush – meat in Nairobi and its environs is zero percent.

The findings of this study which reported the absence of bush-meat among the selected butcheries in Nairobi County and its environs could possibly be as a result of decline in the number of cases regarding bush-meat hunting in the Nairobi national park as well as other wildlife conservancies around the vicinity of Nairobi County possibly due to the enactment of the Wildlife and Conservation Management Act, (2013) which levies stiffer and highest penalties for wildlife crimes and regular patrols by KWS rangers. Similarly, this could imply that most of the harvesting of the wildlife species done among the communities living around the wildlife reserves could be of domestic purpose as reported by Ndibalema and Songorwa, (2007) hence the reason why this stock did not find its way to the butcheries within the study area. Moreover, there is a possibility that those who harvest wildlife species for meat do not supply the butcheries in the selected study areas with meat but rather sell them directly to the end user as documented by Fitzgibbon *et al*. (1995) and Okello and Kiringe (2004). An equally plausible explanation for these findings could be the possibility of the bush-meat harvesting not finding its way into meat outlets in study area is that bush-meat harvesters could be targeting special clientele network within which the products are directly delivered thus cutting out the commercial butcheries that could be considered as middlemen in this case. The probability of bush-meat harvested from Kenya finding its way into “ready markets” across Kenyan borders cannot be underestimated especially in the neighbouring countries’ like Tanzania where wildlife meat is consumptively tolerated and constantly supplied to poor rural communities in Tanzania as reported by Bagachwa *et al*. (1995) as opposed to complete sanction of the same in Kenya (Barnett,1997).

With the increased snaring activities as noted by Fitzgibbon *et al*. (1995), Okello and Kiringe (2004), Wato *et al*. (2006), there are enough indications of ongoing bush-meat harvesting activities. The enforcement agencies will need to focus attention on other possible markets of bush meat such as the exclusive clubs, restaurants or homes. Surveillance at airports should also be intensified.

Contrary to the study findings, Free (2004) reported availability of bush-meat in Kenyan markets at the prevalence rate of 25%, during the wet season. In their study, ouchterlony immunidiffusion method was used to analyze the samples. This method has been reported to have low specificity and usually suffers from cross reactions between closely related species as documented by (Kang’ethe *et al*., 1986).

This study did not put into consideration the effect of seasonality on bush-meat hunting. Moreover, Sutton (2008) could not confirm the results of Free, (2004); a possible indication that probably seasonality could not be a major factor in bush-meat consumption. Of great significance is that the spatial and temporal differences associated with this study and that of Free (2004) cannot be ignored.

The BLAST results from 16 samples representing 11.59% of all the samples in this study did not match their putative identities. This is a scenario where the species the butcher was selling turned out to be a different one on BLAST analysis. These incidences of meat substitutions were observed in ten out of the sixteen sampling sites namely in Ongata Rongai, Kiserian, Ngong, Kangemi, Dandora, Kariobangi, Mlango Kubwa, Huruma, Arthi River and Mlolongo. This could probably be due to retailers pooling their meat samples together during transportation and storage. Secondly, it could be a deliberate move by meat retailers to clear off the stocks since they are perishable or even less preferred like in the case of mutton (which is fatty) being sold in disguise as beef or chevon. Thirdly, the traders could be trying to increase their profit margins by selling cheaper meat such as beef to buyers in disguise of it being from a goat which generally fetches a higher profit margin per kilogram as compared to beef. Lastly, there is a possibility that this mix-up could be resulting from human error in identifying the products being handed over to customers or possible contamination by the butcher given that they use the same knife and meat mincer to process the meat they sell. Besides, it cannot be ruled out that the samples that did not match their putative identities that were identified otherwise by *Cyt-b* assay could be errors that occurred during labeling and sample handling as reported by Eaton *et al.*(2009).

The utilization of the mitochondrial markers for the identification of species has previously been proved to be highly effective (Eaton *et al*., 2009; Olayemi *et al*., 2011).

The results from this study demonstrate sensitivity and specificity of C*yt - b* marker in identifying and resolving various species of meat samples. High- quality sequences were generated from all the samples implying that C*yt - b* marker can be extensively employed in species identification from any suspected animal product confiscated or sampled in surveillance exercises. Akimoto *et al*. (2006) successfully used C*yt - b* to discriminate among fish. Equally successful were Verma and Sign (2003) and Person *et al* (2000) who used C*yt - b* to discriminate amongst avian and mammalian species respectively. In this study, Phylogenetic analysis to determine the evolutionary relationship was done using the maximum likelihood method as documented by (Tamura *et al*., 2013) based on thirty-two haplotypes. Three major clusters were formed representing three distinct species namely, *Bos taurus*, *Ovis aries* and *Capra hircus*. This was congruent with results obtained using BLAST method of identification, a further confirmation of the reliability of C*yt - b* in species identification. The first clade was composed of samples 10,20,19,30,28,70,48 and 47 that clustered together with the *Capra hircus* GenBank reference sequences (KP662716 and JX286551) while the second clade was composed of samples 97 and 40 which clustered together with *Ovis aries* GenBank reference sequence (D84205). The major clade in the tree topology was composed of 22 samples

(17,105,129,76,9,66,88,57,22,127,59,136,44,49,18,135,91,101,23,37,62 and 34), which clustered with the *Bos Taurus* GenBank reference sequences (EU177836 and KJ789953).

The findings of this study have demonstrated that illegal bush-meat is not available in butcheries within Nairobi and its surrounding suburbs. Despite the rise of snaring implying increased illegal poaching as document by Fitzgibbon *et al*., 1995; Okello and Kiringe, 2004; Wato *et al*., 2006 , these products are probably not destined to Nairobi market. Enforcement agencies such as Kenya Wildlife Services will need to focus their attention on other establishments such as the exclusive clubs, restaurants, homes and/or the airport to check if the bush-meat harvested is destined overseas.

5 .2 CONCLUSIONS

i. This study did not document any game meat sold as domestic stock across the various butcheries sampled in Nairobi and its environs.
ii. Findings from this study demonstrated that the commonly consumed meat species in Nairobi and its environs are cattle, sheep and goat.
iii. The results further demonstrated that mitochondrial DNA is a useful tool for accurately identifying the host species from which a meat product was sourced. Phylogenetic analysis of the amplified mtDNA fragments accurately placed all the samples into their respective taxa.

5 .3 RECOMMENDATIONS

i. The frequency of studies similar to this should be increased and also cover large areas. Sampling should also be extended to cover different seasons to ascertain whether the availability of bush-meat products in the local butcheries and meat outlets in Nairobi is influenced by the prevailing seasons.

ii. Surveillance of bush-meat trade should be extended to other towns and market places adjacent to protected areas where a large number of snares have been recovered. This will enable determination of whether the bush-meat trade is at the subsistence level in areas close to the point of harvesting. Trans-boundary surveillance should also be taken into consideration to avert any potential cases of trafficking bush-meat products into “ready markets” across our borders.

5.4 FUTURE RESEARCH

Should aim at developing potential molecular markers that can be used in rapid determination of meat species by the inspectors on site.

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APPENDICES

Appendix I: Consensus sequences.

>1_consensus_sequence Assembly of 2 reads: 1_Mcb869Cytb-Rev_H04_22.ab1 (reversed), 1_Mcb398Cytb-Fwd_G04_19.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>2_consensus_sequence Assembly of 2 reads: 2_Mcb398Cytb-Fwd_A05_02.ab1, 2_Mcb869Cytb-Rev_A06_03.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>3_consensus_sequence Assembly of 2 reads: 3_Mcb398Cytb-Fwd_B05_05.ab1, 3_Mcb869Cytb-Rev_B06_06.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>4_consensus_sequence Assembly of 2 reads: 4_Mcb398Cytb-Fwd_C05_08.ab1, 4_Mcb869Cytb-Rev_C06_09.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>5_consensus_sequence Assembly of 2 reads: 5_Mcb869Cytb-Rev_D06_12.ab1 (reversed), 5_Mcb398Cytb-Fwd_D05_11.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TCCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGAC
ATCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGC
ACCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAAC
ACACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTT
A

>6_consensus_sequence Assembly of 2 reads: 6_Mcb869Cytb-Rev_E06_15.ab1 (reversed), 6_Mcb398Cytb-Fwd_E05_14.ab1

GCAATCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTCT
CAGTAGACAAAGCAACCCTTACCCGATTCTTCGCTTTCCATTTTATCCTTCCAT
TTATCATCATAGCAATTGCCATAGTCCACCTACTATTCCTCCACGAAACAGGC
TCCAACAACCCAACAGGAATTTCCTCAGACGTAGACAAAATCCCATTCCACC
CCTACTATACCATTAAGGACATCTTAGGGGCCCTCTTACTAATTCTAGCTCTA
ATACTACTAGTACTATTCGCACCCGACCTCCTCGGAGACCCAGATAACTACA
CCCCAGCCAATCCACTCAACACACCCCCTCACATCAAACCCGAGTGATACTT
CTTATTTGCATACGCAATCTTA

>7_consensus_sequence Assembly of 2 reads: 7_Mcb398Cytb-Fwd_F05_17.ab1, 7_Mcb869Cytb-Rev_F06_18.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA

TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>8_consensus_sequence Assembly of 2 reads: 8_Mcb869Cytb-Rev_G06_21.ab1 (reversed), 8_Mcb398Cytb-Fwd_G05_20.ab1

AGGGGCAACAGTTATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGAGGGGGATTYTCAGTAGACAAAGCCACTCTCAC
CCGATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCAT
AGTCCACCTGCTTTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATT
CCATCAGACRCAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATAT
CTTAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACC
CGACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACA
CCCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>9_consensus_sequence Assembly of 2 reads: 9_Mcb398Cytb-Fwd_F09_18.ab1, 9_Mcb869Cytb-Rev_F10_16.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>10_consensus_sequence Assembly of 2 reads: 10_Mcb869Cytb-Rev_G10_19.ab1 (reversed), 10_Mcb398Cytb-Fwd_G09_21.ab1

TCAGCAATCCCATATATTGGCACAAACCTAGTCGAATGAATCTGAGGGGGAT
TCTCAGTAGACAAAGCCACTCTCACCCGATTCTTCGCCTTCCACTTTATCCTC
CCATTCATCATCACAGCCCTCGCCATAGTCCACCTGCTCTTCCTCCACGAAAC
AGGATCGAACAACCCCACAGGAATTCCATCAGACACAGATAAAATCCCATTT
CACCCTTACTACACCATTAAAGATATCTTAGGCGCCATGCTACTAATTCTTGT
TCTAATATTACTAGTACTATTCACACCCGACCTACTCGGAGACCCAGACAACT
ATATCCCAGCAAATCCACTCAATACACCCCCTCACATTAAACCTGAGTGGTAT
TTCCTATTTGCATACGCAATCCTA

>11_consensus_sequence Assembly of 2 reads: 11_Mcb398Cytb-Fwd_H09_24.ab1, 11_Mcb869Cytb-Rev_H10_22.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>17_consensus_sequence Assembly of 2 reads: 17_Mcb398Cytb-Fwd_A11_02.ab1, 17_Mcb869Cytb-Rev_A12_03.ab1 (reversed)

AGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAAT
TTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACCC
GATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCTATAG
TCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTTC
CTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACATCT
TAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCACCC
GACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACACAC
CCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>18_consensus_sequence Assembly of 2 reads: 18_Mcb398Cytb-Fwd_B11_05.ab1, 18_Mcb869Cytb-Rev_B12_06.ab1 (reversed)

CAATCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTCTC
AGTAGACAAAGCAACCCTTACCCGATTCTTCGCTTTCCATTTTATCCTTCCATT
TATCATCATAGCAATTGCCATAGTCCACCTACTATTCCTCCACGAAACAGGCT
CCAACAACCCAACAGGAATTTCCTCAGACGTAGACAAAATCCCATTCCACCC
CTACTATACCATTAAGGACATCTTAGGGGCCCTCTTACTAATTCTAGCTCTAA
TACTACTAGTACTATTCGCACCCGACCTCCTCGGAGACCCAGATAACTACACC
CCAGCCAATCCACTCAACACACCCCCTCACATCAAACCCGAGTGATACTTCTT
ATTTGCATACGCAATCTTA

>19_consensus_sequence Assembly of 2 reads: 19_Mcb869Cytb-Rev_C12_09.ab1 (reversed), 19_Mcb398Cytb-Fwd_C11_08.ab1

AGGGGCAACAGTCATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCAC
CCGATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCAT
AGTCCACCTGCTCTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATT
CCATCAGACACAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATAT
CTTAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACC
CGACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACA
CCCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>20_consensus_sequence Assembly of 2 reads: 20_Mcb398Cytb-Fwd_D11_11.ab1, 20_Mcb869Cytb-Rev_D12_12.ab1 (reversed)

GGGCAACAGTCATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAAAC
CTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCACCC
GATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCATAG
TCCACCTGCTCTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATTCC
ATCAGACACAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATATCT
TAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACCC
GACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACAC
CCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>21_consensus_sequence Assembly of 2 reads: 21_Mcb398Cytb-Fwd_E11_14.ab1, 21_Mcb869Cytb-Rev_E12_15.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>22_consensus_sequence Assembly of 2 reads: 22_Mcb398Cytb-Fwd_F11_17.ab1, 22_Mcb869Cytb-Rev_F12_18.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
CTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGAC
ATCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGC
ACCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAAC
ACACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTT
A

>23_consensus_sequence Assembly of 2 reads: 23_Mcb398Cytb-Fwd_G11_20.ab1, 23_Mcb869Cytb-Rev_G12_21.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT

CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>24_consensus_sequence Assembly of 2 reads: 24_Mcb869Cytb-Rev_H12_24.ab1 (reversed), 24_Mcb398Cytb-Fwd_H11_23.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>25_consensus_sequence Assembly of 2 reads: 25_Mcb869Cytb-Rev_A02_02.ab1 (reversed), 25_Mcb398Cytb-Fwd_A01_01.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>26_consensus_sequence Assembly of 2 reads: 26_Mcb869Cytb-Rev_B02_05.ab1 (reversed), 26_Mcb398Cytb-Fwd_B01_04.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>27_consensus_sequence Assembly of 2 reads: 27_Mcb869Cytb-Rev_C02_08.ab1 (reversed), 27_Mcb398Cytb-Fwd_C01_07.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA

CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>28_consensus_sequence Assembly of 2 reads: 28_Mcb398Cytb-Fwd_D01_10.ab1, 28_Mcb869Cytb-Rev_D02_11.ab1 (reversed)

GGGCAACAGTCATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAAAC
CTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCACCC
GATTCTTCGCCCTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCATAG
TCCACCTGCTCTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATTCC
ATCAGACGCAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATATCT
TAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACCC
GACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACAC
CCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>29_consensus_sequence Assembly of 2 reads: 29_Mcb398Cytb-Fwd_E01_13.ab1, 29_Mcb869Cytb-Rev_E02_14.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>30_consensus_sequence Assembly of 2 reads: 30_Mcb398Cytb-Fwd_F01_16.ab1, 30_Mcb869Cytb-Rev_F02_17.ab1 (reversed)

AGGGGCAACAGTCATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCAC
CCGATTCTTCGCCCTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCAT
AGTCCACCTGCTCTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATT
CCATCAGACGCAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATAT
CTTAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACC
CGACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACA
CCCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>31_consensus_sequence Assembly of 2 reads: 31_Mcb398Cytb-Fwd_G01_19.ab1, 31_Mcb869Cytb-Rev_G02_20.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>32_consensus_sequence Assembly of 2 reads: 32_Mcb398Cytb-Fwd_H01_22.ab1, 32_Mcb869Cytb-Rev_H02_23.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>33_consensus_sequence Assembly of 2 reads: 33_Mcb398Cytb-Fwd_A03_03.ab1, 33_Mcb869Cytb-Rev_A04_01.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>34_consensus_sequence Assembly of 2 reads: 34_Mcb398Cytb-Fwd_B03_06.ab1, 34_Mcb869Cytb-Rev_B04_04.ab1 (reversed)

GGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAA
ATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTAC
CCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCAT
AGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATT
TCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGATCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>35_consensus_sequence Assembly of 2 reads: 35_Mcb869Cytb-Rev_C04_07.ab1 (reversed), 35_Mcb398Cytb-Fwd_C03_09.ab1

AGGGGCAACAGTCATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCAC
CCGATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCAT
AGTCCACCTGCTCTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATT
CCATCAGACACAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATAT
CTTAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACC
CGACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACA
CCCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>36_consensus_sequence Assembly of 2 reads: 36_Mcb869Cytb-Rev_D04_10.ab1 (reversed), 36_Mcb398Cytb-Fwd_D03_12.ab1

AGGGGCAACAGTCATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCAC
CCGATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCAT
AGTCCACCTGCTCTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATT
CCATCAGACACAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATAT
CTTAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACC
CGACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACA
CCCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>37_consensus_sequence Assembly of 2 reads: 37_Mcb398Cytb-Fwd_E03_15.ab1, 37_Mcb869Cytb-Rev_E04_13.ab1 (reversed)

GGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAA
ATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTAC
CCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCAT
AGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATT
TCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>38_consensus_sequence Assembly of 2 reads: 38_Mcb869Cytb-Rev_F04_16.ab1 (reversed), 38_Mcb398Cytb-Fwd_F03_18.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA

CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>39_consensus_sequence Assembly of 2 reads: 39_Mcb398Cytb-Fwd_G03_21.ab1, 39_Mcb869Cytb-Rev_G04_19.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>40_consensus_sequence Assembly of 2 reads: 40_Mcb869Cytb-Rev_H04_22.ab1 (reversed), 40_Mcb398Cytb-Fwd_H03_24.ab1

AGGAGCAACAGTTATTACCAACCTCCTTTCAGCAATTCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGGGGAGGATTCTCAGTAGACAAAGCTACCCTCAC
CCGATTTTTCGCCTTTCACTTTATTTTCCCATTCATCATCGCAGCCCTCGCCAT
AGTTCACCTACTCTTCCTCCACGAAACAGGATCCAACAACCCCACAGGAATT
CCATCGGACACAGATAAAATTCCCTTCCACCCTTATTACACCATTAAAGACAT
CCTAGGTGCTATCCTACTAATCCTCATCCTCATGCTACTAGTACTATTCACGC
CTGACTTACTCGGAGACCCAGACAACTACACCCCAGCAAACCCACTTAACAC
TCCCCCTCACATCAAACCTGAATGATACTTCCTATTTGCGTACGCAATCTTA

>41_consensus_sequence Assembly of 2 reads: 41_Mcb869Cytb-Rev_A06_03.ab1 (reversed), 41_Mcb398Cytb-Fwd_A05_02.ab1

AGGGGCAACAGTCATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCAC
CCGATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCAT
AGTCCACCTGCTCTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATT
CCATCAGACACAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATAT
CTTAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACC
CGACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACA
CCCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>42_consensus_sequence Assembly of 2 reads: 42_Mcb869Cytb-Rev_B06_06.ab1 (reversed), 42_Mcb398Cytb-Fwd_B05_05.ab1

AGGGGCAACAGTCATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCAC
CCGATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCAT

AGTCCACCTGCTCTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATT
CCATCAGACACAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATAT
CTTAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACC
CGACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACA
CCCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>43_consensus_sequence Assembly of 2 reads: 43_Mcb398Cytb-Fwd_C05_08.ab1, 43_Mcb869Cytb-Rev_C06_09.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>44_consensus_sequence Assembly of 2 reads: 44_Mcb869Cytb-Rev_D06_12.ab1 (reversed), 44_Mcb398Cytb-Fwd_D05_11.ab1

AGGAGCAACAGTCATCACTAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>45_consensus_sequence Assembly of 2 reads: 45_Mcb398Cytb-Fwd_E05_14.ab1, 45_Mcb869Cytb-Rev_E06_15.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>46_consensus_sequence Assembly of 2 reads: 46_Mcb398Cytb-Fwd_F05_17.ab1, 46_Mcb869Cytb-Rev_F06_18.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>47_consensus_sequence Assembly of 2 reads: 47_Mcb869Cytb-Rev_G06_21.ab1 (reversed), 47_Mcb398Cytb-Fwd_G05_20.ab1

AGGGGCAACAGTTATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCAC
CCGATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCAT
AGTCCACCTGCTTTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATT
CCATCAGACACAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATAT
CTTAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACC
CGACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACA
CCCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>48_consensus_sequence Assembly of 2 reads: 48_Mcb398Cytb-Fwd_H06_24.ab1 (reversed), 48_Mcb398Cytb-Fwd_H05_23.ab1

GGGCAACAGTTATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAAAC
CTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCACCC
GATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCATAG
TCCACCTGCTTTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATTCC
ATCAGACACAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATATCT
TAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACCC
GACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACAC
CCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>49_consensus_sequence Assembly of 2 reads: 49_Mcb398Cytb-Fwd_A07_01.ab1, 49_Mcb869Cytb-Rev_A08_02.ab1 (reversed)

AGGAGCAACAGTCATCACTAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCACAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>50_consensus_sequence Assembly of 2 reads: 50_Mcb869Cytb-Rev_B08_05.ab1 (reversed), 50_Mcb398Cytb-Fwd_B07_04.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>51_consensus_sequence Assembly of 2 reads: 51_Mcb398Cytb-Fwd_C07_07.ab1, 51_Mcb869Cytb-Rev_C08_08.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>52_consensus_sequence Assembly of 2 reads: 52_Mcb398Cytb-Fwd_D07_10.ab1, 52_Mcb869Cytb-Rev_D08_11.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>53_consensus_sequence Assembly of 2 reads: 53_Mcb869Cytb-Rev_E08_14.ab1 (reversed), 53_Mcb398Cytb-Fwd_E07_13.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA

CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>54_consensus_sequence Assembly of 2 reads: 54_Mcb398Cytb-Fwd_F07_16.ab1, 54_Mcb869Cytb-Rev_F08_17.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>55_consensus_sequence Assembly of 2 reads: 55_Mcb869Cytb-Rev_G08_20.ab1 (reversed), 55_Mcb398Cytb-Fwd_G07_19.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>56_consensus_sequence Assembly of 2 reads: 56_Mcb869Cytb-Rev_H08_23.ab1 (reversed), 56_Mcb398Cytb-Fwd_H07_22.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>57_consensus_sequence Assembly of 2 reads: 57_Mcb398Cytb-Fwd_A09_03.ab1, 57_Mcb869Cytb-Rev_A10_01.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCACTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA

TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>58_consensus_sequence Assembly of 2 reads: 58_Mcb398Cytb-Fwd_B09_06.ab1, 58_Mcb869Cytb-Rev_B10_04.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>59_consensus_sequence Assembly of 2 reads: 59_Mcb398Cytb-Fwd_C09_09.ab1, 59_Mcb869Cytb-Rev_C10_07.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAAACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>60_consensus_sequence Assembly of 2 reads: 60_Mcb398Cytb-Fwd_D09_12.ab1, 60_Mcb869Cytb-Rev_D10_10.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>61_consensus_sequence Assembly of 2 reads: 61_Mcb398Cytb-Fwd_E09_15.ab1, 61_Mcb869Cytb-Rev_E10_13.ab1 (reversed)

GGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAA
ATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTAC
CCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCAT
AGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATT
TCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>62_consensus_sequence Assembly of 2 reads: 62_Mcb398Cytb-Fwd_F09_18.ab1, 62_Mcb869Cytb-Rev_F10_16.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACTTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>63_consensus_sequence Assembly of 2 reads: 63_Mcb398Cytb-Fwd_G09_21.ab1, 63_Mcb869Cytb-Rev_G10_19.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>64_consensus_sequence Assembly of 2 reads: 64_Mcb398Cytb-Fwd_H09_24.ab1, 64_Mcb869Cytb-Rev_H10_22.ab1 (reversed)

GGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAA
ATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTAC
CCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCAT
AGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATT
TCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>65_consensus_sequence Assembly of 2 reads: 65_Mcb398Cytb-Fwd_A11_02.ab1, 65_Mcb869Cytb-Rev_A12_03.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>66_consensus_sequence Assembly of 2 reads: 66_Mcb398Cytb-Fwd_B11_05.ab1, 66_Mcb869Cytb-Rev_B12_06.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TCCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGAC
ATCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGC
ACCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAAC
ACACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTT
A

>67_consensus_sequence Assembly of 2 reads: 67_Mcb398Cytb-Fwd_C11_08.ab1, 67_Mcb869Cytb-Rev_C12_09.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>68_consensus_sequence Assembly of 2 reads: 68_Mcb398Cytb-Fwd_D11_11.ab1, 68_Mcb869Cytb-Rev_D12_12.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT

CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>69_consensus_sequence Assembly of 2 reads: 69_Mcb398Cytb-Fwd_E11_14.ab1, 69_Mcb869Cytb-Rev_E12_15.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>70_consensus_sequence Assembly of 2 reads: 70_Mcb398Cytb-Fwd_F11_17.ab1, 70_Mcb869Cytb-Rev_F12_18.ab1 (reversed)

AGGGGCAACAGTTATCACTAATCTTCTCTCAGCAATCCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCAC
CCGATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCAT
AGTCCACCTGCTTTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATT
CCATCAGACACAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATAT
CTTAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACC
CGACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACA
CCCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>71_consensus_sequence Assembly of 2 reads: 71_Mcb398Cytb-Fwd_G11_20.ab1, 71_Mcb869Cytb-Rev_G12_21.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>72_consensus_sequence Assembly of 2 reads: 72_Mcb869Cytb-Rev_H12_24.ab1 (reversed), 72_Mcb398Cytb-Fwd_H11_23.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA

CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>73_consensus_sequence Assembly of 2 reads: 73_Mcb398Cytb-Fwd_A01_01.ab1, 73_Mcb869Cytb-Rev_A02_02.ab1 (reversed)

GGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAA
ATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTAC
CCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCAT
AGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATT
TCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>74_consensus_sequence Assembly of 2 reads: 74_Mcb398Cytb-Fwd_B01_04.ab1, 74_Mcb869Cytb-Rev_B02_05.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>75_consensus_sequence Assembly of 2 reads: 75_Mcb869Cytb-Rev_C02_08.ab1 (reversed), 75_Mcb398Cytb-Fwd_C01_07.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>76_consensus_sequence Assembly of 2 reads: 76_Mcb869Cytb-Rev_D02_11.ab1 (reversed), 76_Mcb398Cytb-Fwd_D01_10.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAATGATACTTCTTATTTGCATACGCAATCTTA

>77_consensus_sequence Assembly of 2 reads: 77_Mcb869Cytb-Rev_E02_14.ab1 (reversed), 77_Mcb398Cytb-Fwd_E01_13.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>78_consensus_sequence Assembly of 2 reads: 78_Mcb398Cytb-Fwd_F01_16.ab1, 78_Mcb869Cytb-Rev_F02_17.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>79_consensus_sequence Assembly of 2 reads: 79_Mcb869Cytb-Rev_G02_20.ab1 (reversed), 79_Mcb398Cytb-Fwd_G01_19.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>80_consensus_sequence Assembly of 2 reads: 80_Mcb869Cytb-Rev_H02_23.ab1 (reversed), 80_Mcb398Cytb-Fwd_H01_22.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>81_consensus_sequence Assembly of 2 reads: 81_Mcb398Cytb-Fwd_A03_03.ab1, 81_Mcb869Cytb-Rev_A04_01.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>82_consensus_sequence Assembly of 2 reads: 82_Mcb398Cytb-Fwd_B03_06.ab1, 82_Mcb869Cytb-Rev_B04_04.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>83_consensus_sequence Assembly of 2 reads: 83_Mcb869Cytb-Rev_C04_07.ab1 (reversed), 83_Mcb398Cytb-Fwd_C03_09.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA

CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>84_consensus_sequence Assembly of 2 reads: 84_Mcb398Cytb-Fwd_D03_12.ab1, 84_Mcb869Cytb-Rev_D04_10.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>85_consensus_sequence Assembly of 2 reads: 85_Mcb869Cytb-Rev_E04_13.ab1 (reversed), 85_Mcb398Cytb-Fwd_E03_15.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>86_consensus_sequence Assembly of 2 reads: 86_Mcb398Cytb-Fwd_F03_18.ab1, 86_Mcb869Cytb-Rev_F04_16.ab1 (reversed)

GGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAA
ATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTAC
CCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCAT
AGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATT
TCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>87_consensus_sequence Assembly of 2 reads: 87_Mcb398Cytb-Fwd_G03_21.ab1, 87_Mcb869Cytb-Rev_G04_19.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA

TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>88_consensus_sequence Assembly of 2 reads: 88_Mcb869Cytb-Rev_H04_22.ab1 (reversed), 88_Mcb398Cytb-Fwd_H03_24.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCCTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>89_consensus_sequence Assembly of 2 reads: 89_Mcb398Cytb-Fwd_A05_02.ab1, 89_Mcb869Cytb-Rev_A06_03.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>90_consensus_sequence Assembly of 2 reads: 90_Mcb398Cytb-Fwd_B05_05.ab1, 90_Mcb869Cytb-Rev_B06_06.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>91_consensus_sequence Assembly of 2 reads: 91_Mcb869Cytb-Rev_C06_09.ab1 (reversed), 91_Mcb398Cytb-Fwd_C05_08.ab1

AGCAATCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTC
TCAGTAGACAAAGCAACCCTTACCCGATTCTTCGCTTTCCATTTTATCCTTCCA
TTTATCATCATAGCAATTGCCATAGTCCACCTACTATTCCTCCACGAAACAGG
CTCCAACAACCCAACAGGAATTTCCTCAGACGTAGACAAAATCCCATTCCAC
CCCTACTATACCATTAAGGACATCTTAGGGGCCCTCTTACTAATTCTAGCTCT
AATACTACTAGTACTATTCGCACCCGACCTCCTCGGAGACCCAGATAACTAC
ACCCCAGCCAATCCACTCAACACACCCCCTCACATCAAACCCGAGTGATACT
TCTTATTTGCATACGCAATCTTA

>92_consensus_sequence Assembly of 2 reads: 92_Mcb398Cytb-Fwd_D05_11.ab1, 92_Mcb869Cytb-Rev_D06_12.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>93_consensus_sequence Assembly of 2 reads: 93_Mcb398Cytb-Fwd_E05_14.ab1, 93_Mcb869Cytb-Rev_E06_15.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>94_consensus_sequence Assembly of 2 reads: 94_Mcb398Cytb-Fwd_F05_17.ab1, 94_Mcb869Cytb-Rev_F06_18.ab1 (reversed)

GGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAA
ATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTAC
CCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCAT
AGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATT
TCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>95_consensus_sequence Assembly of 2 reads: 95_Mcb869Cytb-Rev_G06_21.ab1 (reversed), 95_Mcb398Cytb-Fwd_G05_20.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>96_consensus_sequence Assembly of 2 reads: 96_Mcb398Cytb-Fwd_H05_23.ab1, 96_Mcb869Cytb-Rev_H06_24.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
CTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGAC
ATCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGC
ACCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAAC
ACACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTT
A

>97_consensus_sequence Assembly of 2 reads: 97_Mcb398Cytb-Fwd_A07_01.ab1, 97_Mcb869Cytb-Rev_A08_02.ab1 (reversed)

CAATTCCATATATTGGCACAAACCTAGTCGAATGAATCTGGGGAGGATTCTC
AGTAGACAAAGCTACCCTCACCCGATTTTTCGCCTTTCACTTTATTTTCCCATT
CATCATCGCAGCCCTCGCCATAGTTCACCTACTCTTCCTCCACGAAACAGGAT
CCAACAACCCCACAGGAATTCCATCGGACACAGATAAAATTCCCTTCCACCC
TTATTACACCATTAAAGACATCCTAGGTGCTATCCTACTAATCCTCATCCTCA
TGCTACTAGTACTATTCACGCCTGACTTACTCGGAGACCCAGACAACTACACC
CCAGCAAACCCACTTAACACTCCCCCTCACATCAAACCTGAATGATACTTCCT
ATTTGCGTACGCAATCTTA

>98_consensus_sequence Assembly of 2 reads: 98_Mcb869Cytb-Rev_B08_05.ab1 (reversed), 98_Mcb398Cytb-Fwd_B07_04.ab1

CAATCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTCTC
AGTAGACAAAGCAACCCTTACCCGATTCTTCGCTTTCCATTTTATCCTTCCATT
TATCATCATAGCAATTGCCATAGTCCACCTACTATTCCTCCACGAAACAGGCT
CCAACAACCCAACAGGAATTTCCTCAGACGTAGACAAAATCCCATTCCACCC
CTACTATACCATTAAGGACATCTTAGGGGCCCTCTTACTAATTCTAGCTCTAA

TACTACTAGTACTATTCGCACCCGACCTCCTCGGAGACCCAGATAACTACACC
CCAGCCAATCCACTCAACACACCCCCTCACATCAAACCCGAGTGATACTTCTT
ATTTGCATACGCAATCTTA

>99_consensus_sequence Assembly of 2 reads: 99_Mcb869Cytb-Rev_C08_08.ab1 (reversed), 99_Mcb398Cytb-Fwd_C07_07.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>100_consensus_sequence Assembly of 2 reads: 100_Mcb398Cytb-Fwd_D07_10.ab1, 100_Mcb869Cytb-Rev_D08_11.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>101_consensus_sequence Assembly of 2 reads: 101_Mcb398Cytb-Fwd_E07_13.ab1, 101_Mcb869Cytb-Rev_E08_14.ab1 (reversed)

CTCTTATCAGCAATCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGG
CGGATTCTCAGTAGACAAAGCAACCCTTACCCGATTCTTCGCTTTCCATTTTA
TCCTTCCATTTATCATCATAGCAATTGCCATAGTCCACCTACTATTCCTCCACG
AAACAGGCTCCAACAACCCAACAGGAATTTCCTCAGACGTAGACAAAATCCC
ATTCCACCCCTACTATACCATTAAGGACATCTTAGGGGCCCTCTTACTAATTC
TAGCTCTAATACTACTAGTACTATTCGCACCCGACCTCCTCGGAGACCCAGAT
AACTACACCCCAGCCAATCCACTCAACACACCCCCTCACATCAAACCCGAGT
GATACTTCTTATTTGCATACGCAATCTTA

>102_consensus_sequence Assembly of 2 reads: 102_Mcb869Cytb-Rev_F08_17.ab1 (reversed), 102_Mcb398Cytb-Fwd_F07_16.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA

CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>103_consensus_sequence Assembly of 2 reads: 103_Mcb398Cytb-Fwd_G07_19.ab1, 103_Mcb869Cytb-Rev_G08_20.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>104_consensus_sequence Assembly of 2 reads: 104_Mcb398Cytb-Fwd_H07_22.ab1, 104_Mcb869Cytb-Rev_H08_23.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>105_consensus_sequence Assembly of 2 reads: 105_Mcb398Cytb-Fwd_A09_03.ab1, 105_Mcb869Cytb-Rev_A10_01.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCATGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>106_consensus_sequence Assembly of 2 reads: 106_Mcb398Cytb-Fwd_B09_06.ab1, 106_Mcb869Cytb-Rev_B10_04.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>107_consensus_sequence Assembly of 2 reads: 107_Mcb398Cytb-Fwd_C09_09.ab1, 107_Mcb869Cytb-Rev_C10_07.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>108_consensus_sequence Assembly of 2 reads: 108_Mcb398Cytb-Fwd_D09_12.ab1, 108_Mcb869Cytb-Rev_D10_10.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>109_consensus_sequence Assembly of 2 reads: 109_Mcb398Cytb-Fwd_E09_15.ab1, 109_Mcb869Cytb-Rev_E10_13.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>110_consensus_sequence Assembly of 2 reads: 110_Mcb398Cytb-Fwd_F09_18.ab1, 110_Mcb869Cytb-Rev_F10_16.ab1 (reversed)

CAATCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTCTC
AGTAGACAAAGCAACCCTTACCCGATTCTTCGCTTTCCATTTTATCCTTCCATT
TATCATCATAGCAATTGCCATAGTCCACCTACTATTCCTCCACGAAACAGGCT
CCAACAACCCAACAGGAATTTCCTCAGACGTAGACAAAATCCCATTCCACCC
CTACTATACCATTAAGGACATCTTAGGGGCCCTCTTACTAATTCTAGCTCTAA
TACTACTAGTACTATTCGCACCCGACCTCCTCGGAGACCCAGATAACTACACC
CCAGCCAATCCACTCAACACACCCCCTCACATCAAACCCGAGTGATACTTCTT
ATTTGCATACGCAATCTTA

>111_consensus_sequence Assembly of 2 reads: 111_Mcb869Cytb-Rev_G10_19.ab1 (reversed), 111_Mcb398Cytb-Fwd_G09_21.ab1

AGGGGCAACAGTTATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCAC
CCGATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCAT
AGTCCACCTGCTTTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATT
CCATCAGACACAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATAT
CTTAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACC
CGACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACA
CCCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>112_consensus_sequence Assembly of 2 reads: 112_Mcb869Cytb-Rev_H10_22.ab1 (reversed), 112_Mcb398Cytb-Fwd_H09_24.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>113_consensus_sequence Assembly of 2 reads: 113_Mcb869Cytb-Rev_A12_03.ab1 (reversed), 113_Mcb398Cytb-Fwd_A11_02.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA

CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>114_consensus_sequence Assembly of 2 reads: 114_Mcb398Cytb-Fwd_B11_05.ab1, 114_Mcb869Cytb-Rev_B12_06.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>115_consensus_sequence Assembly of 2 reads: 115_Mcb398Cytb-Fwd_C11_08.ab1, 115_Mcb869Cytb-Rev_C12_09.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>116_consensus_sequence Assembly of 2 reads: 116_Mcb869Cytb-Rev_D12_12.ab1 (reversed), 116_Mcb398Cytb-Fwd_D11_11.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAATGATACTTCTTATTTGCATACGCAATCTTA

>117_consensus_sequence Assembly of 2 reads: 117_Mcb398Cytb-Fwd_E11_14.ab1, 117_Mcb869Cytb-Rev_E12_15.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA

TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>118_consensus_sequence Assembly of 2 reads: 118_Mcb398Cytb-Fwd_F11_17.ab1, 118_Mcb869Cytb-Rev_F12_18.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>119_consensus_sequence Assembly of 2 reads: 119_Mcb869Cytb-Rev_G12_21.ab1 (reversed), 119_Mcb398Cytb-Fwd_G11_20.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>120_consensus_sequence Assembly of 2 reads: 120_Mcb869Cytb-Rev_H12_24.ab1 (reversed), 120_Mcb398Cytb-Fwd_H11_23.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>121_consensus_sequence Assembly of 2 reads: 121_Mcb869Cytb-Rev_A02_02.ab1 (reversed), 121_Mcb398Cytb-Fwd_A01_01.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>122_consensus_sequence Assembly of 2 reads: 122_Mcb398Cytb-Fwd_B01_04.ab1, 122_Mcb869Cytb-Rev_B02_05.ab1

AGCAATCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTC
TCAGTAGACAAAGCAACCCTTACCCGATTCTTCGCTTTCCATTTTATCCTTCCA
TTTATCATCATAGCAATTGCCATAGTCCACCTACTATTCCTCCACGAAACAGG
CTCCAACAACCCAACAGGAATTTCCTCAGACGTAGACAAAATCCCATTCCAC
CCCTACTATACCATTAAGGACATCTTAGGGGCCCTCTTACTAATTCTAGCTCT
AATACTACTAGTACTATTCGCACCCGACCTCCTCGGAGACCCAGATAACTAC
ACCCCAGCCAATCCACTCAACACACCCCCTCACATCAAACCCGAGTGATACT
TCTTATTTGCATACGCAATCTTA

>123_consensus_sequence Assembly of 2 reads: 123_Mcb869Cytb-Rev_C02_08.ab1 (reversed), 123_Mcb398Cytb-Fwd_C01_07.ab1

AGGGGCAACAGTCATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCAC
CCGATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCAT
AGTCCACCTGCTCTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATT
CCATCAGACACAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATAT
CTTAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACC
CGACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACA
CCCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>124_consensus_sequence Assembly of 2 reads: 124_Mcb398Cytb-Fwd_D01_10.ab1, 124_Mcb869Cytb-Rev_D02_11.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>125_consensus_sequence Assembly of 2 reads: 125_Mcb398Cytb-Fwd_E01_13.ab1, 125_Mcb869Cytb-Rev_E02_14.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>126_consensus_sequence Assembly of 2 reads: 126_Mcb869Cytb-Rev_F02_17.ab1 (reversed), 126_Mcb398Cytb-Fwd_F01_16.ab1

AGGAGCAACAGTTATTACCAACCTCCTTTCAGCAATTCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGGGGAGGATTCTCAGTAGACAAAGCTACCCTCAC
CCGATTTTTCGCCTTTCACTTTATTTTCCCATTCATCATCGCAGCCCTCGCCAT
AGTTCACCTACTCTTCCTCCACGAAACAGGATCCAACAACCCCACAGGAATT
CCATCGGACACAGATAAAATTCCCTTCCACCCTTATTACACCATTAAAGACAT
CCTAGGTGCTATCCTACTAATCCTCATCCTCATGCTACTAGTACTATTCACGC
CTGACTTACTCGGAGACCCAGACAACTACACCCCAGCAAACCCACTTAACAC
TCCCCCTCACATCAAACCTGAATGATACTTCCTATTTGCGTACGCAATCTTA

>127_consensus_sequence Assembly of 2 reads: 127_Mcb869Cytb-Rev_G02_20.ab1 (reversed), 127_Mcb398Cytb-Fwd_G01_19.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AACTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>128_consensus_sequence Assembly of 2 reads: 128_Mcb398Cytb-Fwd_H01_22.ab1, 128_Mcb869Cytb-Rev_H02_23.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA

CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>129_consensus_sequence Assembly of 2 reads: 129_Mcb869Cytb-Rev_A04_01.ab1 (reversed), 129_Mcb398Cytb-Fwd_A03_03.ab1

AGCAACAGTCATCACCAACCTTTATCAGCAATCCCATACATCGGCACAAATT
TAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACCCG
ATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATAGT
CCACCTACTATTCCTCCATGAAACAGGCTCCAACAACCCAACAGGAATTTCCT
CAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACATCTT
AGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCACCCG
ACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACACACC
CCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>130_consensus_sequence Assembly of 2 reads: 130_Mcb398Cytb-Fwd_B03_06.ab1, 130_Mcb869Cytb-Rev_B04_04.ab1 (reversed)

CAATCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTCTC
AGTAGACAAAGCAACCCTTACCCGATTCTTCGCTTTCCATTTTATCCTTCCATT
TATCATCATAGCAATTGCCATAGTCCACCTACTATTCCTCCACGAAACAGGCT
CCAACAACCCAACAGGAATTTCCTCAGACGTAGACAAAATCCCATTCCACCC
CTACTATACCATTAAGGACATCTTAGGGGCCCTCTTACTAATTCTAGCTCTAA
TACTACTAGTACTATTCGCACCCGACCTCCTCGGAGACCCAGATAACTACACC
CCAGCCAATCCACTCAACACACCCCCTCACATCAAACCCGAGTGATACTTCTT
ATTTGCATACGCAATCTTA

>131_consensus_sequence Assembly of 2 reads: 131_Mcb398Cytb-Fwd_C03_09.ab1, 131_Mcb869Cytb-Rev_C04_07.ab1 (reversed)

GAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACAAA
TTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTACC
CGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCATA
GTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAATTT
CCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACAT
CTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCAC
CCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACAC
ACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>132_consensus_sequence Assembly of 2 reads: 132_Mcb398Cytb-Fwd_D03_12.ab1, 132_Mcb869Cytb-Rev_D04_10.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA

TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>133_consensus_sequence Assembly of 2 reads: 133_Mcb869Cytb-Rev_E04_13.ab1 (reversed), 133_Mcb398Cytb-Fwd_E03_15.ab1

AGCAATCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTC
TCAGTAGACAAAGCAACCCTTACCCGATTCTTCGCTTTCCATTTTATCCTTCCA
TTTATCATCATAGCAATTGCCATAGTCCACCTACTATTCCTCCACGAAACAGG
CTCCAACAACCCAACAGGAATTTCCTCAGACGTAGACAAAATCCCATTCCAC
CCCTACTATACCATTAAGGACATCTTAGGGGCCCTCTTACTAATTCTAGCTCT
AATACTACTAGTACTATTCGCACCCGACCTCCTCGGAGACCCAGATAACTAC
ACCCCAGCCAATCCACTCAACACACCCCCTCACATCAAACCCGAGTGATACT
TCTTATTTGCATACGCAATCTTA

>134_consensus_sequence Assembly of 2 reads: 134_Mcb869Cytb-Rev_F04_16.ab1 (reversed), 134_Mcb398Cytb-Fwd_F03_18.ab1

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

>135_consensus_sequence Assembly of 2 reads: 135_Mcb869Cytb-Rev_G04_19.ab1 (reversed), 135_Mcb398Cytb-Fwd_G03_21.ab1

GCAATCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTCT
CAGTAGACAAAGCAACCCTTACCCGATTCTTCGCTTTCCATTTTATCCTTCCAT
TTATCATCATAGCAATTGCCATAGTCCACCTACTATTCCTCCACGAAACAGGC
TCCAACAACCCAACAGGAATTTCCTCAGACGTAGACAAAATCCCATTCCACC
CCTACTATACCATTAAGGACATCTTAGGGGCCCTCTTACTAATTCTAGCTCTA
ATACTACTAGTACTATTCGCACCCGACCTCCTCGGAGACCCAGATAACTACA
CCCCAGCCAATCCACTCAACACACCCCCTCACATCAAACCCGAGTGATACTT
CTTATTTGCATACGCAATCTTA

>136_consensus_sequence Assembly of 2 reads: 136_Mcb398Cytb-Fwd_H03_24.ab1, 136_Mcb869Cytb-Rev_H04_22.ab1

ATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGAC
AAAGCAACCCTTACCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATC
ATAGCAATTGCCATAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACA
ACCCAACAGGAATTTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTA
TACCATTAAGGACATCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTAC
TAGTACTATTCGCACCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGC
CAATCCACTCAACACACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTG
CATACGCAATCTTA

>137_consensus_sequence Assembly of 2 reads: 137_Mcb869Cytb-Rev_A06_03.ab1 (reversed), 137_Mcb398Cytb-Fwd_A05_02.ab1

AGGGGCAACAGTCATCACTAATCTTCTTTCAGCAATCCCATATATTGGCACAA
ACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAGCCACTCTCAC
CCGATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCAT
AGTCCACCTGCTCTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATT
CCATCAGACACAGATAAAATCCCATTTCACCCTTACTACACCATTAAAGATAT
CTTAGGCGCCATGCTACTAATTCTTGTTCTAATATTACTAGTACTATTCACACC
CGACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCCACTCAATACA
CCCCCTCACATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>138_consensus_sequence Assembly of 2 reads: 138_Mcb398Cytb-Fwd_B05_05.ab1, 138_Mcb869Cytb-Rev_B06_06.ab1 (reversed)

AGGAGCAACAGTCATCACCAACCTCTTATCAGCAATCCCATACATCGGCACA
AATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCCTTA
CCCGATTCTTCGCTTTCCATTTTATCCTTCCATTTATCATCATAGCAATTGCCA
TAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTCGCA
CCCGACCTCCTCGGAGACCCAGATAACTACACCCCAGCCAATCCACTCAACA
CACCCCCTCACATCAAACCCGAGTGATACTTCTTATTTGCATACGCAATCTTA

Appendix II: *Meat samples collected, location, putative IDs and the BLASTn results in a bush meat study in Nairobi and its environs.*

Sample No.	Location	Putative Species	Blast Species	% ID	GenBank Accession No.	Matched Putative species
1	ONGATA RONGAI	*Capra hircus*	*Bos taurus*	99	KJ709686	NO
2	ONGATA RONGA	*Capra hircus*	*Capra hircus*	99	AB735780	YES
3	ONGATA RONGA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
4	ONGATA RONGA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
5	ONGATA RONGA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
6	ONGATA RONGA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
7	ONGATA RONGA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
8	ONGATA RONGA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
9	ONGATA RONGA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
10	ONGATA RONGA	*Capra hircus*	*Capra hircus*	99	KJ192212	YES
11	KISERIAN	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
12	KISERIAN	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
13	KISERIAN	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
14	KISERIAN	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
15	KISERIAN	*Capra hircus*	*Bos taurus*	99	KJ709686	NO
16	KISERIAN	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
17	KISERIAN	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
18	KISERIAN	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
19	KISERIAN	*Bos taurus*	*Bos taurus*	99	KJ709686	YES

20	KISERIAN	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
21	NGONG	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
22	NGONG	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
23	NGONG	*Capra hircus*	*Ovis aries*	99	DQ903224	NO
24	NGONG	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
25	NGONG	*Bos taurus*	*Bos taurus*	99	KJ709684	YES
26	NGONG	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
27	NGONG	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
28	NGONG	*Bos taurus*	*Capra hircus*	99	GQ141263	NO
29	NGONG	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
30	NGONG	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
31	DAGORETI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
32	DAGORETI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
33	DAGORETI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
34	DAGORETI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
35	DAGORETI	*Bos taurus*	*Bos taurus*	96	KJ709686	YES
36	DAGORETI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
37	DAGORETI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
38	DAGORETI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
39	DAGORETI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
40	DAGORETI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
41	KAWANGWARE	*Bos*	*Bos*	99	KJ709686	YES

		taurus	*taurus*			
42	KAWANGWARE	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
43	KAWANGWARE	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
44	KAWANGWARE	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
45	KAWANGWARE	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
46	KAWANGWARE	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
47	KAWANGWARE	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
48	KAWANGWARE	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
49	KAWANGWARE	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
50	KAWANGWARE	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
51	KANGEMI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
52	KANGEMI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
53	KANGEMI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
54	KANGEMI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
55	KANGEMI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
56	KANGEMI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
57	KANGEMI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
58	KANGEMI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
59	KANGEMI	*Bos taurus*	*Ovis aries*	99	KF977846	NO
60	KANGEMI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
61	DAGORETI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
62	KIBERA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES

63	KIBERA	*Bos taurus*	*Bos taurus*	97	KJ709686	YES
64	KIBERA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
65	KIBERA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
66	KIBERA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
67	KIBERA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
68	KIBERA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
69	KIBERA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
70	KIBERA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
71	KIBERA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
72	BURMA MARKET	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
73	BURMA MARKET	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
74	BURMA MARKET	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
75	BURMA MARKET	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
76	BURMA MARKET	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
77	BURMA MARKET	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
78	BURMA MARKET	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
79	BURMA MARKET	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
80	KALOLENI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
81	DANDORA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
82	DANDORA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
83	DANDORA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
84	DANDORA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES

85	DANDORA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
86	DANDORA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
87	DANDORA	*Capra hircus*	*Capra hircus*	99	KJ192233	YES
88	DANDORA	*Capra hircus*	*Bos taurus*	99	KJ709686	NO
89	DANDORA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
90	KARIOBANGI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
91	KARIOBANGI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
92	KARIOBANGI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
93	KARIOBANGI	*Bos taurus*	*Bos taurus*	100	KJ709686	YES
94	KARIOBANGI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
95	KARIOBANGI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
96	KARIOBANGI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
97	KARIOBANGI	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
98	KARIOBANGI	*Bos taurus*	*Ovis aries*	99	KF977846	NO
99	KARIOBANGI	*Bos taurus*	*Capra hircus*	99	JX286563	NO
100	MLANGO KUBWA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
101	MLANGO KUBWA	*Bos taurus*	*Capra hircus*	99	HM209304	NO
102	MLANGO KUBWA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
103	MLANGO KUBWA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
104	MLANGO KUBWA	*Bos taurus*	*Bos taurus*	99	KJ709685	YES
105	MLANGO KUBWA	*Bos taurus*	*Capra hircus*	99	KJ192212	NO
106	MLANGO KUBWA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES

107	MLANGO KUBWA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
108	MLANGO KUBWA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
109	MLANGO KUBWA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
110	HURUMA	*Bos taurus*	*Capra hircus*	99	AB735780	NO
111	HURUMA	*Bos taurus*	*Capra hircus*	99	AB110596	NO
112	KITENGELA	*Bos taurus*	*Bos taurus*	99	KJ709685	YES
113	KITENGELA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
114	KITENGELA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
115	KITENGELA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
116	KITENGELA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
117	KITENGELA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
118	KITENGELA	*Bos taurus*	*Bos taurus*	98	KJ709686	YES
119	KITENGELA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
120	KITENGELA	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
121	ATHI RIVER	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
122	ATHI RIVER	*Bos taurus*	*Capra hircus*	96	KJ192233	NO
123	ATHI RIVER	*Bos taurus*	*Bos taurus*	97	KJ709686	YES
124	ATHI RIVER	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
125	ATHI RIVER	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
126	ATHI RIVER	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
127	ATHI RIVER	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
128	ATHI RIVER	*Bos taurus*	*Bos taurus*	99	KJ709686	YES

129	ATHI RIVER	*Bos taurus*	*Capra hircus*	99	KJ192212	NO
130	ATHI RIVER	*Capra hircus*	*Capra hircus*	99	KJ192212	YES
131	MLOLONGO	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
132	MLOLONGO	*Bos taurus*	*Capra hircus*	99	KJ192212	NO
133	MLOLONGO	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
134	MLOLONGO	*Capra hircus*	*Bos taurus*	99	KJ709686	NO
135	MLOLONGO	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
136	MLOLONGO	*Bos taurus*	*Bos taurus*	99	KJ709686	YES
137	MLOLONGO	*Capra hircus*	*Capra hircus*	100	HM209304	YES
138	MLOLONGO	*Capra hircus*	*Capra hircus*	100	HM209304	YES

Appendix III: *Study generated haplotypes together with GenBank retrieved sequences used to construct Phylogenetic tree in a bush meat study in Nairobi and its environs.*

>9_Bos taurus
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TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
TCTTAGGGGCCCTCTTA
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CCCAGATAACTACACCC
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>KJ789953_Bos taurus
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TCATCATAGCAATTGCCATAGTCCACCTACTATTCCTCCACGAAACAGGCTCC
AACAACCCAACAGGAAT
TTCCTCAGACGTAGACAAAATCCCATTCCACCCCTACTATACCATTAAGGACA
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CAGCCAATCCACTCAACACACCCCCTCACATCAAACCCGAGTGATACTTCTTA
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>10_Capra hircus
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GCTCTTCCTCCACGAAACAGGATCGAACAACCCCACAGGAATTCCATCAGAC
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TCTAATATTACTAGTAC
TATTCACACCCGACCTACTCGGAGACCCAGACAACTATATCCCAGCAAATCC
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CATTAAACCTGAGTGGTATTTCCTATTTGCATACGCAATCCTA

>KP662716_Carpa hircus
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>17_Bos taurus
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>EU177836 Bos taurus
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GCATACGCAATCTTA

>18_Bos taurus

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>19_Capra hircus
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>KP662716_Capra hircus
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CTTTATCCTCCCATTCA
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CTAATTCTTGTTCTAATATTACTAGTACTATTCACACCCGACCTACTCGGAGA
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>20_Capra hircus
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> JX286551_Capra hircus
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>22_Bos taurus
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>23_Bos taurus
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>28_Capra hircus
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>30_Capra hircus
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>34_Bos taurus
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>37_Bos taurus
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>D84205.1 Ovis aries
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>40_Ovis aries
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>44_Bos taurus
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>47_Capra hircus
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