

**MOLECULAR CHARACTERIZATION OF *THEILERIA* spp.  
USING RIBOSOMAL RNA**

A Thesis

by

**KYLIE GAYLE BENDELE**

Submitted to the Office of Graduate Studies of  
Texas A&M University  
in partial fulfillment of the requirements for the degree of  
**MASTER OF SCIENCE**

August 2004

Major Subject: Veterinary Parasitology

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## ABSTRACT

Molecular Characterization of *Theileria* spp. Using Ribosomal RNA. (August 2004)

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Chair of Advisory Committee: Dr. Patricia Holman

The molecular characterization of twenty six *Theileria* spp. isolates and one *C. felis* isolate were done on the small subunit ribosomal RNA (SSU rRNA) gene, the 5.8S gene, and the two internal transcribed spacer regions using gDNA. The SSU rRNA gene is increasingly accepted as a widely used marker for characterization, taxonomic classification, and phylogenetic analysis and this gene has been sequenced from a variety of different organisms, resulting in a large database for sequence comparisons (Chae et al. 1998; Chae et al., 1999 a,b,c; Stockham et al., 2000; Cossio-Bayugar et al., 2002; Gubbels et al., 2000). The genomic region consists of the internal transcribed spacer 1 (ITS 1), the 5.8S gene, and internal transcribed spacer 2 (ITS 2) (ITS 1-5.8S-ITS 2 gene region) and separates the SSU rRNA gene from the large subunit ribosomal RNA gene. The 5.8S rRNA gene is highly conserved in size and nucleotide sequence, is relatively constant in molecular weight, and has an average chain length of approximately 160 nucleotides and has proven useful in dividing subgenera of *Gyrodactylus* ((Nazar, 1984; Zietara et al., 2002).

Pairwise comparisons were done between the clones of an individual isolate and among the clones of the different isolates. Phylogenetic trees were made from the resulting sequences. This study shows that different SSU rRNA genes may be associated with ITS 1-5.8S-ITS 2 gene regions of distinct sequence in the same isolate. This study

also demonstrates that considerable ITS 1-5.8S-ITS 2 gene region sequence variation may exist within a species. This may be useful for subspeciation designation, or may simply reflect considerable variation within the population. This study shows that the ITS 1-5.8S-ITS 2 gene region may be a useful molecular marker for the taxonomy of *Theileria* spp.

## **DEDICATION**

To my husband, Charlie for all of his love, patience, and support.

To my parents, Warren and Phylliss Ottmers, and Charles and Kathy Bendele for their encouragement and love.

To my grandmother, Marjorie Hofmann for her unconditional love and support.

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## CHAPTER I

### INTRODUCTION

*Theileria* species are found in ruminants worldwide. Taxonomically they are in phylum Apicomplexa, class Piroplasmata, order Piroplasmorida and family Theileriidae (Levine, 1973). *Theileria* are small round, ovoid, irregular or bacilliform shaped parasites with an apical complex comprised only of rhoptries. *Theileria* can be found in both erythrocytes and lymphocytes of their host. The current taxonomic standings of *Theileria* species are based upon morphology, clinical signs, host, tick vector, and geographic area (Levine, 1985). *Theileria* species are vectored by many species of ticks through transstadial transmission. *Theileria* diagnosis is based on identifying parasites in stained smears from blood, spleen or lymph nodes (Levine, 1985).

In the life cycle of *Theileria*, sporozoites are injected into the host with tick saliva during a blood meal. Schizonts, also known as Kock bodies, are then formed inside newly divided lymphocytes producing merozoites. The merozoites break free from the lymphocytes, enter erythrocytes and are then called piroplasms (Mehlhorn and Schein, 1984). Two forms of piroplasms may be seen inside the erythrocytes – a slender comma-shaped or spherical ovoid form (Mehlhorn and Schein, 1984). The merozoite or piroplasm stage is infective to the tick while taking a blood meal from an infected host.

The sexual stage, also called gamogony, of the *Theileria* life cycle occurs in the intestinal cells of the vector ticks. Raybodies or microgamonts are formed from the

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merozoites in the ingested erythrocytes, which are lysed in the intestine of the tick (Mehlhorn and Schein, 1984). The spindle-shaped ray-bodies divide forming a uninucleated microgamete, while macrogamonts form macrogametes. Syngamy occurs with the fusion of two gametes, and results in the formation of a zygote (Mehlhorn and Schein, 1984). The zygote transforms to the motile kinete, club-shaped, stage (Mehlhorn and Schein, 1984).

Sporogony occurs in the salivary glands of the ticks, where the kinetes penetrate the cells of the tick salivary glands after molt. The formation of the sporozoites, which are infective to the ruminant, occurs in the cells of the salivary glands. The sporozoites are injected into the host during feeding. It is estimated that 50,000 sporozoites are found in one salivary gland cell, which leads to large number of sporozoites entering the ruminant host bloodstream during a single blood meal (Mehlhorn and Schein, 1984).

The pathogenic species of *Theileria* infecting cattle are *Theileria parva* and *Theileria annulata*, while *Theileria buffeli*, *Theileria mutans* and *Theileria sergenti* are the benign species found in cattle. The benign species do not cause disease unless the cattle are affected by stress such as that caused by other pathogens or parturition (Kakuda et al., 1998).

*Theileria annulata* causes tropical theileriosis (also known as tropical piroplasmiasis, Egyptian fever or Mediterranean Coast fever) in cattle and water buffalo in North Africa, southern Europe, southern regions of the former USSR and Asia, with a mortality rate from 10-90% (Levine, 1985). *Theileria annulata* is vectored by *Hyalomma detritum*, *Hyalomma excavatum*, *Hyalomma truncatum*, *Hyalomma dromedarii*,

*Hyalomma turanicum*, *Hyalomma marginatum* and *Hyalomma longicornis* ticks, which become infected as a larva or nymph and infection is then passed on by the nymph or adult, respectively (Levine, 1985). The incubation period following tick transmission is nine to twenty-five days, with disease lasting four to twenty days (Levine, 1973).

*Theileria parva* causes East Coast fever (also known as bovine theileriosis, African Coast fever, Rhodesian tick fever, Rhodesian redwater disease or corridor disease) in east and central Africa in cattle, water buffalo and African buffalo (Levine, 1985). *T. parva* is highly pathogenic with a 90-100% mortality rate and is vectored by *Rhipicephalus appendiculatus*, *Rhipicephalus ayrei*, *Rhipicephalus capensis*, *Rhipicephalus eversti*, *Rhipicephalus jeanelli*, *Rhipicephalus neavei*, *Rhipicephalus simus*, *Hyalomma excavatum*, *Hyalomma dromedarii* and *Hyalomma truncatum*, which become infected as larva or nymphs and transmit as nymphs and adults, respectively (Levine, 1985). The incubation time following tick transmission in cattle is eight to twenty-four days and disease lasts for ten to twenty-three days (Levine, 1985).

*Theileria mutans* causes benign bovine theileriosis (also known as Tzaneen disease, Marico calf disease and mild gallsickness) and can be found throughout Africa, Asia, Russia, Australia, Europe and the Caribbean and with a mortality rate of less than 1% (Levine, 1985; Uilenberg, 1995). *Amblyomma variegatum* is the primary vector with *Amblyomma cohaerens*, *Amblyomma hebraeum* and *Amblyomma gemma* also capable of transmitting *T. mutans*. Incubation following tick transmission is ten to twenty days and disease if it occurs lasts three to ten days (Levine, 1985).

*Theileria buffeli* (syn. *Theileria orientalis*; Uilenberg, 1995) is a less pathogenic *Theileria* species infecting cattle in Australia, Africa, the United States, Asia and Europe

(Uilenberg, 1995). It was first described in Indo-China (Vietnam) in an Asian water buffalo by Neveu-Lemaire in 1912 (reviewed by Fujisaki, 1992). *Theileria buffeli* is vectored by *Haemaphysalis punctata*, *Haemaphysalis japonica*, *Haemaphysalis comcinna* and *Haemaphysalis humerosal* in Australia, but the vector ticks in the United States and Africa are still unknown (Fujisaki, 1992).

*Theileria sergenti* causes major losses in grazing cattle in Japan and Korea (Baek et al., 1990). Calves may suffer from chronic anemia and occasionally die in severe cases (Takahashi, 1976). *Haemaphysalis longicornis*, *Haemaphysalis mageshimaensis*, *Haemaphysalis concinna* and *Haemaphysalis bancrofti* are the vector ticks of *T. sergenti* (Fujisaki, 1992). *T. sergenti* was first described in the Vladivostok area of eastern Siberia as *Gonderia (Theileria) sergenti* by Yakimoff and Dekhtereff in 1930 (reviewed by Fujisaki, 1992).

*Theileria taurotragi* is a nonpathogenic species that infects elands (*Taurotragus oryx*) and cattle in East and South Africa (Mehlhorn et al., 1994; Grootenhuis et al., 1981; De Vos and Roos, 1981). Martin and Brocklesby (1960) first described it in an eland in Kenya as *Cytauxzoon taurotragi*, which was later renamed as *T. taurotragi* (Grootenhuis, 1979). It is vectored by *Rhipicephalus appendiculatus* and *Rhipicephalus pulchellus* (Mehlhorn et al., 1994).

The first report of a *Theileria* sp. in a deer was by Bettencourt et al. in 1907 in an erythrocyte of a fallow deer (*Cervus dama*) in Portugal and named it *Theileria cervus* (reviewed by Waldrup, 1991). Kreier et al. (1962) identified a *Theileria* species in a deer (*Dama virginiana*), synonymous with *Odocoileus virginianus*, from Missouri, USA, which was subsequently named *Theileria cervi* (Schaeffler, 1963). Robinson et al.

(1967) found *T. cervi* to be common in white-tailed deer (*Odocoileus virginianus*) herds in Texas, USA. *Theileria cervi* is found in axis deer (*Axis axis*), sika deer (*Cervus nippon*), fallow deer, mule deer (*Odocoileus hemionus*) and elk (*Cervus elaphus canadensis*) (Davidson et al., 1983; Waldrup, 1991; Chae et al., 1999a). *Theileria cervi* is a contributing factor to malnutrition and parasitism in overpopulated deer herds, but can be harbored in healthy animals without any effects (Davidson et al., 1983; Kingston, 1981). Kuttler et al. (1967) showed that *Amblyomma americanum*, Lone Star tick, transmits *T. cervi* with a prepatent period of fourteen to twenty-one days.

*Theileria lestoquardi* (syn *Theileria hirci*; Levine, 1985) is the malignant *Theileria* in sheep and goats while *Theileria ovis* is the benign *Theileria* species. *Theileria ovis* (syn *Theileria recondita*; Levine, 1973) infects sheep and goats in Africa, Europe, the former USSR, India, Sri Lanka and western Asia (Levine, 1985). It is vectored by *Rhicephalus bursa* and *Rhicephalus evertsi evertsi* and can be experimentally vectored by *Rhicephalus haemaphysaloides*. Rodhain in 1916 first described *T. ovis* in tropical Africa (reviewed by Levine, 1985). The incubation period following tick transmission is nine to thirteen days and disease lasts five to sixteen days (Levine, 1973).

*Cytauxzoon* species were first recognized in wild ungulates in Africa by Neitz (reviewed by Brocklesby, 1962). The genus *Cytauxzoon* in the family Theileriidae differs from the genus *Theileria* in the fact that *Cytauxzoon* undergo schizogony in reticuloendothelial macrophages, while *Theileria* undergo schizogony in lymphocytes (Glen et al., 1982). Wagner (1976) first described cytauxzoonosis in a domestic cat (*Felis catus*) in Missouri. Since then, cases of *Cytauxzoon felis* have been reported in Arkansas, Texas, Oklahoma, Mississippi, Georgia, Florida and Louisiana (Bendele et al.,



1976; Kier et al., 1979, 1982a; Hauck et al., 1982). Most cases of *C. felis* are fatal, but there have been reports of cats surviving both natural and experimental infections (Ferris, 1979; Uilenberg et al., 1987; Motzel et al., 1990; Walker and Cowell, 1995; Greene et al., 1999; Meinkoth et al., 2000; Holman et al., submitted). Experimentally, the incubation period is five to twenty days with the clinical course lasting a week in domestic cats (MacWilliams, 1987). *Dermacentor variabilis*, the American dog tick, transstadially transmits *C. felis* (Blouin et al., 1987). *Cytauxzoon felis* has also been found in erythrocytes of bobcats (*Lynx rufus*), cheetahs (*Acinonyx jubatus*), Florida panther (*Felis concolor coryi*), cougars (*Felis concolor stanleyana*), Bengal tiger (*Panthera tigris*), white tiger (*P. tigris*), and ocelots (*Felis pardalis*) (Kier et al., 1982a, 1982b; Zinkl et al., 1981; Butt et al., 1991; Kocan and Kocan, 1991; Jakob and Wesemeier, 1996; Garner et al., 1996; Mercer et al. 1988).

Ribosomal RNA is the most abundant constituent of nucleic acids in any non-viral organism with the eukaryotic RNA transcription unit consisting of the large and small subunit and the 5.8S rRNA gene (Waters and McCutchan, 1990). The small subunit ribosomal RNA (SSU rRNA) gene, also known as the 18S, is a highly conserved region in the nuclear genome and is analogous to the 16S in prokaryotes. The SSU rRNA gene is useful for phylogenetic analysis due to its high levels of conservation (Adam et al., 2000).

Gajadhar et al. (1991) sequenced the SSU rRNA gene of *T. annulata* and compared it to other Apicomplexans, Dinoflagellates and Ciliates, and showed that *Sarcocystis muris* and *T. annulata* were closer related to one another than to *Plasmodium falciparum* or *Plasmodium berghei*, and that a close phylogenetic relationship exists

between Apicomplexa and Dinoflagellata. Allsopp et al. (1993) used SSU rRNA probes to differentiate among six *Theileria* species, which is useful for identification of dual infections and carrier animals. These probes were not able to differentiate between the buffalo and cattle derived *T. parva* stocks.

Kibe et al. (1994) characterized two rRNA transcriptional units from *T. parva* which are located on two different chromosomes and do not consist of tandemly repeated units. Usually eukaryotic organisms have multiple copies of rRNA genes and they are tandemly repeated (Long and Dawid, 1980). The structural organization and content of the *T. parva* Muguga genome has four chromosomes with rRNA being located on chromosomes 1 and 3; preliminary data shows that *T. annulata*, *Theileria taurotragi*, *T. sergenti* and *T. mutans* also have four chromosomes and similar genome size as *T. parva* (Nene et al., 1998).

Chae et al. (1998) classified fourteen *Theileria* isolates into seven different types (A-G) based on a 200bp fragment of the variable (V4) region the SSU rRNA gene. The *Theileria* isolates came from different geographic locations including Korea, Japan and several locations in North America. Types A, B, C, D and E were found in parasites from cattle, type E in parasites from cattle and an elk, and types F and G were found in elk and white-tailed deer. Some individual isolates had more than one SSU rRNA gene type. Chae et al. (1999a) further divided the *Theileria* SSU rRNA gene type G into three subtypes G1, G2 and G3 based on microheterogeneity found in the sequences from white-tailed deer and elk, while the type F was identical in nucleotide sequences from both white-tailed deer and elk.

SSU rRNA gene analysis was used to detect *Theileria* sp. in suspect cattle and ticks collected from cattle in Missouri, USA, when a cow developed clinical theileriosis (Chae et al., 1999b). The index cow had both type A and D *Theileria* sp. SSU rRNA genes and cohort cows had only type D. Both *Dermacentor variabilis* and *Amblyomma americanum* ticks were found on the cohort cows and the type D SSU rRNA gene sequence was obtained from all organs sampled in these ticks. Cossio-Bayugar et al. (2002) reported that the infectious agent causing theileriosis in a cow from Michigan was confirmed as *T. buffeli* with type A SSU rDNA, while a normal steer in Oklahoma also carried type A parasites.

A study was conducted on the SSU rRNA genes of bovine *Theileria* isolates in which a clear taxonomic separation appeared between the pathogenic and the benign to moderately pathogenic *Theileria* species (Chae et al., 1999c). Furthermore this study compared the cattle *Theileria* spp. in the United States to *T. mutans* from Africa and Japanese *T. sergenti*. These *Theileria* spp. had different SSU rRNA gene sequences but are all considered synonymous by Levine (1985).

Phylogenetic trees based on this work on SSU rRNA gene sequences of benign and pathogenic *Theileria* species infecting cattle and deer had two major divisions; division one was further divided into two groups with group one containing *T. buffeli* and other type A SSU rRNA genes while group two contained SSU rRNA gene types B, subtype B1, C, E and H. The second division was divided into four groups; group one contained the pathogenic species *T. annulata*, *T. parva*, *T. taurotragi* and *Theileria* sp. sable; group two contained *T. cervi* with SSU rRNA gene types F, G and G1; group three contained *T. mutans* Intona and *Theileria* sp. MSD from Africa; and group four was

composed of SSU rRNA gene type D. Some isolates had more than one SSU rRNA gene type present suggesting the occurrence of mixed populations.

A molecular characterization was done on seven cattle and five sheep from different geographic areas in Turkey infected with *Theileria*, but without clinical signs (Aktas et al., submitted). The cattle ranged in age from 7 months to 6 years and the sheep were three years old. The SSU rRNA gene of the cattle parasite showed that they were infected with *T. annulata*. The sheep were suspected of having *T. lestoquardi*, but SSU rRNA gene analysis showed that they were infected with another *Theileria* species, *T. ovis* (syn. *T. recondita*).

The 5.8S rRNA gene is located between the small and large subunit of rRNA gene. It is short in length, but is highly conserved and has been proven useful in dividing subgenera of *Gyrodactylus* (Zietara et al., 2002). The first nucleotide sequence of 5.8S rRNA was reported in yeast (Rubin, 1973). The 5.8S rRNA gene is highly conserved in size and nucleotide sequence, is relatively constant in molecular weight, and has an average chain length of approximately 160 nucleotides (Nazar, 1984). The only *Theileria* species 5.8S rRNA gene that has been previously sequenced is that of *T. parva*. The gene was sequenced from several *T. parva* isolate stocks, and all the sequences were identical (Kibe et al., 1994; Collins and Allsopp, 1999).

The internal transcribed spacers (ITS) separate the SSU rRNA gene and 5.8S gene (ITS 1) and the 5.8S gene and the large subunit rRNA gene (ITS 2). ITS regions vary in length and are variable in their nucleotide sequences (Som et al., 2000). The ITS regions are less conserved than the SSU rRNA genes allowing their use for differentiation between species of *Gyrodactylus* (Zietara et al., 2002). The ITS sequences differed

significantly in *T. parva* buffalo 7014 stock, and resulted in two different amplicons with one 50bp larger than the other (Kibe et al., 1994). There were three major polymorphisms found in the *T. parva* sequences, two in the ITS 1 region and one in the ITS 2 region. Kibe et al. (1994) compared the ITS of *T. parva* Muguga and *T. parva* Uganda, which also resulted in two different sizes of amplicons. In this case, one polymorphism occurred in the ITS 1 region and two in the ITS 2 region. Collins and Allsopp (1999) found variable ITS regions in *T. parva parva* and *T. parva lawrenci* isolates in Africa, but the 5.8S rRNA was identical in all isolates.

Zahler et al. (1998) used ITS and 5.8S rRNA gene region to discriminate between geographic and subspecies of *Babesia canis*. The same order of magnitude of polymorphisms was found both among the three subspecies of *B. canis*, and among the three *B. canis* subspecies and *Babesia caballi*, a hemoprotozoon found in horses. These results suggest that the three *B. canis* subspecies might be individual species.

ITS 1 region has been used to distinguish at the species level between *Sarcocystis neurona* and *Sarcocystis falcatula* (Marsh et al., 1999). Miller et al. (2001) used SSU rRNA gene and ITS 1 region to characterize and compare a *Sarcocystis* species found in brain tissue of a southern sea otter and to compare sequences of *S. neurona* from a horse and harbor seal. ITS 2 region has been used for strain differentiation in *Entamoeba histolytica* and species identification between *E. histolytica*, *Entamoeba dispar*, *Entamoeba moshkovskii*, and *Entamoeba invadens* (Som et al., 2000).

## CHAPTER II

### MATERIALS AND METHODS

#### 2.1. Parasites

Thirteen bovine, ten cervine, and three ovine *Theileria* spp. isolates were included in this study and are listed in Table 1 with a description of each, including host, geographic location and clinical status. One *Cytauxzoon felis* sample was also included and is described in Table 1. GenBank accession numbers are listed for those isolates for which previous rRNA gene sequence data is available (Table 1).

#### 2.2. DNA Extractions

Parasite genomic DNA (gDNA) was extracted from blood obtained from the vertebrate host. The blood was transferred to pre-spun Light Spin Phase Lock Gel tubes (Sigma-Aldrich Co. Ltd, St. Louis, MO). An equal amount of DNA lysis buffer (10 mM Tris pH 7.5; 1 mM EDTA pH 8.0; 10% SDS) was added and mixed. RNase A (Sigma-Aldrich Co. Ltd, St. Louis, MO) was then added to a final concentration of 50 µg/ml and the mixture was incubated for 1 h at 37 °C. Proteinase K (Sigma-Aldrich Co. Ltd, St. Louis, MO) was added to a final concentration of 100 µg/ml and the mixture incubated for 3 h at 50 °C with occasional swirling or overnight at room temperature. If incubated at 50 °C, the mixture was allowed to cool to room temperature prior to the addition of an equal volume of Tris-equilibrated phenol (Sigma-Aldrich Co. Ltd, St. Louis, MO) to the mixture. After mixing on a tube rotator (DYNAL, Dynal Inc, New Hyde Park, NY) at 20 rpm for 5 min, the tube was centrifuged for 2 min at 12,000 x g to separate the aqueous and organic phases. The phenol extraction of the resulting aqueous phase was repeated as described. The aqueous phase was then transferred to a Heavy Spin Phase Lock Gel

Table 1  
Description of *Theileria* isolates.

Isolate name	Background	Small subunit rRNA gene (GenBank accession no.)
<i>Theileria annulata</i> Turkey 1	Naturally acquired field isolate, bovine, Elazig, Turkey	<i>Theileria annulata</i> Clone 12 & 24 (AY508462 & AY524666) Aktas et al. submitted
<i>T. annulata</i> Turkey 2	Naturally acquired field isolate, bovine, Elazig, Turkey	<i>Theileria annulata</i> Direct sequence <sup>a</sup> (AY508473) Aktas et al. submitted
<i>T. annulata</i> Turkey 3	Naturally acquired field isolate, bovine, Elazig, Turkey	<i>Theileria annulata</i> Direct sequence <sup>a</sup> (AY508463) Aktas et al. submitted
<i>T. annulata</i> Turkey 5	Naturally acquired field isolate, bovine, Malatya, Turkey	<i>Theileria annulata</i> Clone 31, 33 & 34 (AY508465, AY5088466 & AY508467) Aktas et al. submitted
<i>T. annulata</i> Turkey 6	Naturally acquired field isolate, bovine, Malatya, Turkey	<i>Theileria annulata</i> Clone 15, 22 & 23 (AY508468, AY508470 & AY508469) Aktas et al. submitted
<i>T. annulata</i> Turkey 7	Naturally acquired field isolate, bovine, Malatya, Turkey	<i>Theileria annulata</i> Clone 1 & 11 (AY508471 & AY507472) Aktas et al. submitted
<i>Theileria buffeli</i> Arkansas	Clinical case, bovine, Arkansas, USA	
<i>T. buffeli</i> Michigan	Clinical case, bovine, Eaton County, Michigan, USA; Cossio-Bayugar et al. 2002	
<i>T. buffeli</i> Oklahoma	Clinically normal steer, Oklahoma, USA; Cossio- Bayugar et al. 2002	
<i>T. buffeli</i> Texas	Clinical case, bovine, Texas, USA	
<i>Theileria mutans</i> Intona	Natural infection, bovine, Intona Ranch, Mara, Kenya; Morzaria et al. 1990	<i>Theileria mutans</i> (AF078815) Chae et al. 1999b
<i>Theileria sergenti</i> Chitose	Field isolate, bovine, Chitose, Japan; Kim et al. 1998	
<i>T. sergenti</i> Ikeda	Field isolate, bovine, Ikeda, Japan; Kim et al. 1998	
<i>Cytauxzoon felis</i>	Clinical case, domestic feline, East Texas	<i>Cytauxzoon felis</i> (AY531524) Holman et al. submitted
<i>Theileria ovis</i> Turkey 8	Naturally acquired field isolate, ovine, Erzincan, Turkey	<i>Theileria ovis</i> Direct sequence <sup>a</sup> (AY508455) Clone 12 & 24 (AY508453 & AY508454) Aktas et al. submitted

<sup>a</sup>Direct sequence, sequence obtained directly from PCR product without cloning

Table 1  
continued

Isolate name	Background	Small subunit rRNA gene (GenBank accession no.)
<i>T. ovis</i> Turkey 9	Naturally acquired field isolate, ovine, Erzincan, Turkey	<i>Theileria ovis</i> Clone 21 (AY508457) Aktas et al. submitted
<i>T. ovis</i> Turkey 11	Naturally acquired field isolate, ovine, Erzincan, Turkey	<i>Theileria ovis</i> Clone 1, 3 & 11 (AY508459, AY508460 & AY508461) Aktas et al. submitted
<i>Theileria cervi</i> Oklahoma Bull Elk	Field isolate, free ranging elk, Spavinaw, Oklahoma, USA	Type F (U97054) Type G1 (U97056) Chae et al. 1999a
<i>T. cervi</i> USWTD 1	Clinical case, farmed WTD*, central Texas, USA	Type F (U97054) Type G (U97055) Chae et al. 1998 Type G1 (U97056) Chae et al. 1999a
<i>T. cervi</i> USWTD 2	Clinical case, farmed WTD*, East Texas, USA	Type F (U97054) Chae et al. 1998
<i>T. cervi</i> USWTD 3	Field isolate, wild caught WTD*, Payne County, Oklahoma, USA	Type F (U97054) Type G2 (AF086804) Type G3 (AF086805) Chae et al. 1999a
<i>T. cervi</i> Canada Elk	Field isolate, free ranging elk, Quebec, Canada	Type F (U97054) Type G (U97055) Chae et al. 1998 Type G1 (U97056) Chae et al. 1999a
Indiana Elk Green 5H	Natural infection, farmed elk, Indiana, USA	
Wisconsin Elk (Lulu)	Natural infection, farmed elk, western Wisconsin, USA	
Oklahoma WTD 181	Natural field infection, wild-caught WTD*, Oklahoma, USA	
Oklahoma WTD 183	Natural field infection, wild-caught WTD*, also infected with <i>Babesia odocoilei</i> and <i>Trypanosoma</i> sp., Oklahoma, USA	
Dama Gazelle	Clinical case, farmed gazelle, Texas, USA	

\* WTD, white-tailed deer



tube (Sigma-Aldrich Co. Ltd, St. Louis, MO) and an equal volume of 50:50 chloroform (24 parts chloroform:1 part iso-amyl alcohol):phenol (volume:volume) (Sigma-Aldrich Co. Ltd, St. Louis, MO) was added, and the tube contents mixed and centrifuged as above. A final equal volume of chloroform (24 parts chloroform:1 part iso-amyl alcohol) (Sigma-Aldrich Co. Ltd, St. Louis, MO) was added to the aqueous phase and extracted as described above. The resulting top aqueous layer was then transferred to a 2 ml screw cap centrifuge tube (Continental Lab Products, San Diego, CA), measured and adjusted to a final concentration of 0.3 M NaOAC with mixing. Three volumes of cold absolute ethanol were added and mixed. The DNA was then allowed to precipitate overnight at –70 °C.

The tubes were centrifuged in a pre-cooled refrigerated centrifuge at 12000 x g for 30 min. The ethanol supernatant was removed and saved in 2 ml snap cap tubes (Continental Lab Products, San Diego, CA) and stored in refrigerator until presence of gDNA was confirmed in the pellet. The pellet was rinsed with 500 µl of cold 70% ethanol by centrifugation for 10 min at 12000 x g in a pre-chilled refrigerated centrifuge. The 70% ethanol supernatant was removed and saved as described. The resulting DNA pellet was allowed to air-dry. Once the gDNA pellet was dry, 20-50 µl 1X TBE was added, depending on the size of the pellet, and incubated for at least 1 h at 50 °C to resuspend the DNA before use.

### 2.3. Small Subunit Ribosomal RNA Gene PCR

The small subunit ribosomal RNA (SSU rRNA) gene was amplified from approximately 50 to 100 ng gDNA in a 25 µl reaction volume using the Advantage 2

PCR Enzyme System (BD Bioscience Clontech, Palo Alto, CA) or Proofpro DNA Polymerase (Continental Lab Products, San Diego, CA), with 1 pmol each of forward primer A and reverse primer B (Sogin, 1990) (Table 2). The cycling profile included an initial denaturation at 96 °C for 3 min; 30 cycles of denaturation at 94 °C for 10 sec, annealing at 60 °C for 10 sec, and extension at 72 °C for 2 min; final extension at 72 °C for 10 min and hold at 4 °C in either a Hybaid Express or Hybaid Sprint thermocycler (Continental Lab Products, San Diego, CA). PCR products were electrophoresed through a 1% agarose gel, stained with ethidium bromide (Continental Lab Products, San Diego, CA) and visualized using UV transillumination. Resulting single 1800 bp bands were ligated as described below. If multiple bands or no band resulted, the primary PCR product was subjected to nested PCR as follows.

The nested PCR protocol to amplify a 1650 bp amplicon was similar to the primary PCR, but with primers AN50 and BN1700 (Table 2) and initial denaturation at 96 °C for 2 min was performed. Alternatively, primers 989A and 990A (Table 2) were used following the same protocol as with primers AN50 and BN1700, except with an annealing temperature of 50 °C, which produced a nested 1000 bp amplicon from the primary product.

The resulting amplicons were either directly sequenced after purification (QIAquick PCR Purification Kit; Qiagen, Valencia, CA) or cloned prior to sequencing. The amplicons were cloned by direct ligation into plasmid vector pCR TOPO2.1 and TOP10 One Shot Chemically Competent *Escherichia coli* cells were transformed following manufacturer's instructions (Invitrogen, San Diego, CA). Colonies were then

screened by colony PCR for the correct size insert. Selected clones were grown in overnight cultures and plasmid DNA (pDNA) was purified from the cultures using a modified alkaline lysis mini preparation (QIAprep Spin Miniprep Kit; Qiagen, Valencia, CA) according to manufacturer's instructions.

Table 2  
Primers used for SSU rRNA gene amplification.

Primer name	Primer sequence 5'-3'	Reference
A	AACCTGGTTGATCCTGCCAGT	(Sogin, 1990)
B	GATCCTTCTGCAGGTTACCTAC	(Sogin, 1990)
AN50	GCTTGTCTTAAAGATTAAGCCATGC	(Aktas et al., submitted)
BN1700	CGACTTCTCCTTCCTTTAAGTGATAAG	(Aktas et al., submitted)
989A	GGTAGGGTATTGGCCTACCGT	(Aktas et al., submitted)
990A	AAAGTCCCTCTAAGAAGC	(Aktas et al., submitted)

The pDNA and direct sequencing was done in Big Dye Terminator Cycling Sequencing Ready Reactions (PE Applied Biosystems, Norwalk, CT) with primers listed in Table 3 to obtain the full SSU rRNA gene. Automated sequencing was carried out in an ABI PRISM Model 373A or ABA Model 377 automated sequencer with Version 1.2.2 and 2.1.1 software, respectively or Applied Biosystems 3100 genetic analyzer with DNA analysis software version 3.7. Sequencing reactions and automated sequencing were done by the DNA Technologies Laboratory (Department of Veterinary Pathobiology, Texas A&M University, College Station, TX) or the Gene Technologies Laboratory (Institute of Developmental and Molecular Biology, Department of Biology, Texas A&M University, College Station, TX). The resulting sequences were analyzed using the Sequencher 3.0 software program (Gene Codes Corporation Inc., Ann Harbor, MI) and

submitted to GenBank database (National Center for Biotechnology Information, National Institute of Health) for BLAST homology searches (Altschul et al., 1990).

Table 3  
Primers used for sequencing SSU rRNA gene.

Primers	Primer sequence 5'-3'	Reference
A	AACCTGGTTGATCCTGCCAGT	(Sogin, 1990)
M13F	GTAAAACGACGGCCA	
M13R	CAGGAAACAGCTATGAC	
300F	AGGGTTCGATTCCGGAG	(Elwood et al., 1985)
528F	CGGTAATTCCAGCTCC	(Elwood et al., 1985)
760F	ATCAAGAACGAAAGT	(Elwood et al., 1985)
1055F	GGTGGTGCATGGCCG	(Elwood et al., 1985)
1200R	GGGCATCACAGACCTG	(Elwood et al., 1985)

#### 2.4. Specific Primer Design and Validation for *T. ovis* Detection by PCR

Specific primers were made from the consensus sequence of the SSU rRNA gene for the detection of *T. ovis* using a nested PCR protocol and were compared against other *Theileria* spp. sequences found in GenBank. The primary PCR primers TSsr170F and TSsr670R (Table 4) were used in 25 µl volume reactions with the Advantage 2 Enzyme kits according to manufactures' recommendations to produce an approximately 550 bp band. The cycling profile used with a Hybaid Sprint or Express thermocycler was; initial denaturation at 96 °C for 3 min; 30 cycles of denaturation at 94 °C for 10 sec, annealing at 54 °C for 10 sec, extension at 72 °C for 2 min; final extension at 72 °C for 10 min and hold at 4 °C. The nested primers are TSsr250FN and TSsr630RN (Table 4) produce an approximately 400 bp product using 1 µl of a 1:20 dilution of the primary product, Advantage 2 and with a initial denaturation of 96 °C.

Table 4  
*Theileria ovis* SSU rRNA specific primers.

Primer Name	Primer sequence 5'-3'	Position
TSsr170F	TCGAGCCTTCGGGT	172-187
TSsr760R	TCCGGACATTGTAAAACAAA	673-692
TSsr250FN	CGCGTCTTCGGATG	252-266
TSsr630RN	AAAGACTCGTAAAGGAGCAA	632-651

## 2.5. Internal Transcribed Spacers and 5.8S rRNA Genomic Region PCR

The full ITS and 5.8S gene region was amplified using a nested PCR protocol. The primary PCR was performed as above, but with 1 pmol forward primer 1055F and reverse primer LSUR300 (Table 5). The cycling profile was as follows: 96 °C initial denaturation for 3 min; 30 cycles of denaturation at 94 °C for 30 sec, annealing at 50 °C for 30 sec, and extension at 72 °C for 2 min; final extension at 72 °C for 10 min and hold at 4 °C.

The nested PCR used 1 pmol forward primer ITSF and reverse primer LSUR50 (Table 5), and 1 µl primary PCR product, which was diluted 1:20 if bands were visible in the primary PCR. The cycling profile was initial denaturation for 2 min; 30 cycles of denaturation at 94 °C for 30 sec, annealing at 55 °C for 30 sec, and extension for 72 °C for 2 min; a final extension at 72 °C for 10 min and hold at 4 °C. The resulting amplicon was then cloned, sequenced, and the sequence analyzed as described above with primers used for sequencing listed in Table 6.

Table 5  
Primers used for ITS 1-5.8S-ITS 2 gene region PCR.

Primer Name	Primer Ssequence 5'-3'	Reference
1055F	GGTGGTGCATGGCCG	(Elwood et al., 1985)
LSUR300	T(A/T)GCGCTTCAATCCC	
ITSF	GAGAAGTCGTAACAAGGTTTCCG	
LSUR50	GCTTCACTCGCCGTTACTAGG	

Table 6  
Primers used for sequencing ITS 1-5.8S-ITS 2 gene region.

Primers Primer	Sequence 5'-3'
M13F	GTAAAACGACGGCCA
M13R	CAGGAAACAGCTATGAC
ITSF	GAGAAGTCGTAACAAGGTTTCCG
LSUR50	GCTTCACTCGCCGTTAACTAGG

## 2.6. Partial SSU rRNA and ITS1 Genomic Region PCR

A nested protocol was used to amplify a DNA fragment spanning the variable (V4) SSU rRNA region through the end of ITS1 region from the Oklahoma elk *Theileria* species. A primary PCR was performed as above with 1 pmol of forward primer A (Sogin, 1990) and reverse primer LSUR50 (Table 7) and 50-100 ng gDNA. The cycling profile was initial denaturation of 96 °C for 3 min; 30 cycles of denaturation at 94 °C for 10 sec, annealing at 60 °C for 10 sec, and extension at 72 °C for 2 min; final extension at 72 °C for 10 min and hold at 4 °C.

A nested PCR was performed as above, but using 1 µl of a 1:50 dilution in sterile water of the primary product as template and 1 pmol of forward 528F (Elwood et al., 1985) and reverse iBulleElk520R (Table 7). The nested PCR cycling profile was initial denaturation at 96 °C for 2 min; 30 cycles of denaturation at 94 °C for 10 sec, annealing

at 50 °C for 10 sec, and extension at 72 °C for 2 min; final extension at 72 °C for 10 min and hold at 4 °C.

The resulting product was PCR purified using QIAquick PCR Purification Kit (Qiagen, Valencia, CA) according to manufacturers' instructions to remove primer dimers prior to ligation. The resulting band of approximately 1700bp band was then cloned and sequenced as described above, but with primers listed in Table 8.

Table 7  
Primers used to amplify V4 SSU rRNA through ITS 1 gene fragment.

Primers	Primer Sequence 5'-3'	Reference
A	AACCTGGTTGATCCTGCCAGT	(Sogin, 1990)
LSUR50	GCTTCACTCGCCGTTAACTAGG	
528F	CGGTAATTCCAGCTCC	(Elwood et al., 1985)
iBulleIk520R	GTGTAACCAAGTCTTGTG	

Table 8  
Primers used for sequencing V4 SSU rRNA through ITS 1 gene fragments.

Primers	Primer Sequence 5'-3'	Reference
BN1700	C GACTTCTCCTTCCTTTAAGTGATAAG	
M13F	GTAAAACGACGGCCA	
M13R	CAGGAAACAGCTATGAC	
1200R	GGGCATCACAGACCTG	(Elwood et al., 1985)

## 2.7. Clonal and Phylogenetic Analysis

Sequence results were obtained from at least three clones for each isolate. Genestream comparisons (Pearson et al., 1997) were run among the clones of an isolate, and between clones of different isolates, except for between the *T. annulata* isolates and the benign *Theileria* spp. ClustalX 1.81 (Thompson et al., 1997) was used to make full

alignments of the SSU rRNA genes and full ITS 1-5.8S-ITS 2 gene region. Neighbor joining phylogenetic trees were produced using PAUP 4.0 (Sinauer Associates Inc. Publishers, Sunderland, MA) using *Oxytricha longa* (GenBank Accession number AF508763) as the outgroup. The neighbor joining tree were created using PAUP for the SSU rRNA genes (Figure 2) which included many *Theileria* isolates, list available in GenBank (Table 9). The Neighbor joining tree (Figure 3) constructed from the ITS 1-5.8S-ITS 2 gene region sequences which was made using the alignment found in Appendix 2. The Neighbor joining tree constructed from the 5.8S rRNA gene region sequences is shown in Figure 4 (Appendix 3) of the isolates used in this study.



## CHAPTER III

### RESULTS

#### 3.1. Small Subunit rRNA Genes

The SSU rRNA gene sequences from *Theileria* spp. isolates and their clones obtained during the course of this study can be found aligned with previously reported *Theileria* spp. SSU rRNA sequences from the GenBank database in Appendix I.

The *T. buffeli* Tx SSU rRNA gene was 1740 bp in length and shared 100% identity with the *Theileria* sp. type A SSU rRNA gene sequence (GenBank accession no. U97047) when submitted to a BLAST search (Altschul et al., 1997). The consensus *T. buffeli* Ark SSU rRNA gene sequence shared 99.9% identity with type A SSU rRNA gene, with either cytosine or thymine (Y) at position 1637, where type A has a thymine. The consensus *T. buffeli* Oklahoma SSU rRNA gene sequence also shared 99.9% identity with type A SSU rRNA gene, with cytosine or adenine (M) at position 321 (type A has a cytosine at this position) and adenine or guanine (R) at position 1182 (type A has adenine). The *T. buffeli* Mi SSU rRNA gene sequence was previously reported as identical to the type A SSU rRNA gene sequence (Cossio-Bayugar et al., 2000). All nucleotide changes in the *T. buffeli* isolates SSU rRNA gene sequences are found in conserved SSU rRNA gene regions.

The consensus *T. sergenti* Chitose SSU rRNA gene sequence was 1740 bp long with 99.9% identity to type A *Theileria* sp. SSU rRNA gene with R (adenine or guanine) at position 1383, where type A had guanine. The consensus *T. sergenti* Ikeda SSU rRNA was 1748 bp in length with 99.9% identity to *Theileria* sp. type B SSU rRNA gene (GenBank accession no. U97048) with a single cytosine substitution for a thymine at

position 783. The nucleotide change in the Chitose isolate SSU rRNA gene sequence occurs in a variable region, while the substitution in the Ikeda isolate SSU rRNA gene occurs in a conserved region.

*Theileria annulata* Turkey 1, *T. annulata* Turkey 5, and *T. annulata* Turkey 7 full-length SSU rRNA genes were 1741 bp long. *Theileria annulata* 1 clones 12 and 24 (GenBank accession no. AY508462 and AY524666, respectively) shared 99.9% identity to the Hissar, India *T. annulata* SSU rRNA gene sequence (GenBank accession no. M64243), with a single cytosine insertion at position 1119. This base insertion was found in all Turkey *T. annulata* sequences obtained in this study, making them one nucleotide longer than the Hissar *T. annulata* gene sequence. Additional differences between the Hissar sequence and the Turkey *T. annulata* SSU rRNA gene sequences were noted, but none were fixed differences. Turkey *T. annulata* isolate 5 clones 31, 33 and 34 SSU rRNA genes (GenBank accession no. AY508465, AY508466, and AY508467, respectively) shared 99.8-99.7% identity to the Hissar gene. The clone 31 gene had 3 nucleotide substitutions at positions 453 (guanine for adenine), 1434 (adenine for guanine), and 1703 (cytosine for thymine). The clone 33 gene had substitutions at positions 553 (cytosine for thymine), 657 (cytosine for thymine) and 1022 (thymine for cytosine). The clone 34 gene had 5 nucleotide substitutions at positions 587 (cytosine for thymine), 759 (guanine for adenine), 1167 (guanine for adenine), 1550 (guanine for adenine), 1591 (adenine for guanine) and 1721 (adenine for guanine). *Theileria annulata* 7 clones 1 and 11 (GenBank accession no. AY508471 and AY508472, respectively) had a 99.9% identity to Hissar *T. annulata* with clone 1 having one nucleotide change at position 1431 (cytosine for thymine) and clone 11 having two

nucleotide changes at positions 266 (guanine for adenine) and 1463 (thymine for cytosine) in addition to the insertion at position 119. All of the nucleotide changes were in conserved SSU rRNA gene regions except for the clone 33 nucleotide substitution at position 657.

*Theileria annulata* Turkey isolates 3 and 6 produced 1675 bp SSU rRNA gene sequences from nested PCR with primers AN50 and BN1700. The gene fragment from Turkey isolate 3 (GenBank accession no. AY508463), which was sequenced directly from the PCR product, had a single cytosine insertion at position 1119 and shared 99.9% identity to Hissar *T. annulata*. *Theileria annulata* Turkey isolate 6 clones 15, 22 and 23 SSU rRNA genes (GenBank accession no. AY508468, AY508470, and AY508469, respectively) shared 99.8 to 99.7% identity to the Hissar *T. annulata* sequence. Clone 15 had 2 nucleotide substitutions at positions 200 (guanine for adenine) and 721 (adenine for guanine). The clone 23 gene had substitutions in positions 1347 (thymine for cytosine) and 1543 (adenine for guanine). The clone 22 sequence had two nucleotide substitutions at positions 340 (adenine for guanine) and 947 (guanine for adenine) and a three base deletion at positions 1313 to 1315. Gene sequences from all three clones had the base insertion at position 1119. All the nucleotide changes are found in conserved SSU rRNA gene sequence regions.

Turkey *T. annulata* isolates 2 and 4 SSU rRNA gene fragments of 919 and 967 bp, respectively (GenBank accession no. AY508473 and AY508464, respectively) were derived using primers 989A and 990A. Both fragments were sequenced directly and had the single base insertion at position 1119, thus sharing 99.9% identity with the Hissar *T.*

*annulata* gene sequence. The single base insertion occurs in a conserved SSU rRNA gene region.

Turkey *T. ovis* isolate 8 clones 12 and 24 were full-length 1747 bp SSU rRNA gene sequences that resulted from PCR with primers A and B (GenBank accession no. AY508453 and AY508454, respectively). The clone 12 sequence shared 99.9% identity with the *T. ovis* consensus sequence derived in this study (Appendix 2) due to a single substitution at position 1332 (guanine for adenine). The clone 24 gene shared 99.8% identity with the consensus sequence and had three nucleotide substitutions at positions 572 (guanine for adenine), 1411 (cytosine for thymine) and 1607 (cytosine for thymine). All of the nucleotide changes were found in conserved SSU rRNA gene regions.

A gene fragment from Turkey *T. ovis* isolate 8 was produced using primers AN50 and BN1700 and 1537 bp directly sequenced from the amplicon (Genbank accession no. AY508455). The sequence was identical to the *T. ovis* consensus sequence.

Turkey *T. ovis* isolate 10 clones 15 and 16 (GenBank accession no. AY508457 and AY508458, respectively) were 1682 bp products of primers AN50 and BN1700 and shared 100% identity with the *T. ovis* consensus sequence.

Turkey *T. ovis* isolates 9 and 11 amplicons of 1042 bp and 1046 bp, respectively, were products of primers 989A and 990A. Only one clone was obtained from isolate 9 (GenBank accession no. AY508456) and it shared 99.9% identity with the consensus sequence due to a single nucleotide substitution at position 646 (adenine for guanine). Two clones from *T. ovis* isolate 11, clones 1 and 11 (GenBank accession no. AY508459 AY508461) shared 100% identity with the consensus sequence, and one clone, 3 (GenBank accession no. AY508460), shared 99.9% identity with the consensus sequence

with a single nucleotide substitution at position 1129 (thymine for cytosine). These nucleotide changes were found in conserved SSU rRNA gene regions.

The consensus *T. ovis* SSU rRNA gene sequence shared a 99.9% identity with the *T. ovis* Sudan SSU rRNA gene (GenBank accession no. AY260171), with a single nucleotide substitution at position 786 (thymine for guanine), and a 99.9% identity with the *T. ovis* Turkey SSU rRNA gene (GenBank accession no. AY260172) due to two nucleotide deletions at positions 141 (deleted guanine) and 415 (deleted cytosine). The consensus *T. ovis* SSU rRNA gene had a 99.7% identity to *T. ovis* Spain SSU rRNA (GenBank accession no. AY533144) with six nucleotide differences which include an adenine insertion at position 2, deletion of guanine at position 1288 and cytosine at position 1414, and a nucleotide substitution at position 1274 (adenine for cytosine). The consensus *T. ovis* sequence possessed adenines at positions 1305 and 1531, whereas the *T. ovis* Spain sequence was reported as “n” (any nucleotide) in these positions. An alignment of the full length *T. ovis* SSU rRNA gene clones, *T. ovis* consensus sequence, *T. ovis* Spain, *T. ovis* Sudan, and *T. ovis* Turkey from GenBank can be seen in Figure 1. The *T. ovis* SSU rRNA gene consensus sequence had a 97.4% identity to *T. lestoquardi* SSU rRNA gene sequence (GenBank accession no. AF081135) and a 97.2% identity to *T. separata* SSU rRNA gene sequence (GenBank accession no. AY260175). All of the nucleotide changes were found in conserved SSU rRNA gene regions.

The *T. cervi* white-tailed deer (WTD) 181 SSU rRNA gene was 1748 bp long and had a 99% identity to type F *Theileria* sp. SSU rRNA gene sequence, which is a 1748bp, (GenBank accession no. U97054) with nucleotide substitutions at positions 272 (guanine for thymidine), 223 (thymidine for cytosine), 254 (adenine for guanine) and 1472

T.ovis_Spain	-ACCTGGTTGATCCTGCCAGTAGTCATATGCTTGTCTTAAAGATTAAGCCATGCATGTCT 59
T.ovis_Turkey	AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGTCTTAAAGATTAAGCCATGCATGTCT 60
T.ovis_Sudan	AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGTCTTAAAGATTAAGCCATGCATGTCT 60
T.ovis8_12	AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGTCTTAAAGATTAAGCCATGCATGTCT 60
T.ovis8_24	AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGTCTTAAAGATTAAGCCATGCATGTCT 60
T.ovis_Con	AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGTCTTAAAGATTAAGCCATGCATGTCT 60
T.ovis_Spain	AAGTATAAGCTTTTTATATGGTGAAACTGCGAATGGCTCATTACAACAGTTATAGTTTATT 119
T.ovis_Turkey	AAGTATAAGCTTTTTATATGGTGAAACTGCGAATGGCTCATTACAACAGTTATAGTTTATT 120
T.ovis_Sudan	AAGTATAAGCTTTTTATATGGTGAAACTGCGAATGGCTCATTACAACAGTTATAGTTTATT 120
T.ovis8_12	AAGTATAAGCTTTTTATATGGTGAAACTGCGAATGGCTCATTACAACAGTTATAGTTTATT 120
T.ovis8_24	AAGTATAAGCTTTTTATATGGTGAAACTGCGAATGGCTCATTACAACAGTTATAGTTTATT 120
T.ovis_Con	AAGTATAAGCTTTTTATATGGTGAAACTGCGAATGGCTCATTACAACAGTTATAGTTTATT 120
T.ovis_Spain	TGATGTTTCGTTTTTACATGG-ATAACCGTGCTAATTGTAGGGCTAATACATGTTCCGAGAC 178
T.ovis_Turkey	TGATGTTTCGTTTTTACATGGGATAACCGTGCTAATTGTAGGGCTAATACATGTTCCGAGAC 180
T.ovis_Sudan	TGATGTTTCGTTTTTACATGG-ATAACCGTGCTAATTGTAGGGCTAATACATGTTCCGAGAC 179
T.ovis8_12	TGATGTTTCGTTTTTACATGG-ATAACCGTGCTAATTGTAGGGCTAATACATGTTCCGAGAC 179
T.ovis8_24	TGATGTTTCGTTTTTACATGG-ATAACCGTGCTAATTGTAGGGCTAATACATGTTCCGAGAC 179
T.ovis_Con	TGATGTTTCGTTTTTACATGG-ATAACCGTGCTAATTGTAGGGCTAATACATGTTCCGAGAC 179
T.ovis_Spain	CTTCGGGTGGCGTTTATTAGACCTAAAACCAAACCGCTTGCGGTGTACGGTGATTTCATAA 238
T.ovis_Turkey	CTTCGGGTGGCGTTTATTAGACCTAAAACCAAACCGCTTGCGGTGTACGGTGATTTCATAA 240
T.ovis_Sudan	CTTCGGGTGGCGTTTATTAGACCTAAAACCAAACCGCTTGCGGTGTACGGTGATTTCATAA 239
T.ovis8_12	CTTCGGGTGGCGTTTATTAGACCTAAAACCAAACCGCTTGCGGTGTACGGTGATTTCATAA 239
T.ovis8_24	CTTCGGGTGGCGTTTATTAGACCTAAAACCAAACCGCTTGCGGTGTACGGTGATTTCATAA 239
T.ovis_Con	CTTCGGGTGGCGTTTATTAGACCTAAAACCAAACCGCTTGCGGTGTACGGTGATTTCATAA 239
T.ovis_Spain	TAAACTTGCGAATCGCGTCTTCGGATGCGATGTATCATTCAAGTTTCTGACCTATCAGCT 298
T.ovis_Turkey	TAAACTTGCGAATCGCGTCTTCGGATGCGATGTATCATTCAAGTTTCTGACCTATCAGCT 300
T.ovis_Sudan	TAAACTTGCGAATCGCGTCTTCGGATGCGATGTATCATTCAAGTTTCTGACCTATCAGCT 299
T.ovis8_12	TAAACTTGCGAATCGCGTCTTCGGATGCGATGTATCATTCAAGTTTCTGACCTATCAGCT 299
T.ovis8_24	TAAACTTGCGAATCGCGTCTTCGGATGCGATGTATCATTCAAGTTTCTGACCTATCAGCT 299
T.ovis_Con	TAAACTTGCGAATCGCGTCTTCGGATGCGATGTATCATTCAAGTTTCTGACCTATCAGCT 299
T.ovis_Spain	TTGGACGGTAGGGTATTGGCCTACCGGGGCAACGACGGGTAACGGGGAATTAGGGTTCGA 358
T.ovis_Turkey	TTGGACGGTAGGGTATTGGCCTACCGGGGCAACGACGGGTAACGGGGAATTAGGGTTCGA 360
T.ovis_Sudan	TTGGACGGTAGGGTATTGGCCTACCGGGGCAACGACGGGTAACGGGGAATTAGGGTTCGA 359
T.ovis8_12	TTGGACGGTAGGGTATTGGCCTACCGGGGCAACGACGGGTAACGGGGAATTAGGGTTCGA 359
T.ovis8_24	TTGGACGGTAGGGTATTGGCCTACCGGGGCAACGACGGGTAACGGGGAATTAGGGTTCGA 359
T.ovis_Con	TTGGACGGTAGGGTATTGGCCTACCGGGGCAACGACGGGTAACGGGGAATTAGGGTTCGA 359
T.ovis_Spain	TTCCGGAGAGGGAGCCTGAGAAAACGGCTACCACATCTAAGGAAGGCAGCAGGCGC-GCAA 417
T.ovis_Turkey	TTCCGGAGAGGGAGCCTGAGAAAACGGCTACCACATCTAAGGAAGGCAGCAGGCGC-GCAA 420
T.ovis_Sudan	TTCCGGAGAGGGAGCCTGAGAAAACGGCTACCACATCTAAGGAAGGCAGCAGGCGC-GCAA 418
T.ovis8_12	TTCCGGAGAGGGAGCCTGAGAAAACGGCTACCACATCTAAGGAAGGCAGCAGGCGC-GCAA 418
T.ovis8_24	TTCCGGAGAGGGAGCCTGAGAAAACGGCTACCACATCTAAGGAAGGCAGCAGGCGC-GCAA 418
T.ovis_Con	TTCCGGAGAGGGAGCCTGAGAAAACGGCTACCACATCTAAGGAAGGCAGCAGGCGC-GCAA 418
T.ovis_Spain	ATTACCCAATCCTGACACAGGGAGGTAGTGACAAGAAATAACAATACGGGGCTTAATGTC 477
T.ovis_Turkey	ATTACCCAATCCTGACACAGGGAGGTAGTGACAAGAAATAACAATACGGGGCTTAATGTC 480
T.ovis_Sudan	ATTACCCAATCCTGACACAGGGAGGTAGTGACAAGAAATAACAATACGGGGCTTAATGTC 478
T.ovis8_12	ATTACCCAATCCTGACACAGGGAGGTAGTGACAAGAAATAACAATACGGGGCTTAATGTC 478
T.ovis8_24	ATTACCCAATCCTGACACAGGGAGGTAGTGACAAGAAATAACAATACGGGGCTTAATGTC 478
T.ovis_Con	ATTACCCAATCCTGACACAGGGAGGTAGTGACAAGAAATAACAATACGGGGCTTAATGTC 478

Figure 1

*Theileria ovis* SSU rRNA gene alignment.

Alignment of the full SSU rRNA genes of *Theileria ovis* from this study (T.ovis8\_12, T.ovis8\_24 and T.ovis\_Con) and from GenBank (T.ovis\_Spain, T.ovis\_Turkey and T.ovis\_Sudan).

T.ovis\_Spain TTGTAATTGGAATGATGGGAATTTAAACCTCTTCCAGAGTATCAATTGGAGGGCAAGTCT 537  
 T.ovis\_Turkey TTGTAATTGGAATGATGGGAATTTAAACCTCTTCCAGAGTATCAATTGGAGGGCAAGTCT 540  
 T.ovis\_Sudan TTGTAATTGGAATGATGGGAATTTAAACCTCTTCCAGAGTATCAATTGGAGGGCAAGTCT 538  
 T.ovis8\_12 TTGTAATTGGAATGATGGGAATTTAAACCTCTTCCAGAGTATCAATTGGAGGGCAAGTCT 538  
 T.ovis8\_24 TTGTAATTGGAATGATGGGAATTTAAACCTCTTCCAGAGTATCAATTGGAGGGCAAGTCT 538  
 T.ovis\_Con TTGTAATTGGAATGATGGGAATTTAAACCTCTTCCAGAGTATCAATTGGAGGGCAAGTCT 538

T.ovis\_Spain GGTGCCAGCAGCCGCGGTAATTCAGCTCCAATAGCGTATATTAATAATTGTTGCAGTTAA 597  
 T.ovis\_Turkey GGTGCCAGCAGCCGCGGTAATTCAGCTCCAATAGCGTATATTAATAATTGTTGCAGTTAA 600  
 T.ovis\_Sudan GGTGCCAGCAGCCGCGGTAATTCAGCTCCAATAGCGTATATTAATAATTGTTGCAGTTAA 598  
 T.ovis8\_12 GGTGCCAGCAGCCGCGGTAATTCAGCTCCAATAGCGTATATTAATAATTGTTGCAGTTAA 598  
 T.ovis8\_24 GGTGCCAGCAGCCGCGGTAATTCAGCTCCAATAGCGTATATTAATAATTGTTGCAGTTAA 598  
 T.ovis\_Con GGTGCCAGCAGCCGCGGTAATTCAGCTCCAATAGCGTATATTAATAATTGTTGCAGTTAA 598

T.ovis\_Spain AAAGCTCGTAGTTGAATTTCTGCTGCATTGCTTTTGCTCCTTTACGAGTCTTTGCATTGT 657  
 T.ovis\_Turkey AAAGCTCGTAGTTGAATTTCTGCTGCATTGCTTTTGCTCCTTTACGAGTCTTTGCATTGT 660  
 T.ovis\_Sudan AAAGCTCGTAGTTGAATTTCTGCTGCATTGCTTTTGCTCCTTTACGAGTCTTTGCATTGT 658  
 T.ovis8\_12 AAAGCTCGTAGTTGAATTTCTGCTGCATTGCTTTTGCTCCTTTACGAGTCTTTGCATTGT 658  
 T.ovis8\_24 AAAGCTCGTAGTTGAATTTCTGCTGCATTGCTTTTGCTCCTTTACGAGTCTTTGCATTGT 658  
 T.ovis\_Con AAAGCTCGTAGTTGAATTTCTGCTGCATTGCTTTTGCTCCTTTACGAGTCTTTGCATTGT 658

T.ovis\_Spain GGCTTATTTCCGACTTTGTTTTACAATGTCCGGATGTTTACTTTGAGAAAATTAGAGTGC 717  
 T.ovis\_Turkey GGCTTATTTCCGACTTTGTTTTACAATGTCCGGATGTTTACTTTGAGAAAATTAGAGTGC 720  
 T.ovis\_Sudan GGCTTATTTCCGACTTTGTTTTACAATGTCCGGATGTTTACTTTGAGAAAATTAGAGTGC 718  
 T.ovis8\_12 GGCTTATTTCCGACTTTGTTTTACAATGTCCGGATGTTTACTTTGAGAAAATTAGAGTGC 718  
 T.ovis8\_24 GGCTTATTTCCGACTTTGTTTTACAATGTCCGGATGTTTACTTTGAGAAAATTAGAGTGC 718  
 T.ovis\_Con GGCTTATTTCCGACTTTGTTTTACAATGTCCGGATGTTTACTTTGAGAAAATTAGAGTGC 718

T.ovis\_Spain TCAAAGCAGGCTTTCGCCTTGAATAGTTAGCATGGAATAATAAAGTAGGACTTTGGTTC 777  
 T.ovis\_Turkey TCAAAGCAGGCTTTCGCCTTGAATAGTTAGCATGGAATAATAAAGTAGGACTTTGGTTC 780  
 T.ovis\_Sudan TCAAAGCAGGCTTTCGCCTTGAATAGTTAGCATGGAATAATAAAGTAGGACTTTGGTTC 778  
 T.ovis8\_12 TCAAAGCAGGCTTTCGCCTTGAATAGTTAGCATGGAATAATAAAGTAGGACTTTGGTTC 778  
 T.ovis8\_24 TCAAAGCAGGCTTTCGCCTTGAATAGTTAGCATGGAATAATAAAGTAGGACTTTGGTTC 778  
 T.ovis\_Con TCAAAGCAGGCTTTCGCCTTGAATAGTTAGCATGGAATAATAAAGTAGGACTTTGGTTC 778

T.ovis\_Spain TATTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTA 837  
 T.ovis\_Turkey TATTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTA 840  
 T.ovis\_Sudan TATTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTA 838  
 T.ovis8\_12 TATTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTA 838  
 T.ovis8\_24 TATTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTA 838  
 T.ovis\_Con TATTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTA 838

T.ovis\_Spain TTAACTGTCAGAGGTGAAAATCTTAGATTTGTTAAAGACGAACTACTGCGAAAAGCATT 897  
 T.ovis\_Turkey TTAACTGTCAGAGGTGAAAATCTTAGATTTGTTAAAGACGAACTACTGCGAAAAGCATT 900  
 T.ovis\_Sudan TTAACTGTCAGAGGTGAAAATCTTAGATTTGTTAAAGACGAACTACTGCGAAAAGCATT 898  
 T.ovis8\_12 TTAACTGTCAGAGGTGAAAATCTTAGATTTGTTAAAGACGAACTACTGCGAAAAGCATT 898  
 T.ovis8\_24 TTAACTGTCAGAGGTGAAAATCTTAGATTTGTTAAAGACGAACTACTGCGAAAAGCATT 898  
 T.ovis\_Con TTAACTGTCAGAGGTGAAAATCTTAGATTTGTTAAAGACGAACTACTGCGAAAAGCATT 898

T.ovis\_Spain GCCAAGGATGTTTTCATTAATCAAGAACGAAAAGTTAGGGGATCGAAGACGATCAGATACC 957  
 T.ovis\_Turkey GCCAAGGATGTTTTCATTAATCAAGAACGAAAAGTTAGGGGATCGAAGACGATCAGATACC 960  
 T.ovis\_Sudan GCCAAGGATGTTTTCATTAATCAAGAACGAAAAGTTAGGGGATCGAAGACGATCAGATACC 958  
 T.ovis8\_12 GCCAAGGATGTTTTCATTAATCAAGAACGAAAAGTTAGGGGATCGAAGACGATCAGATACC 958  
 T.ovis8\_24 GCCAAGGATGTTTTCATTAATCAAGAACGAAAAGTTAGGGGATCGAAGACGATCAGATACC 958  
 T.ovis\_Con GCCAAGGATGTTTTCATTAATCAAGAACGAAAAGTTAGGGGATCGAAGACGATCAGATACC 958

T.ovis\_Spain GTCGTAGTCCTAACCATAACTATGCCGACTAGAGATTGGAGGTCGTCAGTTTTTACGAC 1017  
 T.ovis\_Turkey GTCGTAGTCCTAACCATAACTATGCCGACTAGAGATTGGAGGTCGTCAGTTTTTACGAC 1020  
 T.ovis\_Sudan GTCGTAGTCCTAACCATAACTATGCCGACTAGAGATTGGAGGTCGTCAGTTTTTACGAC 1018  
 T.ovis8\_12 GTCGTAGTCCTAACCATAACTATGCCGACTAGAGATTGGAGGTCGTCAGTTTTTACGAC 1018  
 T.ovis8\_24 GTCGTAGTCCTAACCATAACTATGCCGACTAGAGATTGGAGGTCGTCAGTTTTTACGAC 1018  
 T.ovis\_Con GTCGTAGTCCTAACCATAACTATGCCGACTAGAGATTGGAGGTCGTCAGTTTTTACGAC 1018

Figure 1  
continued

T.ovis_Spain	TCCTTCAGCACCTTGAGAGAAATCAAAGTCTTTGGGTCTGGGGGAGTATGGTCGCAAG 1077
T.ovis_Turkey	TCCTTCAGCACCTTGAGAGAAATCAAAGTCTTTGGGTCTGGGGGAGTATGGTCGCAAG 1080
T.ovis_Sudan	TCCTTCAGCACCTTGAGAGAAATCAAAGTCTTTGGGTCTGGGGGAGTATGGTCGCAAG 1078
T.ovis8_12	TCCTTCAGCACCTTGAGAGAAATCAAAGTCTTTGGGTCTGGGGGAGTATGGTCGCAAG 1078
T.ovis8_24	TCCTTCAGCACCTTGAGAGAAATCAAAGTCTTTGGGTCTGGGGGAGTATGGTCGCAAG 1078
T.ovis_Con	TCCTTCAGCACCTTGAGAGAAATCAAAGTCTTTGGGTCTGGGGGAGTATGGTCGCAAG 1078
T.ovis_Spain	GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCGTGGAGCCTGCGGCTTAATT 1137
T.ovis_Turkey	GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCGTGGAGCCTGCGGCTTAATT 1140
T.ovis_Sudan	GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCGTGGAGCCTGCGGCTTAATT 1138
T.ovis8_12	GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCGTGGAGCCTGCGGCTTAATT 1138
T.ovis8_24	GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCGTGGAGCCTGCGGCTTAATT 1138
T.ovis_Con	GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCGTGGAGCCTGCGGCTTAATT 1138
T.ovis_Spain	TGACTCAACACGGGGAAACTCACCAGGTCCAGACAAAAGGAAGGATTGACAGATTGATAGC 1197
T.ovis_Turkey	TGACTCAACACGGGGAAACTCACCAGGTCCAGACAAAAGGAAGGATTGACAGATTGATAGC 1200
T.ovis_Sudan	TGACTCAACACGGGGAAACTCACCAGGTCCAGACAAAAGGAAGGATTGACAGATTGATAGC 1198
T.ovis8_12	TGACTCAACACGGGGAAACTCACCAGGTCCAGACAAAAGGAAGGATTGACAGATTGATAGC 1198
T.ovis8_24	TGACTCAACACGGGGAAACTCACCAGGTCCAGACAAAAGGAAGGATTGACAGATTGATAGC 1198
T.ovis_Con	TGACTCAACACGGGGAAACTCACCAGGTCCAGACAAAAGGAAGGATTGACAGATTGATAGC 1198
T.ovis_Spain	TCCTTCTTGATTCTTTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC 1257
T.ovis_Turkey	TCCTTCTTGATTCTTTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC 1260
T.ovis_Sudan	TCCTTCTTGATTCTTTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC 1258
T.ovis8_12	TCCTTCTTGATTCTTTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC 1258
T.ovis8_24	TCCTTCTTGATTCTTTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC 1258
T.ovis_Con	TCCTTCTTGATTCTTTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC 1258
T.ovis_Spain	TGGTTAATTCGGTTAACGAACGAGACCTTGAACCTGCTAAATAGGGTNCGGGAATAAGCT 1317
T.ovis_Turkey	TGGTTAATTCGGTTAACGAACGAGACCTT-AACCTGCTAAATAGGGTACGGGAATAAGCT 1319
T.ovis_Sudan	TGGTTAATTCGGTTAACGAACGAGACCTT-AACCTGCTAAATAGGGTACGGGAATAAGCT 1317
T.ovis8_12	TGGTTAATTCGGTTAACGAACGAGACCTT-AACCTGCTAAATAGGGTACGGGAATAAGCT 1317
T.ovis8_24	TGGTTAATTCGGTTAACGAACGAGACCTT-AACCTGCTAAATAGGGTACGGGAATAAGCT 1317
T.ovis_Con	TGGTTAATTCGGTTAACGAACGAGACCTT-AACCTGCTAAATAGGGTACGGGAATAAGCT 1317
T.ovis_Spain	TTTGCTGTCCCGTGATCGCTTCTTAGAGGGACTTTGCGGTTATAAATCGCAAGGAAGTTT 1377
T.ovis_Turkey	TTTGCTGTCCCGTGATCGCTTCTTAGAGGGACTTTGCGGTTATAAATCGCAAGGAAGTTT 1379
T.ovis_Sudan	TTTGCTGTCCCGTGATCGCTTCTTAGAGGGACTTTGCGGTTATAAATCGCAAGGAAGTTT 1377
T.ovis8_12	TTTGCTGTCCCGTGATCGCTTCTTAGAGGGACTTTGCGGTTATAAATCGCAAGGAAGTTT 1377
T.ovis8_24	TTTGCTGTCCCGTGATCGCTTCTTAGAGGGACTTTGCGGTTATAAATCGCAAGGAAGTTT 1377
T.ovis_Con	TTTGCTGTCCCGTGATCGCTTCTTAGAGGGACTTTGCGGTTATAAATCGCAAGGAAGTTT 1377
T.ovis_Spain	AAGGCAATAACAGGTCTGTGATGCCCTTAGATGTCCCTGGGCTGCACGCGCGCTACACTG 1437
T.ovis_Turkey	AAGGCAATAACAGGTCTGTGATGCCCTTAGATGTCC-TGGGCTGCACGCGCGCTACACTG 1438
T.ovis_Sudan	AAGGCAATAACAGGTCTGTGATGCCCTTAGATGTCC-TGGGCTGCACGCGCGCTACACTG 1436
T.ovis8_12	AAGGCAATAACAGGTCTGTGATGCCCTTAGATGTCC-TGGGCTGCACGCGCGCTACACTG 1436
T.ovis8_24	AAGGCAATAACAGGTCTGTGATGCCCTTAGATGTCC-TGGGCTGCACGCGCGCTACACTG 1436
T.ovis_Con	AAGGCAATAACAGGTCTGTGATGCCCTTAGATGTCC-TGGGCTGCACGCGCGCTACACTG 1436
T.ovis_Spain	ATGCGTTCATCGAGTTTATCCTTGCCGAGAGGCCCTGGGTAATCTTTAGTACGCATCGTG 1497
T.ovis_Turkey	ATGCGTTCATCGAGTTTATCCTTGCCGAGAGGCCCTGGGTAATCTTTAGTACGCATCGTG 1498
T.ovis_Sudan	ATGCGTTCATCGAGTTTATCCTTGCCGAGAGGCCCTGGGTAATCTTTAGTACGCATCGTG 1496
T.ovis8_12	ATGCGTTCATCGAGTTTATCCTTGCCGAGAGGCCCTGGGTAATCTTTAGTACGCATCGTG 1496
T.ovis8_24	ATGCGTTCATCGAGTTTATCCTTGCCGAGAGGCCCTGGGTAATCTTTAGTACGCATCGTG 1496
T.ovis_Con	ATGCGTTCATCGAGTTTATCCTTGCCGAGAGGCCCTGGGTAATCTTTAGTACGCATCGTG 1496
T.ovis_Spain	ATGGGGATCGATTATTGCAATTATTAATCGTGANCGAGGAATGCCTAGTATGCGCAAGTC 1557
T.ovis_Turkey	ATGGGGATCGATTATTGCAATTATTAATCGTGAACGAGGAATGCCTAGTATGCGCAAGTC 1558
T.ovis_Sudan	ATGGGGATCGATTATTGCAATTATTAATCGTGAACGAGGAATGCCTAGTATGCGCAAGTC 1556
T.ovis8_12	ATGGGGATCGATTATTGCAATTATTAATCGTGAACGAGGAATGCCTAGTATGCGCAAGTC 1556
T.ovis8_24	ATGGGGATCGATTATTGCAATTATTAATCGTGAACGAGGAATGCCTAGTATGCGCAAGTC 1556
T.ovis_Con	ATGGGGATCGATTATTGCAATTATTAATCGTGAACGAGGAATGCCTAGTATGCGCAAGTC 1556

Figure 1  
continued



T.ovis_Spain	ATCAGCTTGTGCAGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTCCTACCGAT 1617
T.ovis_Turkey	ATCAGCTTGTGCAGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTCCTACCGAT 1618
T.ovis_Sudan	ATCAGCTTGTGCAGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTCCTACCGAT 1616
T.ovis8_12	ATCAGCTTGTGCAGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTCCTACCGAT 1616
T.ovis8_24	ATCAGCTTGTGCAGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCCCCCTACCGAT 1616
T.ovis_Con	ATCAGCTTGTGCAGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTCCTACCGAT 1616
T.ovis_Spain	CGAGTGATCCGGTGAATTATTCGGACCGTGATGTTCCCGTCAGGGAGCGTCTAGGGAAGT 1677
T.ovis_Turkey	CGAGTGATCCGGTGAATTATTCGGACCGTGATGTTCCCGTCAGGGAGCGTCTAGGGAAGT 1678
T.ovis_Sudan	CGAGTGATCCGGTGAATTATTCGGACCGTGATGTTCCCGTCAGGGAACGTCTAGGGAAGT 1676
T.ovis8_12	CGAGTGATCCGGTGAATTATTCGGACCGTGATGTTCCCGTCAGGGAGCGTCTAGGGAAGT 1676
T.ovis8_24	CGAGTGATCCGGTGAATTATTCGGACCGTGATGTTCCCGTCAGGGAGCGTCTAGGGAAGT 1676
T.ovis_Con	CGAGTGATCCGGTGAATTATTCGGACCGTGATGTTCCCGTCAGGGAGCGTCTAGGGAAGT 1676
T.ovis_Spain	TTTGTGAACCTTATCACTTAAAGGAAGGAGAAGTCGTAACAAGGTTTCCGTAGGTGAACC 1737
T.ovis_Turkey	TTTGTGAACCTTATCACTTAAAGGAAGGAGAAGTCGTAACAAGGTTTCCGTAGGTGAACC 1738
T.ovis_Sudan	TTTGTGAACCTTATCACTTAAAGGAAGGAGAAGTCGTAACAAGGTTTCCGTAGGTGAACC 1736
T.ovis8_12	TTTGTGAACCTTATCACTTAAAGGAAGGAGAAGTCGTAACAAGGTTTCCGTAGGTGAACC 1736
T.ovis8_24	TTTGTGAACCTTATCACTTAAAGGAAGGAGAAGTCGTAACAAGGTTTCCGTAGGTGAACC 1736
T.ovis_Con	TTTGTGAACCTTATCACTTAAAGGAAGGAGAAGTCGTAACAAGGTTTCCGTAGGTGAACC 1736
T.ovis_Spain	TGCAGAAGGATC 1749
T.ovis_Turkey	TGCAGAAGGATC 1750
T.ovis_Sudan	TGCAGAAGGATC 1748
T.ovis8_12	TGCAGAAGGATC 1748
T.ovis8_24	TGCAGAAGGATC 1748
T.ovis_Con	TGCAGAAGGATC 1748

Figure 1  
continued

(thymidine for cytosine). All of these nucleotide changes occurred in the conserved SSU rRNA gene regions. *T. cervi* WTD 183 clone 5 SSU rRNA gene was 1749 bp in length and had a 99% identity to type F *Theileria* SSU rRNA gene sequence with nucleotide substitutions at positions 37 (cytosine for thymidine), 222 (guanine for thymidine), 223 (thymidine for cytosine), 447 (cytosine for thymidine), 461 (thymidine for cytosine), 1165 (adenine for guanine), 1472 (thymidine for cytosine), 1527 (thymidine for guanine) and a nucleotide insertion at position 250 (guanine). All of the nucleotide changes occurred in conserved SSU rRNA gene regions, except for the changes at positions 222 and 223, which are in V2 variable region. WTD 183 *T. cervi* clone 10 SSU rRNA gene was 1750 bp in length and had a 99% identity to type F *Theileria* SSU rRNA gene sequence with nucleotide substitutions at positions at 183 (thymidine for cytosine), 184

(thymidine for guanine), 188 (thymidine for guanine), 212 (thymidine for adenine), 213 (thymidine for cytosine), 216 (adenine for cytosine), 217 (adenine for thymidine), 225 (adenine for thymidine), 263 (adenine for cytosine) and 1474 (thymidine for cytosine); nucleotide deletions at positions 220 (cytosine), 221 (guanine) and 940 (guanine); and nucleotide insertions at positions 227 to 229 (adenine, adenine, and cytosine; respectively). Most of the nucleotide changes occurred in conserved SSU rRNA gene regions, except for the changes in positions 183, and 184, which are in the V1 variable region, while 188, 225, 220, 221 and 227 to 229 which all occur in V2 variable SSU rRNA gene region.

The *T. cervi* SSU rRNA gene from Indiana elk Green 5H was 1749 bp in length shared 99% identity with the type F *T. cervi* SSU rRNA gene with nucleotide substitutions at positions 222 (guanosine for thymidine), 223 (thymidine for cytosine), 1472 (thymidine for cytosine) and a guanosine insertion at position 1738. Positions 222 and 223 occur in variable SSU rRNA gene regions, while positions 1472 and 1738 were found in conserved SSU rRNA gene regions. The *T. cervi* SSU rRNA gene from the Wisconsin elk was 1748 bp long and shared 99% identity with the type F *T. cervi* SSU rRNA gene with nucleotide substitutions at positions 222 (guanosine for thymidine), 223 (thymidine for cytosine), 1472 (thymidine for cytosine) and 1692 (guanosine for adenine). The two nucleotide changes at positions 222 and 223 were in variable SSU rRNA gene regions, while positions 1472 and 1692 were in conserved SSU rRNA gene regions.

The SSU rRNA gene from the dama gazelle (clones 1 and 55) was 1743 bp long and shared 98% identity to *Theileria* sp. schizont rRNA (GenBank accession no.

L19081). When submitted to Genestream alignments (Pearson et al., 1997), the gene sequences from clones 1 and 55 shared 99.7% identity with each other, 96% with type F *T. cervi* SSU rRNA gene, and 95% with the type G *T. cervi* SSU rRNA gene (GenBank accession no. U97054 and U97055, respectively) sequences. There was a 96% identity to type A and D bovine *Theileria* SSU rRNA gene, *T. annulata*, *T. parva*, *T. lestoquardi* and *T. ovis* from Sudan, Spain and Turkey; while there was a 95% identity to type B, C, and E *Theileria* SSU rRNA gene sequences.

### 3.2. Specific Primers for *T. ovis*

The primary PCR primers TSsr170F and TSsr670R (Table 4) produced a band of approximately 550 bp from all *T. ovis* gDNAs. The nested primers TSsr250FN and TSsr630RN (Table 4) produced a band of approximately 400 bp from the four *T. ovis* isolate gDNAs. Correlate bands were not obtained from *T. annulata* gDNAs under the same PCR conditions used for *T. ovis* samples.

### 3.3. Internal Transcribed Spacers and 5.8S Gene Region

An alignment of the full ITS 1-5.8S gene-ITS2 genomic regions from all *Theileria* spp. and *C. felis* obtained in this study can be found aligned with GENBANK *Theileria* spp. (Table 9) in Appendix 2 . An alignment of the 5.8S gene sequences only are found in Appendix 3.

The full ITS 1-5.8S-ITS 2 gene regions for the *T. buffeli* isolates ranged from 1074 to 1076 bp. The ITS 1 region ranged from 640 to 642 bp, the 5.8S gene was 159 bp, and the ITS 2 region was 275 bp in length. Pairwise comparisons between cloned genes of a particular isolate ranged from 98.1-99.9% identity for the full ITS1-5.8S-ITS2 gene region, 97.2 to 99.8% for ITS 1 region, 99.4 to 100% for the 5.8S gene, and 98.5 to 100%

for the ITS 2 region. The percent identities among the isolates for the full ITS and 5.8S gene region ranges from 97.6 to 99.9%, 96.4 to 99.8% in the ITS 1 region, 99.4 to 100% in the 5.8S gene, and 98.2 to 100% in the ITS 2 region. The 5.8S gene of *T. buffeli* Arkansas clone 20 differed from those of the rest of the isolates by one nucleotide substitution at position 108 (guanosine for adenine). The pairwise comparison values among clones are shown in Tables 10 to 13.

Table 9  
GenBank SSU rRNA gene sequences used in study.

Isolates	GenBank Number
<i>Theileria buffeli</i> Warwick-Australia	AB000272
<i>Theileria annulata</i>	M64243
<i>Theileria buffeli</i> Australia	AF236094
<i>Theileria buffeli</i> China	AF236097
<i>Theileria sergenti</i> Fukushima	AB016074
<i>Theileria buffeli</i> Type A	U97047
<i>Theileria buffeli</i> Type B	U97048
<i>Theileria buffeli</i> Type C	U97051
<i>Theileria buffeli</i> Type D	U97052
<i>Theileria buffeli</i> Type E	U97053
<i>Theileria cervi</i> Type F	U97054
<i>Theileria cervi</i> Type G	U97055
<i>Theileria parva</i>	L02366
<i>Oxytricha longa</i>	AF508763
<i>Theileria mutans</i> Intona	AF078815
<i>Theileria buffeli</i> Marula	Z15106
<i>Cytauxzoon felis</i>	L19080

Table 10

Benign bovine *Theileria* spp. ITS 1-5.8S-ITS 2 gene region pairwise comparisons.

	Ar-15	Ar-20	Ar-25	Mi-3	Mi-5	Mi-14	Mi-15	Ok-8	Ok-9	Ok-10	Tx-5	Tx-6	Tx-11	In-3	In-10	In-13	Ch-1	Ch-2	Ch-3	Ch-4	Ch-5	lk-1	lk-2	lk-6	lk-7
Ar-15	100	99.4	99.4	99.7	98.1	99.4	99.5	97.8	98.2	98.1	97.9	98	98.1	54.3	54.6	54.3	94.2	93.4	93.3	94.5	93.6	36.2	36.3	36.4	36.3
Ar-20		100	99.4	99.5	98	99.3	99.3	97.6	98.1	98	97.7	97.8	97.9	54.8	54.9	54.5	93.9	93.1	93.1	94.3	93.3	36.2	36.3	36.5	36.3
Ar-25			100	99.5	98	99.3	99.3	97.6	98.1	98	97.7	97.8	97.9	54.5	54.5	54.2	93.9	93.1	93.1	94.3	93.3	36.5	36.9	36.3	36.5
Mi-3				100	98.4	99.7	99.8	97.9	98.3	98.2	98	98.1	98.1	54.5	54.6	54.3	94.2	93.4	93.3	94.5	93.6	36.3	36.5	36.6	36.3
Mi-5					100	98.1	98.2	99.3	99.7	99.6	99.3	99.4	99.5	54.4	54	54.2	93.8	93.1	93	94.2	93.2	36.4	36.5	36.7	36.4
Mi-14						100	99.5	97.6	98.1	98	97.7	97.8	97.9	54.4	54.6	54.1	93.9	93.1	93.1	94.3	94.3	36.4	36.7	36.6	36.2
Mi-15							100	97.7	98.1	98.1	97.8	97.9	98	54.4	54.5	54.1	93.9	93.1	93.1	94.3	93.3	36.3	36.6	36.6	36.3
Ok-8								100	99.5	99.4	99.2	99.1	99.3	54.4	54.8	54.2	93.4	92.7	92.6	93.8	92.9	36.2	36.5	36.3	36.3
Ok-9									100	99.9	99.6	99.5	99.8	54.6	54.1	54.3	93.9	93.2	93.1	94.3	93.3	36.3	36.6	36.6	36.4
Ok-10										100	99.5	99.4	99.7	54.5	55	54.3	93.8	93.1	93	94.2	93.2	36.3	36.6	36.6	36.3
Tx-5											100	99.2	99.4	54.7	54.3	54.5	93.5	92.8	92.7	93.9	93	36.3	36.5	36.6	36.4
Tx-6												100	99.3	54.3	55	54.3	93.6	92.9	92.3	94	93.1	36.3	36.4	36.6	36.4
Tx-11													100	54.7	54.3	54.5	93.7	93	92.9	94.1	93.2	36.3	36.3	36.6	36.4
In-3														100	99.5	99.5	54	54.5	54.6	54.3	54.7	35.4	35.4	35.6	35.9
In-10															100	99.8	53.9	54.4	54.2	54.2	54.2	35.4	35.5	35.6	35.7
In-13																100	53.7	54.2	53.9	54.1	54	35.5	35.5	35.6	35.9
Ch-1																	100	98.3	98	98.7	98.3	36.1	36.1	36.3	35.9
Ch-2																		100	99.2	97.9	99.4	35.9	36.1	36.1	35.9
Ch-3																			100	98	99.3	36	36.2	36.2	36
Ch-4																				100	98.1	36.3	36.2	36.2	36.6
Ch-5																					100	36	36.2	36.2	36
lk-1																						100	98.9	98.9	97.5
lk-2																							100	98	96.7
lk-6																								100	97.7
lk-7																									100

Table 11

Benign bovine *Theileria* spp. ITS 1 region pairwise comparisons.

	Ar-15	Ar-20	Ar-25	Mi-3	Mi-5	Mi-14	Mi-15	Ok-8	Ok-9	Ok-10	Tx-5	Tx-6	Tx-11	In-3	In-10	In-13	Ch-1	Ch-2	Ch-3	Ch-4	Ch-5	lk-1	lk-2	lk-6	lk-7
Ar-15	100	99.5	99.4	99.5	96.9	99.4	99.4	96.4	97	96.9	96.9	96.7	96.9	47.6	47.4	46.7	92.9	91.3	91.6	93	91.6	28.2	28.3	28.3	28.4
Ar-20		100	99.5	99.7	97	99.5	99.5	96.6	97.2	97	96.9	97	96.9	47.4	47.9	47.1	92.9	91.3	91.6	93	91.6	28.2	28.3	28.4	28.4
Ar-25			100	99.5	96.9	99.4	99.4	96.4	97	96.9	96.9	96.7	96.9	46.4	46.6	46.2	92.7	91.1	91.5	92.9	91.5	28.5	29	28.5	28.5
Mi-3				100	97.4	99.8	99.8	96.6	97.2	97	96.9	97	96.9	46.9	47.4	46.6	92.9	91.3	91.6	93	91.6	28.3	28.5	28.6	28.4
Mi-5					100	97.2	97.2	98.9	99.5	99.4	99.4	99.2	99.4	46.7	46	46.4	92.2	90.7	91	92.4	91	28.4	28.6	28.7	28.4
Mi-14						100	99.7	96.4	97	96.9	96.9	96.7	96.9	46.8	47.3	46.5	92.7	91.1	91.5	92.9	91.5	28.6	28.9	28.7	28.3
Mi-15							100	96.4	97	96.9	96.9	96.7	96.9	46.8	47.3	46.5	92.5	91	91.3	92.7	91.3	28.3	28.8	28.6	28.4
Ok-8								100	99.4	99.2	99.2	98.8	99.2	46.7	47.3	46.4	91.8	90.2	90.5	91.9	90.5	28.2	28.6	28.1	28.4
Ok-9									100	99.8	99.8	99.4	99.8	47	46.3	46.7	92.4	90.9	91.2	92.6	91.2	28.2	28.7	28.6	28.5
Ok-10										100	99.7	99.2	99.7	46.8	47.7	46.6	92.2	90.7	91	92.4	91	28.3	28.7	28.5	28.4
Tx-5											100	99.2	99.7	47.3	46.7	47.1	92.2	90.7	91	92.4	91	28.5	28.8	28.7	28.6
Tx-6												100	99.2	46.6	47.4	46.3	92.1	90.5	90.9	92.2	90.9	28.3	28.6	28.7	28.5
Tx-11													100	47.3	46.7	47.1	92.2	90.7	91	92.4	91	28.4	28.4	28.7	28.5
In-3														100	99.7	99.7	46.2	46.8	46.9	46.3	46.9	27.1	27.2	27.1	27.8
In-10															100	99.7	46.2	46.8	46.5	46.3	46.5	27.1	27.2	27.2	27.5
In-13																100	45.9	46.3	46	46	46	27.1	27.3	27.2	27.9
Ch-1																	100	97.8	98.1	99.2	98.1	28.1	28.1	28.4	27.8
Ch-2																		100	99.7	97.6	99.7	27.6	28	27.9	27.7
Ch-3																			100	97.9	100	27.8	28.2	28.1	27.9
Ch-4																				100	97.9	28	27.9	27.9	28.5
Ch-5																					100	27.8	28.2	28.1	27.9
lk-1																						100	98.5	98.8	96.6
lk-2																							100	97.6	95.5
lk-6																								100	97.2
lk-7																									100

Table 12  
Benign bovine *Theileria* spp. 5.8S gene pairwise comparisons.

	Ar-15	Ar-20	Ar-25	Mi-3	Mi-5	Mi-14	Mi-15	Ok-8	Ok-9	Ok-10	Tx-5	Tx-6	Tx-11	In-3	In-10	In-13	Ch-1	Ch-2	Ch-3	Ch-4	Ch-5	Ik-1	Ik-2	Ik-6	Ik-7	
Ar-15	100	99.4	100	100	100	100	100	100	100	100	100	100	100	100	97.5	98.1	98.1	98.7	99.4	98.1	99.4	99.4	95	95	95	95
Ar-20		100	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	96.9	97.5	97.5	98.1	98.7	97.5	98.7	98.7	98.7	94.3	94.3	94.3	94.3
Ar-25			100	100	100	100	100	100	100	100	100	100	100	100	97.5	98.1	98.1	98.7	99.4	98.1	99.4	99.4	95	95	95	95
Mi-3				100	100	100	100	100	100	100	100	100	100	100	97.5	98.1	98.1	98.7	99.4	98.1	99.4	99.4	95	95	95	95
Mi-5					100	100	100	100	100	100	100	100	100	100	97.5	98.1	98.1	98.7	99.4	98.1	99.4	99.4	95	95	95	95
Mi-14						100	100	100	100	100	100	100	100	100	97.5	98.1	98.1	98.7	99.4	98.1	99.4	99.4	95	95	95	95
Mi-15							100	100	100	100	100	100	100	100	97.5	98.1	98.1	98.7	99.4	98.1	99.4	99.4	95	95	95	95
Ok-8								100	100	100	100	100	100	100	97.5	98.1	98.1	98.7	99.4	98.1	99.4	99.4	95	95	95	95
Ok-9									100	100	100	100	100	100	97.5	98.1	98.1	98.7	99.4	98.1	99.4	99.4	95	95	95	95
Ok-10										100	100	100	100	100	97.5	98.1	98.1	98.7	99.4	98.1	99.4	99.4	95	95	95	95
Tx-5											100	100	100	100	97.5	98.1	98.1	98.7	99.4	98.1	99.4	99.4	95	95	95	95
Tx-6												100	100	100	97.5	98.1	98.1	98.7	99.4	98.1	99.4	99.4	95	95	95	95
Tx-11													100	100	97.5	98.1	98.1	98.7	99.4	98.1	99.4	99.4	95	95	95	95
In-3														100	99.4	99.4	96.2	96.9	95.6	96.9	96.9	92.5	92.5	92.5	92.5	
In-10															100	100	96.9	97.5	96.2	97.5	97.5	93.1	93.1	93.1	93.1	
In-13																100	96.9	97.5	96.2	97.5	97.5	93.1	93.1	93.1	93.1	
Ch-1																	100	98.1	96.9	98.1	98.1	93.7	93.7	93.7	93.7	
Ch-2																		100	97.5	98.7	98.7	94.3	94.3	94.3	94.3	
Ch-3																			100	98.1	98.1	93.7	93.7	93.7	93.7	
Ch-4																				100	98.7	94.3	94.3	94.3	94.3	
Ch-5																					100	94.3	94.3	94.3	94.3	
Ik-1																						100	100	100	100	
Ik-2																							100	100	100	
Ik-6																								100	100	
Ik-7																									100	

Table 13

Benign bovine *Theileria* spp. ITS 2 region pairwise comparisons.

	Ar-15	Ar-20	Ar-25	Mi-3	Mi-5	Mi-14	Mi-15	Ok-8	Ok-9	Ok-10	Tx-5	Tx-6	Tx-11	In-3	In-10	In-13	Ch-1	Ch-2	Ch-3	Ch-4	Ch-5	Ik-1	Ik-2	Ik-6	Ik-7
Ar-15	100	99.3	99.3	100	100	99.3	99.6	99.6	100	100	98.9	99.6	99.6	50.3	49.7	49.7	94.6	94.9	94.6	95.3	94.9	43.9	43.9	44.3	43.7
Ar-20		100	99.3	99.3	99.3	98.5	98.9	98.9	99.3	99.3	98.2	98.9	98.9	50.6	50	50	93.9	94.2	93.9	94.6	94.2	43.9	43.9	44.3	43.7
Ar-25			100	99.3	99.3	98.5	98.9	98.9	99.3	99.3	98.2	98.9	98.9	50.9	50.3	50.3	93.9	94.2	93.9	94.6	94.2	44.2	44.2	44.5	44
Mi-3				100	100	99.3	99.6	99.6	100	100	98.9	99.6	99.6	50.3	49.7	49.7	94.6	94.9	94.6	95.3	94.9	43.9	43.9	44.3	43.7
Mi-5					100	99.3	99.6	99.6	100	100	98.9	99.6	99.6	50.3	49.7	49.7	94.6	94.9	94.6	95.3	94.9	43.9	43.9	44.3	43.7
Mi-14						100	98.9	98.9	99.3	99.3	98.2	98.9	98.9	50	49.4	49.4	93.9	94.2	93.9	94.6	94.2	43.5	43.5	43.5	43.3
Mi-15							100	99.3	99.6	99.6	98.5	99.3	99.3	50	49.4	49.4	94.2	94.6	94.2	94.9	94.6	43.7	43.7	44	43.5
Ok-8								100	99.6	99.6	98.5	99.3	99.3	50.3	49.7	49.7	94.2	94.6	94.2	94.9	94.6	43.9	43.9	44.3	43.7
Ok-9									100	100	98.9	99.6	99.6	50.3	49.7	49.7	94.6	94.9	94.6	95.3	94.9	43.9	43.9	44.3	43.7
Ok-10										100	98.9	99.6	99.6	50.3	49.7	49.7	94.6	94.9	94.6	95.3	94.9	43.9	43.9	44.3	43.7
Tx-5											100	98.5	98.5	50	49.4	49.4	93.5	93.9	93.5	94.2	93.9	43.3	43.3	43.6	43.1
Tx-6												100	99.3	50	49.4	49.4	94.2	94.6	94.2	94.9	94.6	43.7	43.7	44.1	43.5
Tx-11													100	50	49.4	49.4	94.2	94.6	94.2	94.9	94.6	43.7	43.7	44.1	43.5
In-3														100	99.4	99.4	50.3	50.6	50.9	50.9	50.6	43.9	43.7	44.6	43.7
In-10															100	100	49.7	50	50.3	50.3	50	43.9	43.7	44.4	43.7
In-13																100	49.7	50	50.3	50.3	50	43.9	43.7	44.4	43.7
Ch-1																	100	99.6	98.6	97.8	98.9	43.9	43.9	43.9	43.7
Ch-2																		100	98.9	98.2	99.3	44	44	44.1	43.9
Ch-3																			100	98.6	98.9	44.2	44.2	44.3	44
Ch-4																				100	98.2	44.6	44.6	44.7	44.4
Ch-5																					100	44	44	44.1	43.9
Ik-1																						100	99.8	98.7	99.4
Ik-2																							100	98.9	99.6
Ik-6																								100	98.5
Ik-7																									100



The *T. sergenti* Chitose clones had full ITS 1-5.8S-ITS 2 gene regions ranging from 1064 to 1067 bp. The ITS 1 region ranged from 628 to 631 bp, the 5.8S gene was 159 bp, and the ITS 2 region was 277 bp in length. Pairwise comparisons between clones ranged from 97.9 to 99.4% identity for the full ITS 1-5.8S-ITS 2 gene region, 97.8 to 100% for ITS 1 region, 97.5 to 98.7% for the 5.8S gene, and 97.8 to 99.6% for the ITS 2 region. The pairwise comparisons between the *T. buffeli* isolates and *T. sergenti* Chitose for the ITS 1-5.8S-ITS 2 gene region ranged from 92.3 to 94.5% identity, 90.2 to 93% identity in the ITS 1 region, 97.5 to 99.4% identity in the 5.8S gene, and 93.5 to 95.3% identity in the ITS 2 region. The pairwise comparison values among clones are shown in Tables 10 to 13.

The *T. sergenti* Ikeda clones had full ITS 1-5.8S-ITS 2 gene regions ranging from 2306 to 2312 bp. The ITS 1 region ranged from 1628 to 1634 bp, the 5.8S gene was 153 bp, and the ITS 2 region was 525 bp in length. Pairwise comparisons between cloned genes of the *T. sergenti* Ikeda clones ranged from 96.7 to 98% identity for the full ITS 1-5.8S-ITS 2 gene region, 95.5 to 98.8% identity for the ITS 1 region, and 98.5 to 99.8% identity for the ITS 2 region. The 5.8S genes of the *T. sergenti* Ikeda clones were all identical. The pairwise comparisons between *T. sergenti* Ikeda and Chitose isolates for the full ITS 1-5.8S-ITS 2 gene region ranged from 35.9 to 36.6% identity, 27.6 to 28.5% identity for the ITS 1 region, 93.7 to 94.3% identity for the 5.8S gene, and 43.7 to 44.7% identity for the ITS 2 region. The pairwise comparisons between the *T. sergenti* Ikeda and *T. buffeli* isolates for the full ITS 1-5.8S-ITS 2 gene region ranged from 36.2 to 36.9% identity, 28.5 to 29% identity for the ITS 1 region, 94.3 to 95% identity for the

5.8S gene, and 43.1 to 44.5% identity for the ITS 2 region. The pairwise comparison values among clones are shown in Tables 10 to 13.

The *T. mutans* Intona clones had a full ITS 1-5.8S-ITS 2 gene region that was 1104 bp with the ITS 1 region 598 bp, the 5.8S gene 159 bp, and the ITS 2 region 347 bp in length. The pairwise comparisons among the *T. mutans* clones ranged from 99.5 to 99.8% identity for the full ITS 1-5.8S-ITS 2 gene regions, 99.7% identity for the ITS 1 region, 96.9 to 100% identity for the 5.8S gene, and 94.4 to 100% identity for the ITS 2 region. The pairwise comparisons between *T. mutans* Intona and *T. buffeli* ranged from 54 to 55% identity for the full ITS 1-5.8S-ITS 2 gene regions, 46 to 47.9% identity for the ITS 1 region, 96.9 to 98.1% identity for the 5.8S gene, and 49.4 to 50.9% identity for the ITS 2 region. *Theileria mutans* Intona and *T. sergenti* Chitose pairwise comparisons regions ranged from 53.7 to 54.7% identity for the full ITS 1-5.8S-ITS 2 gene region, 46 to 46.9% identity for the ITS 1 region, 96.2 to 97.5% identity for the 5.8S gene, and 49.7 to 50.9% identity for the ITS 2 region. The pairwise comparisons for *T. mutans* Intona and *T. sergenti* Ikeda ranged from 35.4 to 35.9% identity for the full ITS 1-5.8S-ITS 2 gene region, 27.1 to 27.9% identity for the ITS 1 region, 92.5 to 93.1% identity for the 5.8S gene, and 43.7 to 44.6% identity for the ITS 2 region. The pairwise comparison values among *T. mutans* Intona clones are shown in Tables 10 to 13.

*Theileria annulata* Turkey isolate 1 clones had full ITS 1-5.8S-ITS 2 gene regions ranging from 927 to 946 bp in length, with the ITS 1 region 492 to 512 bp, the 5.8S gene 159 bp and the ITS 2 region 258 to 276 bp in length. The pairwise comparisons ranged from 87.3 to 94.6% identity for the full ITS 1-5.8S-ITS 2 gene regions, 88 to 95.5% identity for the ITS 1 region, 98.7 to 100% identity for the 5.8S gene and 79.5 to 92.8%

for the ITS 2 region among clones. Turkey 1 clones (2, 3, 13 and 14) pairwise comparisons to each other and to clones of the other *T. annulata* isolates can be found in Tables 14 to 17.

The *T. annulata* Turkey isolate 2 clones had full ITS 1-5.8S-ITS 2 gene regions ranging from 918 to 1018 bp, with the ITS 1 region being 482 to 509 bp, the 5.8S gene was 159 bp, and the ITS 2 region was 273 to 354 bp in length. The pairwise comparisons among the isolate 2 clones (3, 5, 7, 11, 12 and 13) for the full ITS 1-5.8S-ITS 2 gene regions ranged from 85.6 to 99.9% identity, 85.5 to 100% identity for the ITS 1 region, 98.7 to 100% identity for the 5.8S gene, and 74.3 to 100% identity for the ITS 2 region. The pairwise comparison values for these clones can be found in Tables 14 to 17.

The *T. annulata* Turkey isolate 3 clones (3, 6, 8 and 9) had full ITS 1-5.8S-ITS 2 gene regions of 928 to 996 bp, including ITS 1 regions of 493 to 511 bp, 5.8S genes of 159 bp, and ITS 2 regions of 264 to 326 bp. The pairwise comparisons among clones ranged from 84.5 to 100% identity for the full ITS 1-5.8S-ITS 2 gene regions, 88.9 to 100% identity for the ITS 1 region, 100% identity for the 5.8S gene, and 70.5 to 100% identity for the ITS 2 region. Pairwise comparison values for these clones can be found in Tables 14 to 17.

The *T. annulata* Turkey isolate 5 clones (7, 8, 11, 12, and 13) had full ITS 1-5.8S-ITS 2 gene regions of 921 to 1004 bp in length, with ITS 1 regions of 488 or 506 bp, 5.8S genes of 159 bp, and ITS 2 regions of 274 to 339 bp. The pairwise comparisons ranged from 86.3 to 99.8% identity for the full ITS 1-5.8S-ITS 2 gene region, 88.1 to 100% identity for ITS 1 region, 98.7 to 100% identity for the 5.8S gene, and 75.9 to 99.6% identity for

Table14

*Theileria annulata* ITS 1-5.8S-ITS 2 gene region pairwise comparisons.

	1-2	1-3	1-13	1-14	2-3	2-5	2-7	2-11	2-12	2-13	3-3	3-6	3-8	3-9	5-7	5-8	5-12	5-13	6-11	6-18	6-24	7-7	7-13	7-18
1-2	100	87.3	89.9	88	87.9	87.6	87.7	84.5	84.4	86.2	87.6	89	87.6	91.1	87.2	87.2	87.2	84.6	90.3	87.2	88.2	86.1	87.9	85.8
1-3		100	92.2	94.6	90.6	94	94.1	87.5	87.4	91.5	87.3	92.3	87.3	91	91.6	92.5	91.3	89.8	93.2	90.3	92.7	88.5	91.2	85.1
1-13			100	91.8	90.6	91.8	91.9	86.5	86.4	90.2	89	90.3	89	93.9	89.7	91.8	89.7	87.1	90.8	90.3	90.9	85.3	90.4	87.8
1-14				100	90.4	93.5	93.6	86.8	86.7	91.9	86.9	92.4	86.9	91.1	91.9	91.8	91.8	89.5	92.7	90.4	93.6	87.4	92.5	85
2-3					100	90	90.1	85.7	85.6	88.8	84.5	92.3	84.5	88.9	92.3	90.8	92.3	86.1	92.5	91.6	92.5	85.9	92.8	82.9
2-5						100	99.9	87.5	87.4	90.5	86.8	90.6	86.8	93.1	91.9	93.2	91.9	88	92.5	90.4	92	86.2	91.1	85.8
2-7							100	87.6	87.5	90.6	86.9	90.7	86.9	93.2	92	93.3	92	88.1	92.6	90.5	92.1	86.3	91.2	85.9
2-11								100	99.9	88.5	91.8	85.9	91.8	86	85.6	89.4	85.6	93.5	86.1	84.3	86.7	91.1	85.5	93.2
2-12									100	88.4	91.7	85.8	91.7	86	85.5	89.3	85.5	93.4	86	84.2	86.6	91	85.4	93.1
2-13										100	87.7	89.7	87.7	89.1	88.9	92.2	88.9	89.2	89.7	88.8	90.9	86	89.9	87.2
3-3											100	84.5	100	88.5	85.7	87.9	85.7	92.1	85.4	85.8	84.9	91.1	84.6	93.1
3-6												100	84.5	89.4	90.1	90.8	90	87.6	94.1	89.8	95.1	88	95.1	83.3
3-8													100	88.5	85.7	87.9	85.7	92.1	85.4	85.8	84.9	91.1	84.6	93.1
3-9														100	89.8	92.1	89.8	85.8	90.9	88.8	90.3	83.5	89.4	87.2
5-7															100	90.3	99.8	86.3	91.1	93.5	90	84.3	89.1	82.7
5-8																100	90.3	89	91.9	89.5	91.6	86	90.3	87.4
5-12																	100	86.3	91.1	93.5	90	84.4	89.3	82.7
5-13																		100	87.6	85.3	88.6	93.5	87.7	90.6
6-11																			100	90.2	93.4	87.2	93.4	83.6
6-18																				100	90.3	84.2	89	83.3
6-24																					100	88.4	94.6	83.7
7-7																						100	87.1	89.2
7-13																							100	83.4
7-18																								100

Table 15

*Theileria annulata* ITS 1 region pairwise comparisons.

	1-2	1-3	1-13	1-14	2-3	2-5	2-7	2-11	2-12	2-13	3-3	3-6	3-8	3-9	5-7	5-8	5-12	5-13	6-11	6-18	6-24	7-7	7-13	7-18
1-2	100	88	88.3	88.3	87.7	86.9	86.9	89.2	89.2	88.2	88.3	90.9	88.3	88.4	86	87.6	86	88.3	92.3	85.8	89.9	90.2	88.7	88.6
1-3		100	95.5	93.9	88.4	93.9	93.9	94.3	94.3	93.2	95.3	89.9	95.3	91.9	89.2	93.7	89.2	95.3	91.9	89.6	91.3	93.1	89.2	93.9
1-13			100	93	89	92.9	92.9	94.5	94.5	93.6	93.9	90.3	93.9	92.9	88.3	95.1	88.3	94.1	90.7	88.3	91.7	91.3	89.6	95.3
1-14				100	87.2	92	92	92.8	92.8	93	93.8	88.5	93.8	93	89.3	92.4	89.3	93.4	90.8	88.5	91.2	89.1	88.9	93
2-3					100	85.5	85.5	87.8	87.8	87.5	87.4	89	87.4	86.9	88.2	87.8	88.2	87.8	89.6	88.6	89.5	87.8	89.7	87.6
2-5						100	100	92.9	92.9	92	91.7	87.4	91.7	93.9	87.4	93.7	87.4	93.3	90	87.1	90	88.6	89.1	93.1
2-7							100	92.9	92.9	92	91.7	87.4	91.7	93.9	87.4	93.7	87.4	93.3	90	87.1	90	88.6	89.1	93.1
2-11								100	100	93.2	92.4	90.1	92.4	93.1	89	93.5	89	93.7	90.1	87.3	91.9	89.6	89.4	93.1
2-12									100	93.2	92.4	90.1	92.4	93.1	89	93.5	89	93.7	90.1	87.3	91.9	89.6	89.4	93.1
2-13										100	94.4	88.2	94.4	92.8	89.1	93.2	89.1	92.8	90.8	88.9	90.9	89.7	88.7	93.9
3-3											100	88.9	100	91.7	90	92.8	90	93	90	90	90.4	91	88.9	92.8
3-6												100	88.9	89.4	85.7	89.3	85.7	89.6	94	86.6	92.6	90.2	92.8	89.3
3-8													100	91.7	90	92.8	90	93	90	90	90.4	91	88.9	92.8
3-9														100	88.3	94.1	88.3	92.5	90.5	86.8	91	88.3	90	92.9
5-7															100	88.1	100	88.9	87.5	92.7	85.7	85.7	84.5	88.4
5-8																100	88.1	94.7	90.5	87.4	90.9	88.6	89.2	94.1
5-12																	100	88.9	87.5	92.7	85.7	85.7	84.5	88.4
5-13																		100	91.3	88.7	91.1	90	89.6	93.7
6-11																			100	87.6	93.2	91	93	90.3
6-18																				100	87.8	86.4	85.5	87.9
6-24																					100	91.8	92.4	90.7
7-7																						100	88.6	90
7-13																							100	89.6
7-18																								100

Table 16

*Theileria annulata* 5.8S gene pairwise comparisons.

	1-2	1-3	1-13	1-14	2-3	2-5	2-7	2-11	2-12	2-13	3-3	3-6	3-8	3-9	5-7	5-8	5-12	5-13	6-11	6-18	6-24	7-7	7-13	7-18
1-2	100	99.4	98.7	99.4	99.4	98.7	99.4	99.4	98.7	98.7	99.4	99.4	99.4	99.4	99.4	98.7	98.7	99.4	99.4	98.7	99.4	98.7	99.4	99.4
1-3		100	99.4	100	100	99.4	100	100	99.4	99.4	100	100	100	100	100	99.4	99.4	100	100	99.4	100	99.4	100	100
1-13			100	99.4	99.4	98.7	99.4	99.4	98.7	98.7	99.4	99.4	99.4	99.4	99.4	98.7	98.7	99.4	99.4	98.7	99.4	98.7	99.4	99.4
1-14				100	100	99.4	100	100	99.4	99.4	100	100	100	100	100	99.4	99.4	100	100	99.4	100	99.4	100	100
2-3					100	99.4	100	100	99.4	99.4	100	100	100	100	100	99.4	99.4	100	100	99.4	100	99.4	100	100
2-5						100	99.4	99.4	98.7	98.7	99.4	99.4	99.4	99.4	99.4	98.7	98.7	99.4	99.4	98.7	99.4	98.7	99.4	99.4
2-7							100	100	99.4	99.4	100	100	100	100	100	99.4	99.4	100	100	99.4	100	99.4	100	100
2-11								100	99.4	99.4	100	100	100	100	100	99.4	99.4	100	100	99.4	100	99.4	100	100
2-12									100	98.7	99.4	99.4	99.4	99.4	99.4	98.7	98.7	99.4	99.4	98.7	99.4	98.7	99.4	99.4
2-13										100	99.4	99.4	99.4	99.4	99.4	98.7	98.7	99.4	99.4	98.7	99.4	98.7	99.4	99.4
3-3											100	100	100	100	100	99.4	99.4	100	100	99.4	100	99.4	100	100
3-6												100	100	100	100	99.4	99.4	100	100	99.4	100	99.4	100	100
3-8													100	100	100	99.4	99.4	100	100	99.4	100	99.4	100	100
3-9														100	100	99.4	99.4	100	100	99.4	100	99.4	100	100
5-7															100	99.4	99.4	100	100	99.4	100	99.4	100	100
5-8																100	98.7	99.4	99.4	98.7	99.4	98.7	99.4	99.4
5-12																	100	99.4	99.4	98.7	99.4	98.7	99.4	99.4
5-13																		100	100	99.4	100	99.4	100	100
6-11																			100	99.4	100	99.4	100	100
6-18																				100	99.4	100	99.4	99.4
6-24																					100	99.4	100	100
7-7																						100	99.4	99.4
7-13																							100	100
7-18																								100

Table 17

*Theileria annulata* ITS 2 region pairwise comparisons.

	1-2	1-3	1-13	1-14	2-3	2-5	2-7	2-11	2-12	2-13	3-3	3-6	3-8	3-9	5-7	5-8	5-12	5-13	6-11	6-18	6-24	7-7	7-13	7-18
1-2	100	79.5	87.7	81.4	82.1	82.6	82.6	71.2	71.2	76.5	80.1	80.3	80.1	91.3	82.6	80.6	83	72.1	81.8	83.2	79.2	74.2	80.3	75.4
1-3		100	82	92.8	89.4	91	91	72.2	72.2	83.7	69.4	92.2	69.4	84.2	91	86.7	90.6	76.9	91.8	86.4	91.8	76.6	89.7	66.3
1-13			100	85.1	88.5	85.8	85.8	69.2	69.2	80	76.1	85	76.1	92.5	86.9	82.1	87.3	71	85.9	89	84.6	70	86.1	71.6
1-14				100	91.8	92.8	92.8	72.4	72.4	86	70.3	95.3	70.3	82.4	92	86.6	92	78.8	92.1	88.8	94.3	79.4	95	66.9
2-3					100	92.8	92.8	76.3	76.3	85.3	72.7	93.9	72.7	86.2	95	91.4	95.3	77.1	93.2	92.4	93.5	76.8	94.3	68.7
2-5						100	100	74.3	74.3	83.7	73.3	91.4	73.3	88	96	89.3	96.4	75.4	93.1	91.7	90.7	76.8	90.7	68.7
2-7							100	74.3	74.3	83.7	73.3	91.4	73.3	88	96	89.3	96.4	75.4	93.1	91.7	90.7	76.8	90.7	68.7
2-11								100	100	77	87.3	73.6	87.3	69.8	74.3	79.1	74.6	90.2	74.1	73.2	73.3	89.6	73.6	90.2
2-12									100	77	87.3	73.6	87.3	69.8	74.3	79.1	74.6	90.2	74.1	73.2	73.3	89.6	73.6	90.2
2-13										100	72.3	87	72.3	77.4	82.9	87	88.3	79.1	82.8	83.3	86.6	74.9	87	72.1
3-3											100	70.5	100	78	72.4	75.1	72.7	87.1	71.7	72.8	69.9	87.4	70.8	90.4
3-6												100	70.5	83.3	92.5	88.7	92.5	78.9	91.1	90	96.8	79.4	96.4	67.5
3-8													100	78	72.4	75.1	72.7	87.1	71.7	72.8	69.9	87.4	70.8	90.4
3-9														100	86.7	84.6	87.1	69.3	86.5	86.5	83.6	69.1	82.3	72.8
5-7															100	89.3	99.6	75.9	93.5	91.7	92.1	75.8	91.4	67
5-8																100	89.7	75.9	90.1	88.3	88.4	76.4	87.4	72.6
5-12																	100	76.2	93.9	92.1	92.5	76.5	92.1	67.3
5-13																		100	76.3	73.5	79.4	95.9	79.4	82
6-11																			100	89.6	90.1	76	90.4	67.1
6-18																				100	89.6	73.5	89.6	69.6
6-24																					100	78.2	95.4	66.7
7-7																						100	79.1	83.6
7-13																							100	67.4
7-18																								100

the ITS 2 region. The pairwise comparison values for Turkey 5 clones can be found in Tables 14 to 17.

*Theileria annulata* Turkey isolate 6 clones (11, 18, and 24) had full ITS 1-5.8S-ITS 2 gene regions of 915 to 935 bp, with ITS 1 regions of 486 to 498 bp, 5.8S genes of 159 bp, and ITS 2 regions of 270 to 278 bp. The pairwise comparisons for these clones ranged from 90.2 to 93.4% identity for the full ITS 1-5.8S-ITS 2 gene regions, 87.6 to 93.2% identity for ITS 1 region, 99.4 to 100% identity for the 5.8S gene, and 89.6 to 90.1% identity for ITS 2 region. The pairwise comparison values for these clones can be found in Tables 14 to 17.

Turkey 7 *T. annulata* clones (7, 13, and 18) had full ITS 1-5.8S-ITS 2 gene regions of 935 to 1008 bp in length, which included 490 to 504 bp ITS 1 regions, 159 bp 5.8S genes, and 279 to 339 bp ITS 2 regions. The pairwise comparisons of these clones ranged from 83.4 to 89.2% identity for the full ITS 1-5.8S-ITS 2 gene regions, 88.6 to 90% identity for the ITS 1 region, 99.4 to 100% identity in the 5.8S gene, and 67.4 to 83.6% identity in the ITS 2 region. The pairwise comparison values for *T. annulata* Turkey 7 clones can be found in Tables 14 to 17.

Comparisons among the Elazig, Turkey *T. annulata* isolates 1, 2 and 3 resulted in percent identities of 84.4 to 94.1 for the full ITS 1-5.8S-ITS 2 gene region, 85.5 to 95.3 for the ITS 1 region, 98.7 to 100 for the 5.8S gene, and 69.2 to 93.9 for the ITS 2 region. Similarly, comparisons among the Malatya, Turkey *T. annulata* isolates 5, 6 and 7 resulted in full ITS 1-5.8S-ITS 2 gene region identities ranging from 82.7 to 94.6%, 84.5 to 94.1% for the ITS 1 region, 98.7 to 100% for the 5.8S gene, and 66.7 to 95.9% for the ITS 2 region. The full ITS 1-5.8S-ITS 2 gene regions between the Elazig *T. annulata*



isolates and Malatya isolates ranged from 82.7 to 95.1%, 85.5 to 94.4% for the ITS 1 region, 98.7 to 100% for the 5.8S gene, and 67.5 to 96.8% for the ITS 2 region. Each of these comparisons showed no differences than the clonal comparisons.

*Theileria ovis* Turkey 8 clones (4, 8, and 9) had full ITS 1-5.8S-ITS 2 gene regions ranging from 1356 to 1357 bp, with ITS 1 regions from 763 to 764 bp, 5.8S genes of 159 bp, and ITS 2 regions of 434 bp. The pairwise comparisons among these clones ranged from 99.3 to 99.5% identity for the full ITS 1-5.8S-ITS 2 gene regions, 99.5 to 99.7% identity for ITS 1 region, 98.1 to 99.4% identity for the 5.8S gene, and 98.8 to 99.5% identity for ITS 2 region. *Theileria ovis* 9 clones (10, 11, 12, 13 and 14) had full ITS 1-5.8S-ITS 2 gene regions of 1344 to 1357 bp, which included a 751 to 764 bp ITS 1 region, a 159 bp 5.8S gene, and a 434 bp ITS 2 region. The pairwise comparison identities for these clones ranged from 98.2.9 to 99.9% for the full ITS 1-5.8S-ITS 2 gene region, and 97 to 99.9% for the ITS 1 region, 99.4 to 100% for the 5.8S gene, and 99.3 to 99.8% for the ITS 2 region. *Theileria ovis* 11 clones (1, 2 and 5) had full ITS 1-5.8S-ITS 2 gene regions of 1357 bp, and 764 bp ITS 1 regions, 159 bp 5.8S genes, and 434 bp ITS 2 regions. The percent identities among the clones were 99.5 to 99.7 for the full ITS 1-5.8S-ITS 2 gene region, 99.6 to 99.9 for the ITS 1 region, 99.4 for the 5.8S gene, and 99.3 to 99.5 for the ITS 2 region. All the pairwise comparison values for the *T. ovis* clones can be found in Tables 18 to 21.

The dama gazelle *Theileria* sp. clones (10 -14) had full length ITS 1-5.8S-ITS 2 gene regions of 670 to 688 bp, with ITS 1 regions of 305 to 310 bp, 5.8S genes of 158 bp, and ITS 2 regions of 207 to 220 bp. Percent identities for the clones ranged from 92.9 to 97.9 for the full ITS 1-5.8S-ITS 2 gene region, and 94.5 to 98.4 for ITS 1, 99.4 to 100 for

Table 18

*Theileria ovis* ITS 1-5.8S-ITS 2 gene region pairwise comparisons.

	To8-4	To8-8	To8-9	To9-10	To9-11	To9-12	To9-13	To9-14	To11-1	To11-2	To11-5
To8-4	100	99.3	99.5	98.2	98.2	99.2	98.4	99.5	99.8	99.6	99.7
To8-8		100	99.5	98.2	98	99	98.4	99.5	99.5	99.3	99.4
To8-9			100	98.6	98.2	99.4	98.7	99.7	99.7	99.5	99.6
To9-10				100	99.3	98.3	99.9	98.5	98.5	98.2	98.4
To9-11					100	98.2	99.5	98.2	98.4	98.2	98.3
To9-12						100	98.4	99.3	99.4	99.2	99.3
To9-13							100	98.6	98.6	98.4	98.5
To9-14								100	99.8	99.9	99.7
To11-1									100	99.7	99.5
To11-2										100	99.6
To11-5											100

Table 19

*Theileria ovis* ITS 1 region pairwise comparisons.

	To8-4	To8-8	To8-9	To9-10	To9-11	To9-12	To9-13	To9-14	To11-1	To11-2	To11-5
To8-4	100	99.5	99.7	97.6	97.1	99.1	97.8	99.7	99.9	99.6	99.7
To8-8		100	99.5	97.4	96.9	98.8	97.5	99.5	99.6	99.3	99.5
To8-9			100	97.6	97.1	99.3	97.8	99.7	99.9	99.6	99.7
To9-10				100	99.2	97.5	99.9	97.6	97.8	97.5	97.6
To9-11					100	97	99.3	97.1	97.3	97	97.1
To9-12						100	97.6	99.1	99.2	99	99.1
To9-13							100	97.8	97.9	97.6	97.8
To9-14								100	99.7	99.9	99.6
To11-1									100	99.9	99.6
To11-2										100	99.7
To11-5											100

Table 20

*Theileria ovis* 5.8S gene pairwise comparisons.

	To8-4	To8-8	To8-9	To9-10	To9-11	To9-12	To9-13	To9-14	To11-1	To11-2	To11-5
To8-4	100	98.1	98.8	98.8	99.4	99.4	98.8	98.8	99.4	99.4	99.4
To8-8		100	99.4	99.4	98.7	98.7	99.4	99.4	98.7	98.7	98.7
To8-9			100	100	99.4	99.4	100	100	99.4	99.4	99.4
To9-10				100	99.4	99.4	100	100	99.4	99.4	99.4
To9-11					100	100	99.4	99.4	100	100	100
To9-12						100	99.4	99.4	100	100	100
To9-13							100	100	99.4	99.4	99.4
To9-14								100	100	100	100
To11-1									100	99.4	99.4
To11-2										100	99.4
To11-5											100

Table 21

*Theileria ovis* ITS 2 region pairwise comparisons.

	To8-4	To8-8	To8-9	To9-10	To9-11	To9-12	To9-13	To9-14	To11-1	To11-2	To11-5
To8-4	100	98.8	98.8	98.6	99.3	99.1	99.1	99.1	99.5	99.3	99.5
To8-8		100	99.5	99.3	99.8	99.5	99.5	99.5	99.5	99.3	99.5
To8-9			100	99.8	99.8	99.5	100	99.5	99.5	99.3	99.5
To9-10				100	99.5	99.3	99.8	99.3	99.3	99.1	99.3
To9-11					100	99.8	99.8	99.8	99.8	99.5	99.8
To9-12						100	99.5	99.5	99.5	99.3	99.5
To9-13							100	99.5	99.5	99.3	99.5
To9-14								100	99.8	100	99.8
To11-1									100	99.5	99.3
To11-2										100	99.5
To11-5											100

the 5.8S gene, and 84.4 to 96.2 for the ITS 2 region. The pairwise comparison values can be found in Tables 22 to 25.

*Theileria cervi* WTD 1 clones (16, 17, and 24) had full length ITS 1-5.8S-ITS 2 gene regions of 905 bp, which included a 514 bp ITS 1 region, a 158 bp 5.8S gene, and a 233 bp ITS 2 region. The percent identities for these clones ranged from 99.1 to 100 for the full ITS 1-5.8S-ITS 2 gene regions, 98.8 to 100 for ITS 1 regions, 100 for the 5.8S genes, and 99.1 to 100 for the ITS 2 regions. *Theileria cervi* WTD 2 clones (3, 9, and 10) had full ITS 1-5.8S-ITS 2 gene regions of 904 to 906 bp in length, with ITS 1 regions of 513 to 515 bp, a 158 bp 5.8S gene, and a 233 bp ITS 2 region. The percent identities for WTD 2 clones for the full ITS 1-5.8S-ITS 2 gene regions ranged from 96.9 to 97.5, and 95.9 to 96.7 for ITS 1 regions, 100 for the 5.8S genes, and 97 to 97.4 for the ITS 2 regions. WTD 3 *T. cervi* clones (2, 7, and 8) had full ITS 1-5.8S-ITS 2 gene regions of 905 to 906 bp, with ITS 1 regions of 514 to 515 bp, a 158 bp 5.8S gene, and a 233 bp ITS 2 region. Percent identities for these clones range from 97 to 99.4 for the full ITS 1-5.8S-ITS 2 gene regions, 96.1 to 99.6 for the ITS 1 regions, 100 for the 5.8S gene, and 97 to 98.7 for the ITS 2 regions. WTD 181 *T. cervi* clones (1, 2, and 10) had a full ITS 1-5.8S-ITS 2 gene region of 905 bp with percent identities that ranged from 99 to 99.4 for the full ITS 1-5.8S-ITS 2 gene region; an ITS 1 region that was 514 bp with percent identities from 98.8 to 99.8; a 5.8S gene of 158 bp with percent identities from 99.4 to 100; and a 233 bp ITS 2 region with percent identities from 98.7 to 99.6. WTD 183 *T. cervi* clones had full ITS 1-5.8S-ITS 2 gene regions that were 904 to 906 bp, including a ITS 1 region of 513 to 515 bp, a 158 bp 5.8S gene, and a 233 bp ITS 2 region. *Theileria cervi* WTD 183 clones percent identities ranged from 97.7 to 98.8 for the full ITS 1-5.8S-

Table 22

*Theileria cervi* and *dama gazelle Theileria sp.* ITS 1-5.8S-ITS 2 gene region pairwise comparisons.

	OkE-10	OkE-11	OkE-12	OkE-13	W1-16	W1-17	W1-24	W2-3	W2-9	W2-10	W3-2	W3-7	W3-8	181-1	181-2	181-10	183-5	183-7	
OkE-10	100	99.9	64.5	97.1	99.4	98.8	99.4	97.5	97.1	99.3	97.2	99.3	99.4	99	99.3	99.4	97.2	99.4	
OkE-11		100	64.6	97	99.3	98.7	99.3	97.4	97	99.3	97.1	99.2	99.3	98.9	99.2	99.3	97.1	99.3	
OkE-12			100	64.6	64.8	64.7	64.8	64.3	66.2	64.6	66.3	64.8	64.7	64.9	64.8	64.8	64.2	64.8	
OkE-13				100	97.1	96.8	97.1	98.9	96.8	97	96.9	97	97.1	97	97	97.1	98.2	97.1	
W1-16					100	99.1	100	97.5	97	99.9	97.1	99.9	99.6	99.3	99.4	100	97.7	100	
W1-17						100	99.1	97.2	96.8	99	96.9	99	98.9	99.8	99.8	99.1	97.2	99.1	
W1-24							100	97.5	97	99.9	97.1	99.9	99.6	99.3	99.4	100	97.7	100	
W2-3								100	97.5	97.4	97.6	97.4	97.5	97.5	97.4	97.5	97.8	97.5	
W2-9									100	96.9	99.9	96.9	97	97	96.9	97	96.8	97	
W2-10										100	97	99.8	99.4	99.2	99.3	99.9	97.6	99.9	
W3-2											100	97	97.1	97.1	97	97.1	96.9	97.1	
W3-7												100	99.4	99.2	99.3	99.9	97.6	99.9	
W3-8													100	99.1	99.4	99.6	97.2	99.6	
181-1														100	99	99.3	97.5	99.3	
181-2															100	99.4	97.1	99.4	
181-10																100	97.7	100	
183-5																	100	97.7	
183-7																			100
183-8																			
CanE-1																			
CanE-6																			
CanE-7																			
CanE-8																			
CanE-10																			
CanE-11																			
WisE-3																			
WisE-4																			
WisE-5																			
InE-1																			
InE-2																			
InE-3																			
DG-10																			
DG-11																			
DG-12																			
DG-13																			
DG-14																			

Table 22  
continued

	183-8	CanE-1	CanE-6	CanE-7	CanE-8	CanE-10	CanE-11	WisE-3	WisE-4	WisE-5	InE-1	InE-2	InE-3	DG-10	DG-11	DG-12	DG-13	DG-14
OkE-10	98.8	63.8	63.7	63.8	98.6	98.6	98.3	98.7	98.7	98.7	94.1	94.1	94.2	55.2	55.1	55.2	55.7	56.4
OkE-11	98.7	63.7	63.6	63.7	98.5	98.5	98.2	98.6	98.6	98.6	94	94	94.1	55.2	55.1	55.3	55.7	56.4
OkE-12	65.3	95.2	95	95.1	65.5	65.4	65.1	65.5	65.5	65.5	64.7	65	64.8	52.9	51.7	51.7	51.1	51.3
OkE-13	98	62.6	62.5	62.6	97.8	97.8	97.6	97.9	97.9	97.9	95.8	95.8	95.9	54.7	54.9	55.1	55.4	56
W1-16	98.8	63.6	63.5	63.6	98.7	98.7	98.5	98.8	98.8	98.8	94.1	94.1	94.2	54.9	55	55.1	55.5	56.2
W1-17	98.6	63.6	63.5	63.6	98	98	97.8	98.1	98.1	98.1	94.1	93.9	94	55.3	55.3	55.6	56	56.6
W1-24	98.8	63.6	63.5	63.6	98.7	98.7	98.5	98.8	98.8	98.8	94.1	94.1	94.2	54.9	55	55.1	55.5	56.2
W2-3	98.5	62.7	62.6	62.7	97.2	97.2	97	97.4	97.4	97.4	95.4	95.4	95.5	54.6	54.7	54.9	55.3	55.8
W2-9	98.1	64.5	64.5	64.5	96.7	96.7	96.5	96.8	96.8	96.8	94.7	94.7	94.8	54.7	55	54.9	54.9	55.8
W2-10	98.7	63.4	63.3	63.4	98.6	98.6	98.3	98.7	98.7	98.7	94	94	94.1	55	55	55.1	55.6	56.2
W3-2	98.2	64.6	64.6	64.6	96.8	96.8	96.6	96.9	96.9	96.9	94.8	94.8	95	54.7	55	54.9	54.9	55.8
W3-7	98.7	63.6	63.5	63.6	98.6	98.6	98.3	98.7	98.7	98.7	94	94	94.1	54.9	55	55.1	55.5	56.2
W3-8	98.8	63.5	63.4	63.5	98.7	98.7	98.5	98.8	98.8	98.8	94.1	94.1	94.2	54.8	54.9	54.8	55.5	56.2
181-1	98.8	63.7	63.6	63.7	98.2	98.2	98	98.3	98.3	98.3	94.1	94.1	94.2	55.2	55.2	55.3	55.8	56.5
181-2	98.7	63.6	63.5	63.6	98.6	98.6	98.3	98.7	98.7	98.7	94	94	94.1	54.7	54.8	54.8	55.4	55.9
181-10	98.8	63.6	63.5	63.6	98.7	98.7	98.5	98.8	98.8	98.8	94.1	94.1	94.2	54.9	55	55.1	55.5	56.2
183-5	97.8	62.8	62.7	62.8	97.7	97.7	97.5	97.8	97.8	97.8	95.9	95.9	96	54.6	54.9	54.7	55.1	56.3
183-7	98.8	63.6	63.5	63.6	98.7	98.7	98.5	98.8	98.8	98.8	94.1	94.1	94.2	54.9	55	55.1	55.5	56.2
183-8	100	63.4	63.3	63.4	98.6	98.6	98.3	98.7	98.7	98.7	95.2	95.2	95.3	54.9	55	54.9	55.2	56.3
CanE-1		100	99.8	99.9	63.7	63.6	63.4	63.5	63.5	63.5	64.2	64.2	64.2	51.2	50.6	50.6	50.6	50.5
CanE-6			100	99.7	63.6	63.5	63.3	63.4	63.4	63.4	64.2	64.2	64.2	51.1	50.9	50.4	50.4	50.4
CanE-7				100	63.7	63.6	63.4	63.5	63.5	63.5	64.2	64.2	64.2	51.2	50.6	50.6	50.6	50.5
CanE-8					100	99.8	99.6	99.9	99.9	99.9	94.8	94.8	95	54.9	55.1	55.2	55.7	56.2
CanE-10						100	99.6	99.9	99.9	99.9	94.8	94.8	95	55	55.2	55.3	55.8	56.5
CanE-11							100	99.7	99.7	99.7	94.6	94.6	94.7	54.9	55.2	54.8	55.3	56.2
WisE-3								100	100	100	95	95	95.1	55	55.2	55.3	55.8	56.4
WisE-4									100	100	95	95	95.1	55	55.2	55.3	55.8	56.4
WisE-5										100	95	95	95.1	55	55.2	55.3	55.8	56.4
InE-1											100	99.6	99.6	54.7	54.6	54.6	54.5	55.7
InE-2												100	99.6	54.4	54.8	54.5	54.6	55.7
InE-3													100	54.4	54.6	54.5	54.7	55.7
DG-10														100	94.8	94.2	93.9	92.9
DG-11															100	97.9	96.3	95
DG-12																100	97.6	95.3
DG-13																	100	95.3
DG-14																		100

Table 23

*Theileria cervi* and dama gazelle *Theileria* sp. ITS 1 gene region pairwise comparisons.

	OkE-10	OkE-11	OkE-12	OkE-13	W1-16	W1-17	W1-24	W2-3	W2-9	W2-10	W3-2	W3-7	W3-8	181-1	181-2	181-10	183-5	183-7
OkE-10	100	99.8	63.4	95	99.4	98.2	99.4	96.3	95.9	99.2	96.1	99.2	99.2	98.4	99.2	99.4	95.7	99.4
OkE-11		100	63.4	95.3	99.2	98.1	99.2	96.1	95.7	99.2	95.9	99	99	98.2	99	99.2	95.5	99.2
OkE-12			100	61.9	63.6	63.6	63.6	62.9	64.9	63.2	65.1	63.6	63.4	63.7	63.4	63.6	62.3	63.6
OkE-13				100	95.9	95.3	95.9	98.6	95.3	95.7	95.5	95.7	95.7	95.5	95.7	95.9	97.7	95.9
W1-16					100	98.8	100	96.7	96.1	99.8	96.3	99.8	99.8	99	99.8	100	96.1	100
W1-17						100	98.8	96.3	95.7	98.6	95.9	98.6	98.6	99.8	98.6	98.8	95.7	98.8
W1-24							100	96.7	96.1	99.8	96.3	99.8	99.8	99	99.8	100	96.1	100
W2-3								100	96.7	96.5	96.9	96.5	96.5	96.5	96.5	96.7	97.5	96.7
W2-9									100	95.9	99.8	95.9	95.9	95.9	95.9	96.1	95.9	96.1
W2-10										100	96.1	99.6	99.6	98.8	99.6	99.8	95.9	99.8
W3-2											100	96.1	96.1	96.1	96.1	96.3	96.1	96.3
W3-7												100	99.6	98.8	99.6	99.8	95.9	99.8
W3-8													100	98.8	99.6	99.8	95.9	99.8
181-1														100	98.8	99	95.9	99
181-2															100	99.8	95.9	99.8
181-10																100	96.1	100
183-5																	100	96.1
183-7																		100
183-8																		
CanE-1																		
CanE-6																		
CanE-7																		
CanE-8																		
CanE-10																		
CanE-11																		
WisE-3																		
WisE-4																		
WisE-5																		
InE-1																		
InE-2																		
InE-3																		
DG-10																		
DG-11																		
DG-12																		
DG-13																		
DG-14																		

Table 23  
continued

	183-8	CanE-1	CanE-6	CanE-7	CanE-8	CanE-10	CanE-11	WisE-3	WisE-4	WisE-5	InE-1	InE-2	InE-3	DG-10	DG-11	DG-12	DG-13	DG-14
OkE-10	98.2	63.6	63.6	63.6	98.4	98.2	98.1	98.4	98.4	98.4	95.2	95	95	45.3	44.9	45.1	45.5	46.4
OkE-11	98.1	63.4	63.4	63.4	98.2	98.1	97.9	98.2	98.2	98.2	95	94.8	94.8	45.3	44.9	45.1	45.5	46.4
OkE-12	63.2	96.3	96.3	96.1	63.4	63.2	62.8	63.4	63.4	63.4	62.1	61.9	61.9	46.4	45.8	45.2	44.5	45.9
OkE-13	96.7	61.5	61.5	61.5	96.5	96.3	96.1	96.5	96.5	96.5	97.9	97.7	97.7	44.9	44.6	44.9	45.1	45.9
W1-16	98.6	63.3	63.3	63.3	99	98.8	98.6	99	999	99	95.5	95.3	95.3	45	44.6	44.8	45.2	46.2
W1-17	98.2	63.5	63.5	63.5	97.9	97.7	97.5	97.9	97.9	97.9	95.2	95	95	45.7	45.3	45.7	46.1	46.8
W1-24	98.6	63.3	63.3	63.3	99	98.8	98.6	99	99	99	95.5	95.3	95.3	45	44.6	44.8	45.2	46.2
W2-3	97.7	62.2	62.2	62.2	96.1	95.9	95.7	96.1	96.1	96.1	97.7	97.5	97.5	44.7	44.4	44.7	44.9	45.7
W2-9	97.5	64.8	64.8	64.8	95.5	95.3	95.1	95.5	95.5	95.5	95.7	95.5	95.5	44.5	44.7	44.9	45.1	46.2
W2-10	98.4	62.9	62.9	62.9	98.8	98.6	98.4	98.8	98.8	98.8	95.3	95.2	95.2	45.1	44.7	44.9	45.3	46.3
W3-2	97.7	65	65	65	95.7	95.5	95.3	95.7	95.7	95.7	95.9	95.7	95.7	44.5	44.7	44.9	45.1	46.2
W3-7	98.4	63.3	63.3	63.3	98.8	98.6	98.4	98.8	98.8	98.8	95.3	95.2	95.2	45	44.6	44.8	45.2	46.2
W3-8	98.4	63.1	63.1	63.1	98.8	98.6	98.4	98.8	98.8	98.8	95.3	95.2	95.2	44.8	44.4	44.6	45	46
181-1	98.4	63.5	63.5	63.5	98.1	97.9	97.7	98.1	98.1	98.1	95.3	95.2	95.2	45.7	45.3	45.5	45.9	46.8
181-2	98.4	63.1	63.1	63.1	98.8	98.6	98.4	98.8	98.8	98.8	95.3	95.2	95.2	44.8	44.8	44.7	45.4	46
181-10	98.6	63.3	63.3	63.3	99	98.8	98.6	99	99	99	95.3	95.3	95.3	45	44.6	44.8	45.2	46.2
183-5	97.1	61.9	61.9	61.9	97.1	96.9	96.7	97.1	97.1	97.1	98.6	98.4	98.4	44.9	44.4	44.1	44.3	46.2
183-7	98.6	63.3	63.3	63.3	99	98.8	98.6	99	99	99	95.5	95.3	95.3	45	44.6	44.8	45.2	46.2
183-8	100	62.9	62.9	62.9	98.1	97.9	97.7	98.1	98.1	98.1	96.9	96.7	96.7	45.3	42.6	44.8	42.7	45.2
CanE-1		100	100	99.8	62.9	62.8	62.6	62.9	62.9	62.9	61.6	61.4	61.9	45.6	45.6	45.2	45	46.4
CanE-6			100	99.8	62.9	62.8	62.6	62.9	62.9	62.9	61.6	61.4	61.9	45.6	45.6	45.2	45	46.4
CanE-7				100	62.9	62.8	62.6	62.9	62.9	62.9	61.6	61.4	61.9	45.6	45.6	45.2	45	46.4
CanE-8					100	99.8	99.6	100	100	100	96.5	96.3	96.3	45.5	45.1	45.3	45.7	46.4
CanE-10						100	99.4	99.8	99.8	99.8	96.3	96.1	96.1	45.5	45.1	45.3	45.7	46.6
CanE-11							100	99.6	99.6	99.6	96.1	95.9	95.9	45.6	45.2	44.6	45	46.3
WisE-3								100	100	100	96.5	96.3	96.3	45.5	45.1	45.3	45.7	46.4
WisE-4									100	100	96.5	96.3	96.3	45.5	45.1	45.3	45.7	46.4
WisE-5										100	96.5	96.3	96.3	45.5	45.1	45.3	45.7	46.4
InE-1											100	99.8	99.8	44.8	44.4	44.4	44.6	46.2
InE-2												100	99.6	44.8	44.7	44.4	44.6	46.2
InE-3													100	44.8	44.4	44.4	44.6	46.2
DG-10														100	98.4	96.1	94.8	95.2
DG-11															100	96.4	95.7	95.2
DG-12																100	97.7	94.8
DG-13																	100	94.5
DG-14																		100



Table 24

*Theileria cervi* and dama gazelle *Theileria* sp. 5.8S gene pairwise comparisons.

	OkE-10	OkE-11	OkE-12	OkE-13	W1-16	W1-17	W1-24	W2-3	W2-9	W2-10	W3-2	W3-7	W3-8	181-1	181-2	181-10	183-5	183-7
OkE-10	100	100	90.6	99.4	100	100	100	100	100	100	100	100	100	100	99.4	100	100	100
OkE-11		100	90.6	99.4	100	100	100	100	100	100	100	100	100	100	99.4	100	100	100
OkE-12			100	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6	91.2	90.6	90.6	90.6
OkE-13				100	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	98.8	99.4	99.4	99.4
W1-16					100	100	100	100	100	100	100	100	100	100	99.4	100	100	100
W1-17						100	100	100	100	100	100	100	100	100	99.4	100	100	100
W1-24							100	100	100	100	100	100	100	100	99.4	100	100	100
W2-3								100	100	100	100	100	100	100	99.4	100	100	100
W2-9									100	100	100	100	100	100	99.4	100	100	100
W2-10										100	100	100	100	100	99.4	100	100	100
W3-2											100	100	100	100	99.4	100	100	100
W3-7												100	100	100	99.4	100	100	100
W3-8													100	100	99.4	100	100	100
181-1														100	99.4	100	100	100
181-2															100	99.4	99.4	99.4
181-10																100	100	100
183-5																	100	100
183-7																		100
183-8																		
CanE-1																		
CanE-6																		
CanE-7																		
CanE-8																		
CanE-10																		
CanE-11																		
WisE-3																		
WisE-4																		
WisE-5																		
InE-1																		
InE-2																		
InE-3																		
DG-10																		
DG-11																		
DG-12																		
DG-13																		
DG-14																		

Table 24  
continued

	183-8	CanE-1	CanE-6	CanE-7	CanE-8	CanE-10	CanE-11	WisE-3	WisE-4	WisE-5	InE-1	InE-2	InE-3	DG-10	DG-11	DG-12	DG-13	DG-14
OkE-10	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
OkE-11	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
OkE-12	90.6	99.4	98.8	99.4	90.6	90.6	90	90.6	90.6	90.6	90.6	90.6	90.6	86.9	86.9	86.9	87.5	86.9
OkE-13	99.4	91.2	90.6	91.2	98.8	99.4	98.8	99.4	99.4	99.4	99.4	99.4	99.4	94.4	94.4	94.4	95	94.4
W1-16	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
W1-17	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
W1-24	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
W2-3	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
W2-9	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
W2-10	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
W3-2	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
W3-7	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
W3-8	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
181-1	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
181-2	99.4	91.9	91.2	91.9	98.7	99.4	98.7	99.4	99.4	99.4	99.4	99.4	99.4	94.3	94.3	94.3	95	94.3
181-10	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
183-5	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
183-7	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
183-8	100	91.2	90.6	91.2	99.4	100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
CanE-1		100	99.4	100	91.2	91.2	90.6	91.2	91.2	91.2	91.2	91.2	91.2	87.5	87.5	87.5	88.1	87.5
CanE-6			100	99.4	90.6	90.6	90	90.6	90.6	90.6	90.6	90.6	90.6	86.9	86.9	86.9	87.5	86.9
CanE-7				100	91.2	91.2	90.6	91.2	91.2	91.2	91.2	91.2	91.2	87.5	87.5	87.5	88.1	87.5
CanE-8					100	99.4	98.7	99.4	99.4	99.4	99.4	99.4	99.4	94.3	94.3	94.3	95	94.3
CanE-10						100	99.4	100	100	100	100	100	100	95	95	95	95.6	95
CanE-11							100	99.4	99.4	99.4	99.4	99.4	99.4	94.3	94.3	94.3	95	94.3
WisE-3								100	100	100	100	100	100	95	95	95	95.6	95
WisE-4									100	100	100	100	100	95	95	95	95.6	95
WisE-5										100	100	100	100	95	95	95	95.6	95
InE-1											100	100	100	95	95	95	95.6	95
InE-2												100	100	95	95	95	95.6	95
InE-3													100	95	95	95	95.6	95
DG-10														100	100	100	99.4	100
DG-11															100	100	99.4	100
DG-12																100	99.4	100
DG-13																	100	99.4
DG-14																		100

Table 25

*Theileria cervi* and dama gazelle *Theileria* sp. ITS 2 region pairwise comparisons.

	OkE-10	OkE-11	OkE-12	OkE-13	W1-16	W1-17	W1-24	W2-3	W2-9	W2-10	W3-2	W3-7	W3-8	181-1	181-2	181-10	183-5	183-7
OkE-10	100	100	53.7	98.3	99.1	99.1	99.1	98.3	97.9	99.1	97.9	99.1	99.6	99.6	99.6	99.1	98.7	99.1
OkE-11		100	54.5	98.3	99.1	99.1	99.1	98.3	97.9	99.1	97.9	99.1	99.6	99.6	99.6	99.1	98.7	99.1
OkE-12			100	56.3	53.4	53.4	53.4	52.8	55.3	53.4	55.3	53.4	53.4	53.4	53.4	53.4	53.5	53.4
OkE-13				100	97.4	97.9	97.4	98.3	97.4	97.4	97.4	97.4	97.9	97.9	97.9	97.4	97.9	97.4
W1-16					100	99.1	100	97.4	97	100	97	100	98.7	99.6	98.7	100	99.6	100
W1-17						100	99.1	97.4	97	99.1	97	99.1	98.7	99.6	98.7	99.1	98.7	99.1
W1-24							100	97.4	97	100	97	100	98.7	99.6	98.7	100	99.6	100
W2-3								100	97.4	97.4	97.4	97.4	97.9	97.9	97.9	97.4	97	97.4
W2-9									100	97	100	97	97.4	97.4	97.4	97	96.6	97
W2-10										100	97	100	98.7	99.6	98.7	100	99.6	100
W3-2											100	97	97.4	97.4	97.4	97	97	98.3
W3-7												100	98.7	99.6	98.7	100	99.6	100
W3-8													100	99.1	99.1	98.7	98.3	98.7
181-1														100	99.1	99.6	99.1	99.6
181-2															100	98.7	98.3	98.7
181-10																100	99.6	100
183-5																	100	99.6
183-7																		100
183-8																		
CanE-1																		
CanE-6																		
CanE-7																		
CanE-8																		
CanE-10																		
CanE-11																		
WisE-3																		
WisE-4																		
WisE-5																		
InE-1																		
InE-2																		
InE-3																		
DG-10																		
DG-11																		
DG-12																		
DG-13																		
DG-14																		

Table 25  
continued

	183-8	CanE-1	CanE-6	CanE-7	CanE-8	CanE-10	CanE-11	WisE-3	WisE-4	WisE-5	InE-1	InE-2	InE-3	DG-10	DG-11	DG-12	DG-13	DG-14
OkE-10	99.1	51.9	51.9	51.9	98.3	98.3	98.3	98.3	98.3	98.3	88.4	88.7	89.1	50.6	51	51	51.4	52.3
OkE-11	99.1	51.9	51.9	51.9	98.3	98.3	98.3	98.3	98.3	98.3	88.4	88.7	89.1	50.6	51	51	51.4	52.3
OkE-12	55.3	91.5	91.2	91.5	55.7	55.7	55.7	56.5	56.5	56.5	56.6	57.5	56.9	46.4	43.6	44.5	43.6	42
OkE-13	99.1	51.9	51.9	51.9	99.1	99.1	99.1	99.1	99.1	99.1	89.1	89.1	89.5	48.4	50	50	50.4	51.2
W1-16	98.3	51.6	51.6	51.6	97.4	97.4	97.4	97.4	97.4	97.4	87.6	87.9	88.3	50.2	51	51	51.4	52.3
W1-17	98.3	51.6	51.6	51.6	97.4	97.4	97.4	97.4	97.4	97.4	88.4	87.9	88.3	50.2	51	51	51.4	52.3
W1-24	98.3	51.6	51.6	51.6	97.4	97.4	97.4	97.4	97.4	97.4	87.6	87.9	88.3	50.2	51	51	51.4	52.3
W2-3	99.1	50.7	50.7	50.7	98.3	98.3	98.3	98.3	98.3	98.3	88	88.3	88.7	49.6	50.8	50.8	51.2	52.1
W2-9	98.3	51.9	52.2	51.9	97.4	97.4	97.4	97.4	97.4	97.4	89.5	89.9	90.3	50.4	51	50.2	49.6	52.1
W2-10	98.3	51.6	51.6	51.6	97.4	97.4	97.4	97.4	97.4	97.4	87.6	87.9	88.3	50.2	51	51	51.4	52.3
W3-2	96.6	51.9	52.2	51.9	97.4	97.4	97.4	97.4	97.4	97.4	89.5	89.9	90.3	50.4	51	50.2	49.6	52.1
W3-7	98.3	51.6	51.6	51.6	97.4	97.4	97.4	97.4	97.4	97.4	87.6	87.9	88.3	50.2	51	51	51.4	52.3
W3-8	98.7	51.6	51.6	51.6	97.9	97.9	97.9	97.9	97.9	97.9	88	88.3	88.7	50.2	51.2	50.6	52	52.8
181-1	98.7	51.6	51.6	51.6	97.9	97.9	97.9	97.9	97.9	97.9	88	88.3	88.7	49.8	50.6	50.6	51	51.9
181-2	98.7	51.6	51.6	51.6	97.9	97.9	97.9	97.9	97.9	97.9	88	88.3	88.7	50.2	50.6	50.6	51	51.9
181-10	98.3	51.6	51.6	51.6	97.4	97.4	97.4	97.4	97.4	97.4	87.6	87.9	88.3	50.2	51	51	51.4	52.3
183-5	97.9	51.7	51.7	51.7	97.9	97.9	97.9	97.9	97.9	97.9	88	87.6	88.8	49.2	51.4	51.4	51.8	52.7
183-7	98.3	51.6	51.6	51.6	97.4	97.4	97.4	97.4	97.4	97.4	88.3	87.9	89.1	50.2	51	51	51.4	52.3
183-8	100	51.6	51.6	51.5	99.1	99.1	99.1	99.1	99.1	99.1	88.7	88.3	89.5	49.4	50.6	50.6	51	51.9
CanE-1		100	99.7	100	51.3	51.3	51.3	52	52	52	56.1	55.9	55.9	42.9	41.1	41.7	41.5	39.5
CanE-6			100	99.7	51.3	51.3	51.3	52	52	52	56.4	56.2	56.2	42.9	42.3	41.4	41.3	39.5
CanE-7				100	51.3	51.3	51.3	52	52	52	56.1	55.9	55.9	42.9	41.1	41.7	41.5	39.5
CanE-8					100	100	100	100	100	100	88.8	89.1	89.5	49.3	51	51	51.4	52.3
CanE-10						100	100	100	100	100	88.8	89.1	89.5	49.4	51	51	51.4	52.3
CanE-11							100	100	100	100	88.8	89.1	89.5	49.4	51	51	51.4	52.3
WisE-3								100	100	100	88.8	88.8	88.8	49.4	51	51	51.4	52.3
WisE-4									100	100	89.1	89.1	89.1	49.4	51	51	51.4	52.3
WisE-5										100	89.5	89.5	89.5	49.4	51	51	51.4	52.3
InE-1											100	98.8	98.8	50.2	49.6	50.4	49.2	51
InE-2												100	99.2	48.9	50.6	50.2	49.8	51
InE-3													100	48.9	50.2	50.2	49.8	51
DG-10														100	86.1	87.4	88.8	84.8
DG-11															100	98.6	94.7	90.9
DG-12																100	96.2	92.3
DG-13																	100	93.3
DG-14																		100

ITS 2 gene regions, 96.1 to 98.6 for the ITS 1 region, 100 for the 5.8S gene, and 97.9 to 99.6 for ITS 2 region. Among the *T. cervi* WTD clones, the full ITS 1-5.8S-ITS 2 gene region percent identities ranged from 96.8 to 100, 95.7 to 100 for the ITS 1 region, 99.4 to 100 for the 5.8S gene, and 96.9 to 100 for the ITS 2 region. The pairwise comparison values among WTD *T. cervi* isolate clones can be found in Tables 22 to 25.

Oklahoma elk *T. cervi* clones had an ITS 1-5.8S-ITS 2 gene region of 902 to 1017 bp, with an ITS 1 region length ranging from 511 to 517 bp, a 5.8S gene length ranging from 158 to 159 bp, and an ITS 2 region length ranging from 233 to 341 bp. The pairwise comparisons for these clones ranged from 64.5 to 99.9% identity for the ITS 1-5.8S-ITS 2 gene region, ranged from 61.9 to 99.8% identity for the ITS 1 region, 90.6 to 100% identity for the 5.8S gene, and 53.7 to 100% identity for the ITS 2 region. The *T. cervi* Canadian elk clones had an ITS 1-5.8S-ITS 2 gene region of 904 to 1017 bp, which included a 513 to 516 bp ITS 1 region, a 5.8S gene of 158 to 159 bp, and an ITS 2 region length of 233 to 340 bp. *Theileria cervi* Canadian elk clones pairwise comparisons that ranged from 63.3 to 99.9% identity for the ITS 1-5.8S-ITS 2 gene region, 62.6 to 100% identity for the ITS 1 region, 90 to 100% for the 5.8S gene, and 51.3 to 100% identity for the ITS 2 gene region. Two distinct ITS 1-5.8S-ITS 2 gene region sequences were obtained from *T. cervi* isolates from the Oklahoma and Canadian elk. These two ITS types were associated with the two *T. cervi* SSU rRNA gene types, F and G. The type F ITS 1-5.8S-ITS 2 gene region was found in clones 10, 11 and 13 from the Oklahoma elk and was 902 to 906 bp in length, while the type G ITS 1-5.8S-ITS 2 gene region was found in clone 12 of Oklahoma elk and was 1017 bp in length. The ITS 1-5.8S-ITS 2 gene region for the type F *T. cervi* Oklahoma elk clones was 902 to 906 bp in length, with

an ITS 1 region ranging from 511 to 515 bp, a 158 bp 5.8S gene, and an ITS 2 region of 233bp, while the G type *T. cervi* Oklahoma elk ITS 1-5.8S-ITS 2 gene region of 1017 bp in length, with an ITS 1 region of 517 bp, a 159 bp 5.8S gene, and an ITS 2 region of 341 bp. The individual clone lengths for the Oklahoma elk *T. cervi* can be found in Table 26. The *T. cervi* type F ITS1-5.8S-ITS 2 gene region was found in clones 8, 10 and 11 from the Canadian elk and was 904 bp in length, while type G ITS 1-5.8S-ITS 2 gene region was found in clones 1, 6 and 7 of Canadian elk and was 1014 to 1015 bp in length. The F type *T. cervi* Canadian elk clones had an ITS 1-5.8S-ITS 2 gene region of 904 bp, with an ITS 1 region of 513 bp, a 158 bp 5.8S gene, and an ITS 2 region of 233 bp. The G type *T. cervi* Canadian elk clones had an ITS 1-5.8S-ITS 2 gene region of 1014 to 1015 bp, with an ITS 1 region of 515 to 516 bp in length, a 159 bp 5.8S gene, and an ITS 2 region of 340 bp and individual clone lengths can be found in Table 26. The pairwise comparison values for these *T. cervi* isolates are shown in Tables 22 to 25.

The Indiana elk clones (1, 2, and 3) had full ITS 1-5.8S-ITS 2 gene regions of 929 to 930 bp, which included a 515 bp ITS 1 region, 158 bp 5.8S gene, and a 256 to 257 bp ITS 2 region. Percent identities among the Indiana elk *T. cervi* clones were 99.6 for the full ITS 1-5.8S-ITS 2 gene region, 99.6 to 99.8 for the ITS 1 region, 100 for the 5.8S gene, and 98.8 to 99.2 for the ITS 2 region. The *T. cervi* Wisconsin elk clones (3, 4 and 5) were all identical with 100 identity to each other in the full ITS 1-5.8S-ITS 2 gene region of 994 bp, which was divided into a 513 bp ITS 1 region, 158 bp 5.8S gene, and 323 bp ITS 2 region.

The pairwise comparisons among the *T. cervi* type G ITS 1-5.8S-ITS 2 gene regions ranged from 96.1 to 99.9% identity for the full region, 96.1 to 100% identity for

Table 26  
*Theileria cervi* ITS 1-5.8S-ITS 2 types.

Isolate	ITS Types	Clones	BP ITS 1	BP 5.8S	BP ITS 2
Oklahoma elk	F	10, 11, 13	511-515	158	233
	G	12	517	159	341
Canadian elk	F	8, 10, 11	513	158	233
	G	1, 6, 7	515-516	159	340

the ITS 1 region, 98.8 to 100% identity for the 5.8S gene, and 91.2 to 100% identity for the ITS 2 region. Percent identities among all the *T. cervi* ITS type F ITS 1-5.8S-ITS 2 gene region ranged from 93.9 to 100 for the full gene region, 94.8 to 100 for the ITS 1 region, 98.7 to 100 for the 5.8S gene, and 87.6 to 100 for the ITS 2 region. The pairwise comparisons for these clones can be found in Tables 22 to 25.

The percent identities for the ITS 1-5.8S-ITS 2 gene regions (including both the type F and type G sequences) among all the elk *T. cervi* clones ranged from 62.5 to 99.9 for the full gene region, 61.5 to 99.8 for the ITS 1 region, 90 to 100 for the 5.8S gene, and 51.3 to 100 for the ITS 2 region. The pairwise comparison values for the elk *T. cervi* isolates can be found in Tables 22 to 25.

### 3.4. Phylogenetic Trees

The Neighbor joining tree (Figure 2) of the *Theileria* spp. and *C. felis* full SSU rRNA gene sequences with *O. longa* as the outgroup shows that *O. longa*, is ancestral to the other lineages, giving rise to two branches: *Cytauxzoon felis* (GenBank accession no. L19080) and the *Theileria* spp. (Figure 2). The *Theileria* spp. divides into six major clades with the *Theileria* sp. from the dama gazelle and *T. separata* as one

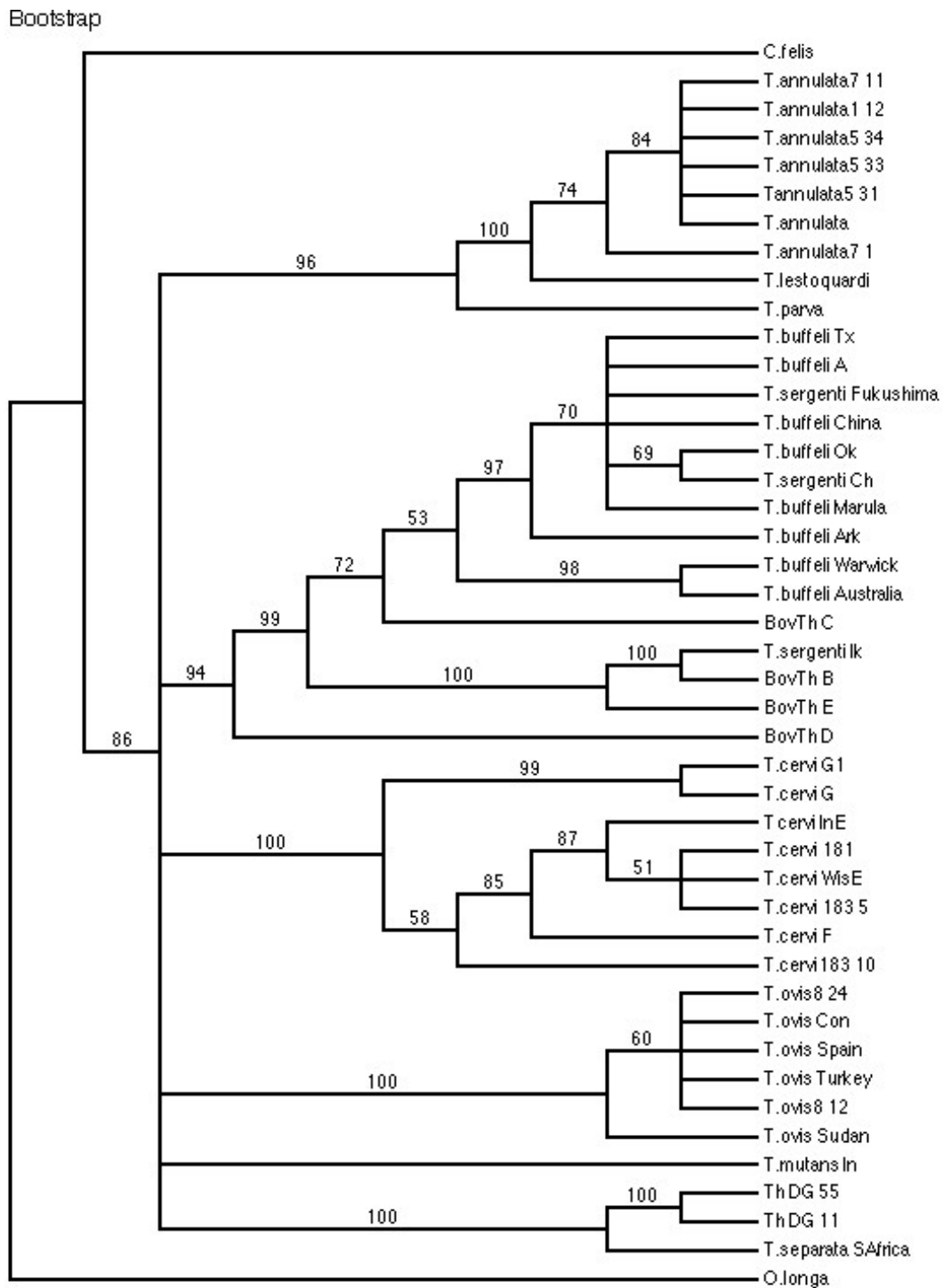


Figure 2

Neighbor joining tree based on SSU rRNA gene.

This tree is comprised of the SSU rRNA genes from the isolates used in this study from Table 1 and the GenBank sequences in Table 9.



clade, *T. mutans* Intona as a second clade, *T. ovis* as a third clade, *T. cervi* type F and G as a fourth clade, the benign bovine *Theileria* spp. as the fifth clade, and the pathogenic *Theileria* spp. as the sixth clade. *Cytauxzoon felis* branches ancestrally from the *Theileria* spp. One *Theileria* spp. clade is composed of the benign and moderately pathogenic bovine agents. Within the benign and moderately pathogenic bovine *Theileria* spp. clade, both *T. sergenti* Chitose and *T. sergenti* Fukushima (GenBank accession no. AB016074) grouped within the clade holding the type A *T. buffeli* SSU rRNA gene sequence (GenBank accession no. U97047), the *T. buffeli* isolates from the U.S., *T. buffeli* from China (GenBank accession no. AF236097), and *T. buffeli* Marula (GenBank accession no. Z15106). The Australian *T. buffeli* (Australia and Warwick) are closely related, but separate from the other *T. buffeli* isolates. The bovine *Theileria* type D (GenBank accession no. U97052) branched separately from the type A and the type B SSU rRNA gene sequences (GenBank accession no. U97048, respectively).

*Theileria sergenti* Ikeda shared branched with the type B SSU rRNA *Theileria* sp. gene and separate from the type A SSU rRNA gene *Theileria* spp. The bovine *Theileria* type E SSU rRNA gene sequence branched separately, but with the with the type B SSU rRNA gene isolates.

The six full length SSU rRNA gene sequences obtained from clones of Turkey *T. annulata* isolates 1, 5 and 7 grouped together with the Hissar, India, *T. annulata* (GenBank accession no. M64243). *Theileria annulata* Turkey 7 clone 1 was divergent from the other Turkey *T. annulata* gene sequences. The *Theileria parva* (GenBank accession no. L02366) and *T. lestoquardi* (GenBank accession no. AF081135) each branched separately, but within this group.

The full length SSU rRNA gene sequences obtained from *T. ovis* Turkey 8 clones 12 and 24 and the consensus *T. ovis* SSU rRNA gene sequence grouped with the *T. ovis* SSU rRNA gene sequences from Spain, Sudan and Turkey isolates (GenBank accession no. AY533144, AY260171, and AY260172; respectively; these sequences appeared in the GenBank database during the course of this study). This group was well separated from the ovine parasite, *T. separata*, of South African origin (GenBank accession no. AY260175).

The SSU rRNA gene sequences from the U.S. dama gazelle *Theileria* sp. clones grouped with *T. separata*, as a clade well separated from the clade containing the North American WTD and elk *T. cervi* SSU rRNA gene type F (GenBank accession no. U97054), the North American elk *T. cervi* SSU rRNA gene type G (GenBank accession no. U907055), and subtype G1 (GenBank accession no. U97056) sequences.

The Neighbor joining tree constructed from the ITS 1-5.8S-ITS 2 gene region sequences shows the outgroup *O. longa* and *C. felis* divergent from the *Theileria* spp. (Figure 3). The *Theileria* spp. divide into 2 major clades - one consisting of the *Theileria* spp. of cattle, and the other of *Theileria* spp. infecting cervids and sheep.

The bovine *Theileria* spp. further divide into two major branches, one branch consists of the pathogenic species, including six *T. annulata* sequences from Turkey isolates, two *T. parva* isolates (GenBank accession no. AF086734 (Hluhluwe strain) and U03602 (sporozoite stablate 3081)), plus *T. mutans* Intona. The second branch consists of the benign and moderately pathogenic bovine *Theileria* spp., which further divides into two major branches, one consisting of the *T. sergenti* Ikeda clones and the second consisting of the U.S. *T. buffeli* isolates and *T. sergenti* Chitose clones.

Bootstrap

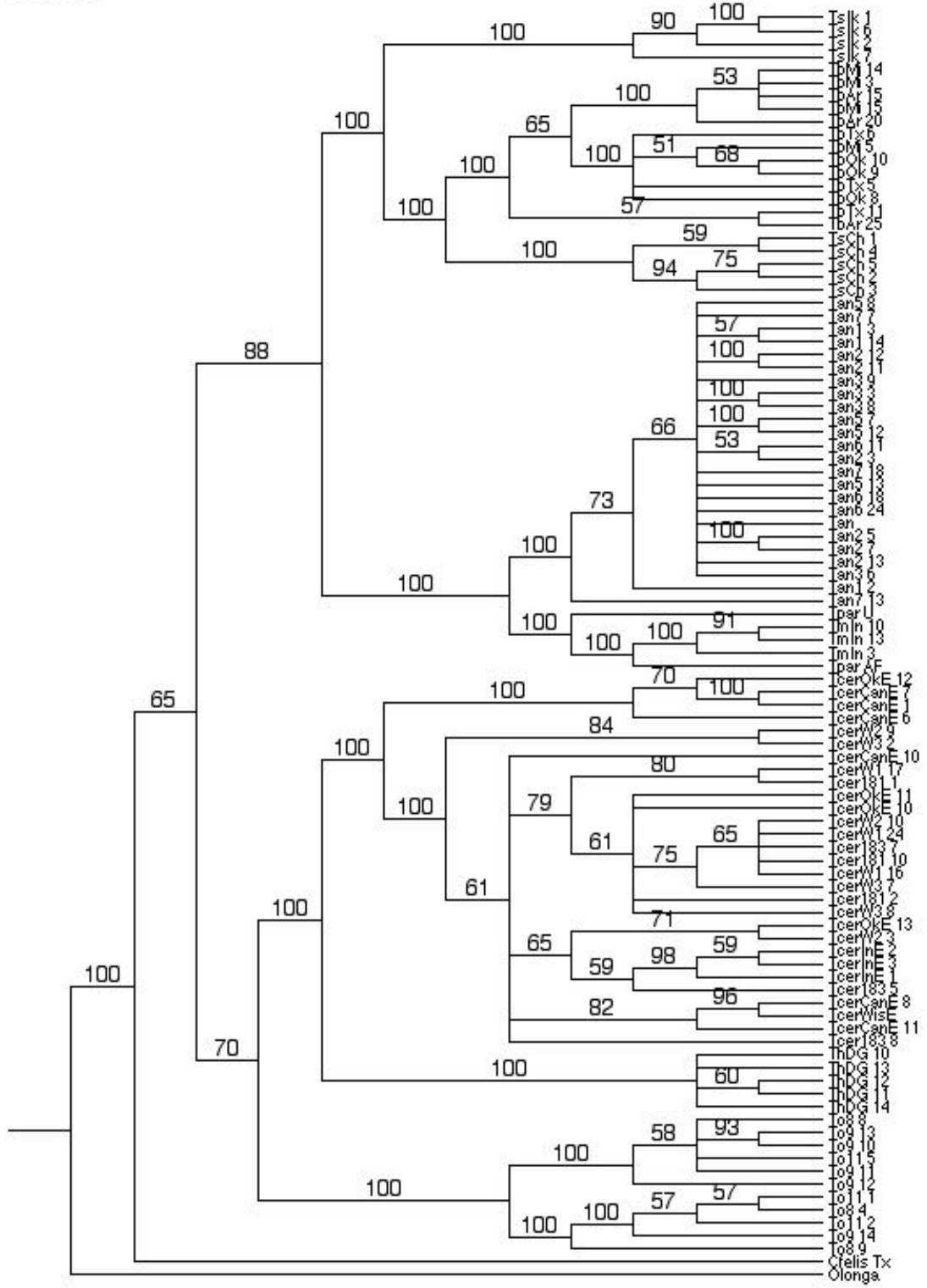


Figure 3  
Neighbor joining tree based on ITS 1-5.8S-ITS 2 gene region.  
This tree was created from the ITS 1-5.8S-ITS 2 gene regions of the isolates listed in Table 1, each isolate has at least three clones from every isolate and the two *Theileria parva* from GenBank

The cervid and sheep *Theileria* spp. branch divides into two major groups with one consisting of the four Turkey *T. ovis* isolates (from this study) and the other consisting of the *T. cervi* isolates and the dama gazelle *Theileria* sp. The cervid branch divides into two well-supported groups, one containing the dama gazelle *Theileria* sp. clones and the second containing the *T. cervi* isolates. Within the *T. cervi* group, the type F and type G ITS 1-5.8S-ITS 2 gene region sequences branch separately.

The Neighbor joining tree constructed from the 5.8S rRNA gene region sequences is shown in Figure 4. Individual isolates that had an identical 5.8S gene were run as a single entry; clones that differed used clone identification number. The outgroup *O. longa* is ancestral to *C. felis* and the *Theileria* spp. This group divides into the *T. cervi* type G 5.8S branch and a large branch holding the remaining species. The large branch subdivides into a *T. ovis* branch and a branch containing the bovine and deer *Theileria* spp. along with *C. felis*. This latter branch then splits the *T. cervi* type F 5.8S group from the group containing the bovine and dama gazelle *Theileria* spp. and *C. felis*. This last group then subdivides into three groups: Group one consists of the U.S. *T. buffeli* isolates and *T. sergenti* Chitose. Group two contains only *T. sergenti* Ikeda. Group three consists of *T. annulata*, *T. mutans* Intona, *T. parva* (GenBank accession no. AF086734), dama gazelle *Theileria* sp., and *C. felis*.

Bootstrap

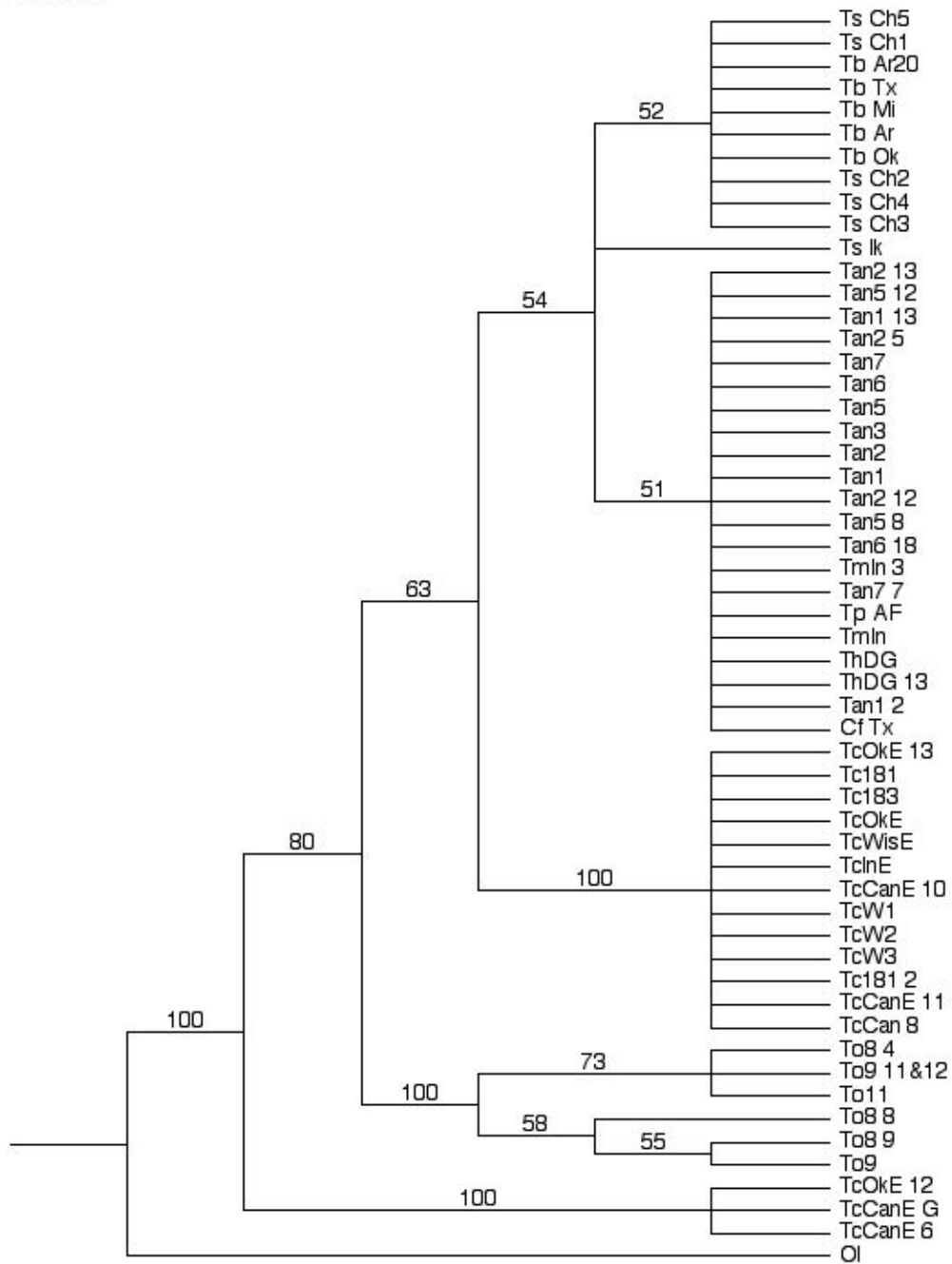


Figure 4

Neighbor joining tree based on 5.8S gene.

The 5.8S gene neighbor joining tree in which individual isolates that had an identical 5.8S gene were run as a single entry; clones that differed used clone identification number.

## CHAPTER IV

### DISCUSSION AND CONCLUSIONS

This is the first thorough molecular study of *Theileria* spp. using the internal transcribed spacers and 5.8S rRNA gene sequences for taxonomic analysis. To date, the only *Theileria* species for which this region has been investigated is *Theileria parva* (Kibe et al., 1994; Collins and Allsopp, 1999). The genomic region consisting of internal transcribed spacer 1 (ITS 1), the 5.8S gene, and internal transcribed spacer 2 (ITS 2) (ITS 1-5.8S-ITS 2 gene region) separates the SSU rRNA gene from the large subunit ribosomal RNA gene. The 5.8S rRNA gene is highly conserved in size and nucleotide sequence, is relatively constant in molecular weight, and has an average chain length of approximately 160 nucleotides and was proven useful in dividing subgenera of *Gyrodactylus* ((Nazar, 1984; Zietara et al., 2002).

The only theilerial 5.8S rRNA gene that has been previously sequenced is that of *T. parva*. The gene was sequenced from several *T. parva* isolate stocks, and all the sequences were identical (Kibe et al., 1994; Collins and Allsopp, 1999). However, the ITS sequences differed significantly in *T. parva* buffalo 7014 stock. Two different sizes were reported, with one 50 bp larger than the other (Kibe et al., 1994). There were three major polymorphisms found in the *T. parva* ITS sequences, two in the ITS 1 region and one in the ITS 2 region. Similarly, when Kibe et al. (1994) compared the ITS regions of *T. parva* Muguga and *T. parva* Uganda, the Uganda isolate ITS was 50 bp larger than that of the Muguga stock. In these isolate, however, one polymorphism occurred in the ITS 1 region and two in the ITS 2 region. Collins and Allsopp (1999) found variable ITS

regions in *T. parva parva* and *T. parva lawrenci* isolates in Africa, but the 5.8S rRNA genes were identical in all isolates.

The classification of piroplasms traditionally has been based on microscopic observations, ultrastructural characteristics, lifecycle, geographic location and vertebrate host (Allopp et al., 1994). Levine (1985) classifies the benign bovine *Theileria* spp. as *T. mutans* (syn. *T. buffeli*, *T. orientalis* and *T. sergenti*), however, the exact taxonomic standings of the benign and moderately pathogenic *Theileria* spp. have been problematic to establish and the subject of considerable controversy (Kim et al., 1998; Gubbels et al., 2002, Kawazu et al., 1992). A number of factors contribute to the complexity of assigning taxonomic positions, including similar morphology among this group of parasites regardless of vertebrate host, incomplete lifecycle data, serologic tests that are not specific enough to discriminate individual species in the presence of mixed infections, and the difficulty of obtaining pure isolates for studies when the circulating parasitemia may be very low (Chae et al., 1999c). The SSU rRNA gene is increasingly accepted as a widely used marker for characterization, taxonomic classification, and phylogenetic analysis and this gene has been sequenced from a variety of different organisms, resulting in a large database for sequence comparisons (Chae et al. 1998; Chae et al., 1999a,b,c; Stockham et al., 2000; Cossio-Bayugar et al., 2002; Gubbels et al., 2000).

Although *T. sergenti* and *T. buffeli* have been synonymized with *T. mutans*, it was previously shown that the SSU rRNA gene sequence of *T. mutans* is distinct from those of *T. sergenti* and *T. buffeli* (Levine, 1985; Chae et al., 1998; Chae et al., 1999c; Gubbels et al., 2000). Furthermore, it was shown that not all *T. sergenti* isolates possess the same

SSU rRNA gene sequence, but, rather, some possess what was termed the type A sequence (which is the same as that of *T. buffeli*) and some type B (arguably designated that of *T. sergenti*) (Chae et al., 1998; Chae et al., 1999c). These findings were confirmed in this study where it is shown that *T. sergenti* Chitose possesses the benign bovine *T. buffeli* type A SSU rRNA gene sequence, but that *T. sergenti* Ikeda possesses the type B SSU rRNA gene sequence, and that both are clearly distinct from the *T. mutans* SSU rRNA gene sequence.

Analysis of the ITS 1-5.8S-ITS 2 gene region in the current study adds proof to the SSU rRNA gene sequences analysis for the taxonomic classification of the benign bovine *Theileria* spp. In a phylogenetic tree based on the full ITS 1-5.8S-ITS 2 gene region sequence, the *T. sergenti* Chitose sequences grouped with the *T. buffeli* sequences, with *T. sergenti* Ikeda branching off separately, but still within the benign *Theileria* spp. clade. However, the *Theileria mutans* Intona sequences were located within the pathogenic *T. annulata* and *T. parva* clade, which clearly shows that *T. mutans* cannot be synonymous with *T. buffeli*.

Based on these molecular data, it is clear that *T. mutans*, *T. sergenti* and *T. buffeli* are not synonymous. Renaming of the benign bovine *Theileria* spp. is needed, especially since the name *T. sergenti* is invalid due to the fact that is synonymous for *Babesia sergenti*, a parasite of sheep and goats (Levine, 1985 ).

This is the first molecular characterization of *T. annulata* from clinically normal cattle in Turkey. Some microheterogeneity was found among the *T. annulata* isolates SSU rRNA isolates and clones, but no fixed differences were found. The SSU rRNA gene sequence from *Theileria annulata* Turkey 7 clone 1 was divergent from the other



Turkey *T. annulata* gene sequences, likely reflecting the presence of duplicate gene copies in *T. annulata* as previously described for *T. parva* (Kibe et al., 1994; Collins and Allsopp, 1999).

*Theileria ovis* and *T. separata* (GenBank Accession no. AY260175) are different benign *Theileria* spp. infecting sheep based on SSU rRNA gene sequence analysis. The difference is clearly indicated by the observation that *T. separata* grouped with the U.S. dama gazelle *Theileria* sp. instead of with the *T. ovis* isolates in the phylogenetic tree constructed from SSU rRNA gene sequences. *Theileria ovis* is found in Africa, former USSR, India, Sri Lanka, Europe, and western Asia, including Turkey (Levine, 1985), while *T. separata* is found in South Africa.

SSU rRNA sequences obtained in this study from *T. ovis* isolates from Erzincan, Turkey, shared high percent identities with the SSU rRNA gene sequences from *T. ovis* isolates from Spain, Sudan, and Turkey (GenBank Accession no. AY533144, AY260171, and AY260172; respectively). The *T. ovis* SSU rRNA gene sequences have a higher percent identity to *T. cervi* type F SSU rRNA gene sequence (GenBank Accession no. U97054) than the pathogenic sheep parasite *T. lestoquardi* (GenBank Accession no. AF081135).

The SSU rRNA gene specific primers created from the consensus *T. ovis* SSU rRNA gene sequence have been tested on field samples in Turkey using nested PCR and detected a higher percentage of infected sheep than by microscopic examination (Altay et al., submitted). The use of these primers allowed the authors to identify 54% of the field samples as being infected, while microscopic examinations only detected 19%. The specificity of these primers was also tested against other *Theileria* and *Babesia* spp. that

are found in the same area as *T. ovis*, and the nested PCR only produced expected amplicons from the *T. ovis*-infected samples. These primers could be used to detect *T. ovis* in mixed infections and for epidemiological studies of *Theileria* spp.

Two *T. cervi* SSU rRNA gene types, F and G, have been described (Chae et al., 1998; Chae et al., 1999a,c). Previous studies show the two types branching with one another on phylogenetic trees constructed from SSU rRNA gene sequences, as was the case in the current study. Both type F and G SSU rRNA gene sequences have been found in the same isolates (Chae et al., 1999a), which is not surprising since the existence of multiple SSU rRNA gene sequence types that represent genes from multiple copy units has been found in *T. parva* (Kibe et al., 1994). Additional studies in this laboratory found both type F *T. cervi* SSU rRNA gene sequence and type G *T. cervi* SSU rRNA gene sequences in nine known *T. cervi* isolates from WTD and elk by PCR using specific primer sets for each (unpublished data).

An interesting finding in this study is that each SSU rRNA type possesses a distinctive ITS 1-5.8S-ITS 2 gene region sequence. Of particular note is that the 5.8S gene sequence for each type is in itself distinct, a characteristic not seen in any of the other *Theileria* isolates in this study. Despite these differences, the two *T. cervi* types are more closely related to one another on the ITS 1-5.8S-ITS 2 gene region neighbor joining tree than to any other *Theileria* spp. Whether or not these transcriptional units are on separate chromosomes as with *T. parva* SSU rRNA genes (Nene et al., 1998) is unknown. Since both transcriptional units of *T. cervi* SSU rRNA genes and ITS 1-5.8S-ITS 2 gene regions have found in the same isolates, it is possible that the these different

transcriptional units are expressed at different developmental stages of the lifecycle as seen in *Plasmodium* spp. (Li et al., 1997; Waters et al., 1989; Corredor and Enea, 1994).

The SSU rRNA genes amplified from the *T. cervi* isolates in this study were all *T. cervi* type F sequences, yet *T. cervi* type G SSU rRNA gene sequences were identified in all nine of the isolates using specific G type SSU rRNA gene primers (unpublished data). Of note, among the ITS 1-5.8S-ITS 2 gene regions amplified from these nine isolates, only two produced the type G ITS 1-5.8S-ITS 2 gene region. From these results it seems likely that the type F *T. cervi* SSU rRNA gene sequence is the more predominant sequence found in *T. cervi* isolates. Southern blots probed with specific SSU rRNA gene primers might be utilized to reveal if a particular SSU rRNA gene type predominates in *T. cervi* isolates.

Although similar data was not obtained for other *Theileria* spp. in this study, the lack of additional ITS1-5.8S-ITS 2 gene region sequences could have been due to possible nucleotide variation in the areas where primers attach. Also, it is possible that minor bands might have been present on agarose gels that were not considered significant. Such bands might have been overlooked, or it is even possible that large single-appearing bands actually might have consisted of two single bands.

Unlike the ITS 1-5.8S-ITS 2 gene region, the 5.8S gene is a less informative marker, probably due to the short length and high amount of conservation. The 5.8S gene groups the pathogenic *T. annulata* and *T. parva*, together with *T. mutans* Intona, the dama gazelle *Theileria* sp., and *C. felis*. In this study, only in the Neighbor joining tree based on 5.8S gene sequences is *C. felis* included in a clade with *Theileria* spp. In the trees constructed from SSU rRNA gene sequences or ITS regions, *C. felis* branched separately

ancestral to the other piroplasms. The genus *Cytauxzoon* is in the family Theileriidae, but differs from other theilerial parasites in the fact that *Cytauxzoon* undergo schizogony in reticuloendothelial macrophages, while *Theileria* undergo schizogony in lymphocytes (Glen et al., 1982). Thus, the 5.8S gene tree groups species from two different genera together, making it less informative at a species level.

The *Theileria* sp. from the dama gazelle grouped with different *Theileria* spp. in the phylogenetic trees depending on which molecular marker was used. The phylogenetic tree based on SSU rRNA gene sequences analysis paired it with *T. separata*, a benign parasite of sheep and goats in South Africa. The phylogenetic tree based on the ITS 1-5.8S-ITS 2 gene region placed the dama gazelle *Theileria* sp. on its own branch parallel with the *T. cervi* clade. The phylogenetic tree based on the 5.8S gene placed it in the group with *T. annulata*, *T. parva*, *T. mutans* Intona, and *C. felis*. The dama gazelle *Theileria* sp. appears to be a previously unreported isolate and a different species from the others used in this study, but until more isolates are studied and more information on the biology of the parasite is known, no name should be given.

Currently, there is no consensus on how much difference in the SSU rRNA gene there must be for an isolate to be called a species. The use of multiple molecular markers, such as the ITS 1-5.8S-ITS 2 gene region and the 5.8S gene alone, can more clearly demonstrate differences and similarities among isolates.

The results of this study show that *T. sergenti* Chitose is probably not a correct taxonomic name, since this isolate is molecularly indistinguishable from *T. buffeli*. This study shows that different SSU rRNA genes may be associated with ITS 1-5.8S-ITS 2 gene regions of distinct sequence in the same isolate. This study also demonstrates that

considerable ITS 1-5.8S-ITS 2 gene region sequence variation may exist within a species. This may be useful for subspeciation designation, or may simply reflect considerable variation within the population. This study shows that the ITS 1-5.8S-ITS 2 gene region may be a useful molecular marker for the taxonomy of *Theileria* spp.

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## APPENDIX 1

## Small subunit rRNA gene alignment

C.felis AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.annulata7\_11 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.buffeli\_Tx AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.cervi\_G1 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.buffeli\_A AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.sergenti\_Fukushima AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.buffeli\_China AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.ovis8\_24 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.cervi\_InE AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.annulata1\_12 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.cervi\_181 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.annulata7\_1 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.cervi\_WisE AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.mutans\_In AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 Th\_DG\_55 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.cervi\_F AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.annulata5\_34 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.buffeli\_Warwick AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.annulata5\_33 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 BovTh\_C AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.buffeli\_Ok AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.cervi\_183\_5 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 O.longa AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
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 T.buffeli\_Australia AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
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 T.lestoquardi AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.buffeli\_Marula AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.cervi183\_10 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
 T.ovis8\_12 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCTAAAGATTAAGCCATGCATGTCT 60  
  
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 T.annulata7\_11 AAGTATAAGCTTTTATATGGTGAAACTGCGAATGGCTCATTACAACAGTTATAGTTTATT 120  
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 T.ovis8\_24 AAGTATAAGCTTTTATATGGTGAAACTGCGAATGGCTCATTACAACAGTTATAGTTTATT 120  
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 T.buffeli\_Warwick AAGTATAAGCTTTTATATGGTGAAACTGCGAATGGCTCATTATAACAGTTATAGTTTATT 120  
 T.annulata5\_33 AAGTATAAGCTTTTATATGGTGAAACTGCGAATGGCTCATTACAACAGTTATAGTTTATT 120





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 T.parva GCGGT--GTCCGGTATTGATTATAATAAAATATGCG-AATCG-----TACTTAG--TGCGATG 268  
 BovTh\_B ACGGT--TCCCAGGTGATTGATTATAATAAACTTGCG-AATCGCTT--TACTTA----GCGATG 274  
 T.ovis\_Spain -CGGTGTAC--GGTGATTGATTATAATAAACTTGCG-AATCGCGT----CTTCGGATGCGATG 270  
 Tannulata5\_31 -CGGTGTCC--GGTGATTGATTATAATAAAATATGCG-AATCGTAC----TCT--GTACGATG 268  
 T.buffeli\_Australia -CGGTAACC--GGTGATTGATTATAATAAACTTGCG-AATCGCAT----TATT--TTGCGATG 269  
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 T.ovis\_Sudan -CGGTGTAC--GGTGATTGATTATAATAAACTTGCG-AATCGCGT----CTTCGGATGCGATG 271  
 Th\_DG\_11 -CGGTGGCC--GGTGATTGATTATAATAAAATTTGCG-AATCGCAG----TTTT--CTGCGATG 269  
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 T.cervi183\_10 TCGAAA--ACCGGTGATTGATTATAATAAACTTGCG-AATCGCGG----CTTAGGCTGCGATG 272  
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 T.ovis\_Spain CATCTAAGGAAGGCAGCAGGCG-CGCAAATTACCCAATCCTGACACAGGGAGGTAGTGAC 449  
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T.annulata5_33	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 507
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T.buffeli_Ok	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 507
T.cervi_183_5	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 511
O.longa	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 525
T.ovis_Con	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 510
BovTh_D	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 508
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T.parva	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 507
BovTh_B	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 513
T.ovis_Spain	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 509
Tannulata5_31	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 507
T.buffeli_Australia	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 508
T.annulata	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 507
T.ovis_Sudan	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 510
Th_DG_11	AAGAAATAACAATACGGGGCTCAATGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 508
T.cervi_G	AAGAAATAACAATACGGGACGTA-TGTTTTGTAATTGGAATGATGGGAATTTAAACCTCT 509
BovTh_E	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 513
T.ovis_Turkey	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 512
T.buffeli_Ar	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 507
T.sergenti_Ch	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 507
T.separata_SAfrica	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 509
T.lesstoquardi	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 507
T.buffeli_Marula	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 507
T.cervi183_10	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 511
T.ovis8_12	AAGAAATAACAATACGGGGCTTAAAGTCTTGTAATTGGAATGATGGGAATTTAAACCTCT 510
C.felis	TCCGAGTATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGTAATTCCAGCTCCAA 584
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T.buffeli_Tx	TCCAGAGTATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGTAATTCCAGCTCCAA 567
T.cervi_G1	TCCAGAGTATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGTAATTCCAGCTCCAA 571
T.buffeli_A	TCCAGAGTATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGTAATTCCAGCTCCAA 567
T.sergenti_Fukushima	TCCAGAGTATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGTAATTCCAGCTCCAA 567
T.buffeli_China	TCCAGAGTATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGTAATTCCAGCTCCAA 567
T.ovis8_24	TCCAGAGTATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGTAATTCCAGCTCCAA 570
T_cervi_InE	TCCAGAGTATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGTAATTCCAGCTCCAA 570
T.annulata1_12	TCCAGAGTATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGTAATTCCAGCTCCAA 567



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 T.lestoquardi TAGCGTATATTTAAATTTGTTGCAGTTAAAAAGCTCGTAGTTGAATTTCTGCTGCATTGCT 627  
 T.buffeli\_Marula TAGCGTATATTTAAATTTGTTGCAGTTAAAAAGCTCGTAGTTGAATTTCTGCTGCATTCA 627  
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 T.ovis8\_12 TAGCGTATATTTAAATTTGTTGCAGTTAAAAAGCTCGTAGTTGAATTTCTGCTGCATTGCT 630

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 T.annulata7\_11 TG--TGTCCCTCTGG--GGTCTGT-GCA-TGT--GGCTT-----TTTT 662  
 T.buffeli\_Tx CA--TTTCTCTTTCTG--AGTTTGT-TTT-TGC--GGCTT-----ATTT 661  
 T.cervi\_G1 CTATCTTCCCCTTATGGAGGTTTGT-CGC-CGT--GGCTT-----ATTT 671  
 T.buffeli\_A ---TTTCTCTTTCTG--AGTTTGT-TTT-TGC--GGCTT-----ATTT 661  
 T.sergenti\_Fukushima ---TTTCTCTTTCTG--AGTTTGT-TTT-TGC--GGCTT-----ATTT 661  
 T.buffeli\_China ---TTTCTCTTTCTG--AGTTTGT-TTT-TGC--GGCTT-----ATTT 661  
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 T.cervi\_InE ---TTTTCCCTTTGAGGGGTTTTT-GCGCTGT--GGCTT-----ATTT 667  
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 T.mutans\_In ---GCGGCCCTCC--CGGGCCAG-CGGTTGC--GGCTT-----ATTT 660  
 Th\_DG\_55 ---TCTCCTCCTTGATGGATTGGT-GCATTGC--GGCTT-----GTTT 665  
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 T.cervi\_183\_5 ---TTTTCCCTTTGAGGGGTTTTT-GCGCTGT--GGCTT-----ATTT 668  
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 T.ovis\_Con ---TTTGCTCCTTTACGAGTCTTT-GCATTGT--GGCTT-----TTTT 667  
 BovTh\_D ---G-CATCTCTGCTGAGTGCTT--CGTTTC--GGCTT-----ATTT 663  
 T.sergenti\_Ik ---TTTCTCTTGTTTGAGTTTGT---ATTGT--GGCTT-----ATTT 668  
 T.parva ---TGTGTCCCTTCGGGTCTCTG---CATGT--GGCTT-----ATTT 662  
 BovTh\_B ---TTTCTCTTGTTTGAGTTTGT---ATTGT--GGCTT-----ATTT 668  
 T.ovis\_Spain --CTTTTGCTCCTTTACGAGTCTTT-GCATTGT--GGCTT-----ATTT 666  
 T.annulata5\_31 --CTTGTGTCCCTCTG-GGGTCTGT-GCAT-GT--GGCTT-----TTTT 662  
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 T.ovis\_Turkey ----TTTGCTCCTTTACGAGTCTTT-GCATTGT--GGCTT-----ATTT 669  
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 T.buffeli\_Marula -----TTTCTCTTCTGAGTTTGT--TTTTGC--GGCTT-----ATTT 661  
 T.cervi183\_10 ----TTTTCCCTTTGAGGGGTTTTT-GCGCTGT--GGCTT-----ATTT 668  
 T.ovis8\_12 ----TTTGCTCCTTTACGAGTCTTT-GCATTGT--GGCTT-----ATTT 667

C.felis TGGTGATTATATTTCCGGTATGATTATCCAGATTGTT-ACTTTGAGAAAATTAGAGTGCTT 742  
 T.annulata7\_11 CGG--ACGAGTCTTCT-----TTGCTGAATGTTT-ACTTTGAGAAAATTAGAGTGCTC 713  
 T.buffeli\_Tx CGGT--TTGATTTTTT-----CTTCCGGATGATT-ACTTTGAGAAAATTAGAGTGCTC 712  
 T.cervi\_G1 CGGACTGTGTTATGCA-----CTGTCCGGATGTTT-ACTTTGAGAAAATTAGAGTGCTC 724  
 T.buffeli\_A CGG--TTTGATTTTTT-----CTTCCGGATGATT-ACTTTGAGAAAATTAGAGTGCTC 712  
 T.sergenti\_Fukushima CGG--TTTGATTTTTT-----CTTCCGGATGATT-ACTTTGAGAAAATTAGAGTGCTC 712  
 T.buffeli\_China CGG--TTTGATTTTTT-----CTTCCGGATGATT-ACTTTGAGAAAATTAGAGTGCTC 712  
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 T.cervi\_InE CGGACTGTGTTATGCA-----CTGTCCGGATGTTT-ACTTTGAGAAAATTAGAGTGCTC 720  
 T.annulata1\_12 CGGACGGAGTTT--CT-----TTGCTGAATGTTT-ACTTTGAGAAAATTAGAGTGCTC 713  
 T.cervi\_181 CGGACTGTGTTATGCA-----CTGTCCGGATGTTT-ACTTTGAGAAAATTAGAGTGCTC 720  
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 T.mutans\_In CGGACTCGCTTGCCT-----C-TCCGAATGTTT-ACTTTGAGAAAATTAGAGTGCTC 710  
 Th\_DG\_55 CGGCTGTGGTTTCT-----CGTCCGGATGTTT-ACTTTGAGAAAATTAGAGTGCTC 716

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 T.annulata5\_34 CGGACGGAGTT--TCTT-----TGTCGAATGTTT-ACTTTGAGAAAATTAGAGTGCTC 713  
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 BovTh\_D CGGATTGATTTTTTCT-----TTCCGGATGATT-ACTTTGAGAAAATTAGAGTGCTC 714  
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 T.parva CGGACGGAGTTCGCTT-----TGTCGGATGTTT-ACTTTGAGAAAATTAGAGTGCTC 714  
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 T.ovis\_Sudan CGGACTTTGTTTTACA-----ATGTCCGGATGTTT-ACTTTGAGAAAATTAGAGTGCTC 720  
 Th\_DG\_11 CGGTCGTGTTTTCCT-----CGTCCGGATGTTT-ACTTTGAGAAAATTAGAGTGCTC 716  
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 T.ovis\_Turkey CGGACTTTGTTTTACAA-----TGTCGGGATGTTT-ACTTTGAGAAAATTAGAGTGCTC 722  
 T.buffeli\_Ar CGGTTTGATTTTTTC-----TTTCCGGATGATT-ACTTTGAGAAAATTAGAGTGCTC 712  
 T.sergenti\_Ch CGGTTTGATTTTTTC-----TTTCCGGATGATT-ACTTTGAGAAAATTAGAGTGCTC 712  
 T.separata\_SAfrica CGGTCGTGTTTTCCT-----CGTCCGGATTTTT-ACTTTGAGAAAATTAGAGTGCTC 718  
 T.lestoquardi CGGACGGAGTTTCTT-----TGTCGAATGTTT-ACTTTGAGAAAATTAGAGTGCTC 713  
 T.buffeli\_Marula CGGTTTGATTTTTTC-----TTTCCGGATGATT-ACTTTGAGAAAATTAGAGTGCTC 712  
 T.cerviI83\_10 CGGACTGTGTTATGCA-----CTGTCCGGATGTTT-ACTTTGAGAAAATTAGAGTGCTC 721  
 T.ovis8\_12 CGGACTTTGTTTTACAA-----TGTCGGGATGTTT-ACTTTGAGAAAATTAGAGTGCTC 720

C.felis AAAGCAGGCTTTGCGCTTGAATACTTTAGCATGGAATAACTAAGTAGGACTTTGGTTCTA 802  
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 T.buffeli\_Tx AAAGCAGGCTTTGCGCTTGAATAGTTTAGCATGGAATAATAAAGTAGGACTTTGGTTCTA 772  
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 T.cervi\_183\_5 TTTTGTGGTTTAAAGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTATT 841  
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C.felis  
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C.felis  
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 T.buffeli\_China  
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 T.mutans\_In  
 Th\_DG\_55  
 T.cervi\_F  
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 T.buffeli\_Warwick  
 T.annulata5\_33  
 BovTh\_C  
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 BovTh\_D  
 T.sergenti\_Ik  
 T.parva  
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C.felis  
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 T.annulata5\_33  
 BovTh\_C  
 T.buffeli\_Ok  
 T.cervi\_183\_5  
 O.longa  
 T.ovis\_Con  
 BovTh\_D  
 T.sergenti\_Ik  
 T.parva  
 BovTh\_B  
 T.ovis\_Spain  
 Tannulata5\_31  
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 T.cervi183\_10 CACCAGCTTGTGCAGATTACGTCCCTGCCCTTTGTACACACCCGCCCGTCGCTCCTACCGA 1615  
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 BovTh\_C T--CGAGTGATCCGGTGAATTATTCGGACCGTGATGT-TCCCGTC-AG---GGAACGTCT 1670  
 T.buffeli\_Ok T--CGAGTGATCCGGTGAATTATTCGGACCGTGATGT-TCCCGTC-AG---GGAACGTCT 1660  
 T.cervi\_183\_5 T--CGAGTGATCCGGTGAATTATTCGGACCGTGATGT-TCCCGTC-AG---GGAACGTCT 1669  
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 T.sergenti\_ik T--CGAGTGATCCGGTGAATTATTCGGACCGTGATGT-TCCCGTC-AG---GGAACGTCT 1668  
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 T.sergenti\_Fukushima GGTGAACCTG-CAGAAGGATC 1740  
 T.buffeli\_China GGTGAACCTG-CAGAAGGATC 1740  
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 Th\_DG\_55 GGTGAACCTG-CAGAAGGATC 1743  
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 T.sergenti\_Ch GGTGAACCTG-CAGAAGGATC 1740  
 T.separata\_SAfrica GGTGAACCTG-CAGAAGGATC 1745  
 T.lestoquardi GGTGAACCTG-CAGAAGGATC 1741  
 T.buffeli\_Marula GGTGAACCTG-CAGAAGGATC 1740  
 T.cervi183\_10 GGTGAACCTG-CAGAAGGATC 1748  
 T.ovis8\_12 GGTGAACCTG-CAGAAGGATC 1748

## APPENDIX 2

*Theileria ovis* Consensus Alignment

T.ovis8-12 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGTCTTAAAGATTAAGCCATGCATGTCT 60  
 T.ovis11-1 -----  
 T.ovis10-16 -----GCTTGTCTTAAAGATTAAGCCATGCATGTCT 31  
 T.ovis10-15 -----GCTTGTCTTAAAGATTAAGCCATGCATGTCT 31  
 T.ovis11-11 -----  
 T.ovis11-3 -----  
 T.ovis9-21 -----GCTTGTCTTAAAGATTAAGCCATGCATGTCT 31  
 T.ovis8 -----TGTCT 5  
 T.ovis8-24 AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGTCTTAAAGATTAAGCCATGCATGTCT 60  
 T.ovisConsen AACCTGGTTGATCCTGCCAGTAGTCATATGCTTGTCTTAAAGATTAAGCCATGCATGTCT 60

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 T.ovis10-16 AAGTATAAGCTTTTATATGGTGAAACTGCGAATGGCTCATTACAACAGTTATAGTTTATT 91  
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 T.ovis11-11 -----  
 T.ovis11-3 -----  
 T.ovis9-21 AAGTATAAGCTTTTATATGGTGAAACTGCGAATGGCTCATTACAACAGTTATAGTTTATT 91  
 T.ovis8 AAGTATAAGCTTTTATATGGTGAAACTGCGAATGGCTCATTACAACAGTTATAGTTTATT 65  
 T.ovis8-24 AAGTATAAGCTTTTATATGGTGAAACTGCGAATGGCTCATTACAACAGTTATAGTTTATT 120  
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 T.ovis11-11 -----  
 T.ovis11-3 -----  
 T.ovis9-21 TGATGTTTCGTTTTTACATGGATAACCGTGCTAATTGTAGGGCTAATACATGTTTCGAGACC 151  
 T.ovis8 TGATGTTTCGTTTTTACATGGATAACCGTGCTAATTGTAGGGCTAATACATGTTTCGAGACC 125  
 T.ovis8-24 TGATGTTTCGTTTTTACATGGATAACCGTGCTAATTGTAGGGCTAATACATGTTTCGAGACC 180  
 T.ovisConsen TGATGTTTCGTTTTTACATGGATAACCGTGCTAATTGTAGGGCTAATACATGTTTCGAGACC 180

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 T.ovis10-15 TTCGGGTGGCGTTTATTAGACCTAAAACCAAACCGCTTGCGGTGTACGGTGATTTCATAAT 211  
 T.ovis11-11 -----  
 T.ovis11-3 -----  
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 T.ovis8 TTCGGGTGGCGTTTATTAGACCTAAAACCAAACCGCTTGCGGTGTACGGTGATTTCATAAT 185  
 T.ovis8-24 TTCGGGTGGCGTTTATTAGACCTAAAACCAAACCGCTTGCGGTGTACGGTGATTTCATAAT 240  
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 T.ovis11-3 -----  
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 T.ovis8 AAACCTGCGAATCGCGTCTTCGGATGCGATGTATCATTCAAGTTTCTGACCTATCAGCTT 245  
 T.ovis8-24 AAACCTGCGAATCGCGTCTTCGGATGCGATGTATCATTCAAGTTTCTGACCTATCAGCTT 300  
 T.ovisConsen AAACCTGCGAATCGCGTCTTCGGATGCGATGTATCATTCAAGTTTCTGACCTATCAGCTT 300



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 T.ovis10-15 TGGACGGTAGGGTATTGGCCTACCGGGGCAACGACGGGTAACGGGGGAATTAGGGTTCGAT 331  
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 T.ovis11-3 -----GGTAGGGTATTGGCCTACCGGGGCAACGACGGGTAACGGGGGAATTAGGGTTCGAT 55  
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 T.ovis8 TGGACGGTAGGGTATTGGCCTACCGGGGCAACGACGGGTAACGGGGGAATTAGGGTTCGAT 305  
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 T.ovis10-16 TCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCTAAGGAAGGCAGCAGGCCGCGCAAAT 391  
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 T.ovis10-15 TACCCAATCCTGACACAGGGAGGTAGTGACAAGAAATAACAATACGGGGCTTAATGTCTT 451  
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 T.ovis8 TACCCAATCCTGACACAGGGAGGTAGTGACAAGAAATAACAATACGGGGCTTAATGTCTT 425  
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 T.ovis10-15 AAAGCAGGCTTTTCGCCTTGAATAGTTTAGCATGGAATAATAAAGTAGGACTTTGGTTCTA 751  
 T.ovis11-11 AAAGCAGGCTTTTCGCCTTGAATAGTTTAGCATGGAATAATAAAGTAGGACTTTGGTTCTA 475  
 T.ovis11-3 AAAGCAGGCTTTTCGCCTTGAATAGTTTAGCATGGAATAATAAAGTAGGACTTTGGTTCTA 475  
 T.ovis9-21 AAAGCAGGCTTTTCGCCTTGAATAGTTTAGCATGGAATAATAAAGTAGGACTTTGGTTCTA 751  
 T.ovis8 AAAGCAGGCTTTTCGCCTTGAATAGTTTAGCATGGAATAATAAAGTAGGACTTTGGTTCTA 725  
 T.ovis8-24 AAAGCAGGCTTTTCGCCTTGAATAGTTTAGCATGGAATAATAAAGTAGGACTTTGGTTCTA 780  
 T.ovisConsen AAAGCAGGCTTTTCGCCTTGAATAGTTTAGCATGGAATAATAAAGTAGGACTTTGGTTCTA 780

T.ovis8-12 TTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTATT 840  
 T.ovis11-1 TTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTATT 535  
 T.ovis10-16 TTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTATT 811  
 T.ovis10-15 TTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTATT 811  
 T.ovis11-11 TTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTATT 535  
 T.ovis11-3 TTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTATT 535  
 T.ovis9-21 TTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTATT 811  
 T.ovis8 TTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTATT 785  
 T.ovis8-24 TTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTATT 840  
 T.ovisConsen TTTTGTGGTTTTAGGTACCAAAGTAATGGTTAATAGGAACAGTTGGGGGCATTTCGTATT 840

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 T.ovis11-1 TAACTGTCAGAGGTGAAATTCCTAGATTTGTTAAAGACGAACTACTGCGAAAGCATTTCG 595  
 T.ovis10-16 TAACTGTCAGAGGTGAAATTCCTAGATTTGTTAAAGACGAACTACTGCGAAAGCATTTCG 871  
 T.ovis10-15 TAACTGTCAGAGGTGAAATTCCTAGATTTGTTAAAGACGAACTACTGCGAAAGCATTTCG 871  
 T.ovis11-11 TAACTGTCAGAGGTGAAATTCCTAGATTTGTTAAAGACGAACTACTGCGAAAGCATTTCG 595  
 T.ovis11-3 TAACTGTCAGAGGTGAAATTCCTAGATTTGTTAAAGACGAACTACTGCGAAAGCATTTCG 595  
 T.ovis9-21 TAACTGTCAGAGGTGAAATTCCTAGATTTGTTAAAGACGAACTACTGCGAAAGCATTTCG 871  
 T.ovis8 TAACTGTCAGAGGTGAAATTCCTAGATTTGTTAAAGACGAACTACTGCGAAAGCATTTCG 845  
 T.ovis8-24 TAACTGTCAGAGGTGAAATTCCTAGATTTGTTAAAGACGAACTACTGCGAAAGCATTTCG 900  
 T.ovisConsen TAACTGTCAGAGGTGAAATTCCTAGATTTGTTAAAGACGAACTACTGCGAAAGCATTTCG 900

T.ovis8-12 CAAGGATGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGACGATCAGATACCGT 960  
 T.ovis11-1 CAAGGATGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGACGATCAGATACCGT 655  
 T.ovis10-16 CAAGGATGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGACGATCAGATACCGT 931  
 T.ovis10-15 CAAGGATGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGACGATCAGATACCGT 931  
 T.ovis11-11 CAAGGATGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGACGATCAGATACCGT 655  
 T.ovis11-3 CAAGGATGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGACGATCAGATACCGT 655  
 T.ovis9-21 CAAGGATGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGACGATCAGATACCGT 931  
 T.ovis8 CAAGGATGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGACGATCAGATACCGT 905  
 T.ovis8-24 CAAGGATGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGACGATCAGATACCGT 960  
 T.ovisConsen CAAGGATGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGACGATCAGATACCGT 960

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 T.ovis10-16 CGTAGTCCTAACCATAAACTATGCCGACTAGAGATTGGAGGTCGTCAGTTTTTACGACTC 991  
 T.ovis10-15 CGTAGTCCTAACCATAAACTATGCCGACTAGAGATTGGAGGTCGTCAGTTTTTACGACTC 991  
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 T.ovis11-3 CGTAGTCCTAACCATAAACTATGCCGACTAGAGATTGGAGGTCGTCAGTTTTTACGACTC 715  
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 T.ovis8 CGTAGTCCTAACCATAAACTATGCCGACTAGAGATTGGAGGTCGTCAGTTTTTACGACTC 965  
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 T.ovisConsen CGTAGTCCTAACCATAAACTATGCCGACTAGAGATTGGAGGTCGTCAGTTTTTACGACTC 1020

T.ovis8-12 CTTACGACCTTGAGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGC 1080  
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 T.ovis10-16 CTTACGACCTTGAGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGC 1051  
 T.ovis10-15 CTTACGACCTTGAGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGC 1051  
 T.ovis11-11 CTTACGACCTTGAGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGC 775  
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 T.ovis9-21 CTTACGACCTTGAGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGC 1051  
 T.ovis8 CTTACGACCTTGAGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGC 1025  
 T.ovis8-24 CTTACGACCTTGAGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGC 1080  
 T.ovisConsen CTTACGACCTTGAGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGC 1080

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 T.ovis11-1 TGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCCGTGGAGCCTGCGGCTTAATTTG 835  
 T.ovis10-16 TGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCCGTGGAGCCTGCGGCTTAATTTG 1111  
 T.ovis10-15 TGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCCGTGGAGCCTGCGGCTTAATTTG 1111  
 T.ovis11-11 TGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCCGTGGAGCCTGCGGCTTAATTTG 835  
 T.ovis11-3 TGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCCGTGGAGCCTGCGGCTTAATTTG 835  
 T.ovis9-21 TGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCCGTGGAGCCTGCGGCTTAATTTG 1111  
 T.ovis8 TGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCCGTGGAGCCTGCGGCTTAATTTG 1085  
 T.ovis8-24 TGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCCGTGGAGCCTGCGGCTTAATTTG 1140  
 T.ovisConsen TGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGCCGTGGAGCCTGCGGCTTAATTTG 1140

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 T.ovis11-11 ACTCAACACGGGGAAACTCACCAGGTCCAGACAAAGGAAGGATTGACAGATTGATAGCTC 895  
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 T.ovis9-21 ACTCAACACGGGGAAACTCACCAGGTCCAGACAAAGGAAGGATTGACAGATTGATAGCTC 1171  
 T.ovis8 ACTCAACACGGGGAAACTCACCAGGTCCAGACAAAGGAAGGATTGACAGATTGATAGCTC 1145  
 T.ovis8-24 ACTCAACACGGGGAAACTCACCAGGTCCAGACAAAGGAAGGATTGACAGATTGATAGCTC 1200  
 T.ovisConsen ACTCAACACGGGGAAACTCACCAGGTCCAGACAAAGGAAGGATTGACAGATTGATAGCTC 1200

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 T.ovis10-15 TTTCCTTGATTCCTTTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTG 1231  
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 T.ovis8 TTTCCTTGATTCCTTTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTG 1205  
 T.ovis8-24 TTTCCTTGATTCCTTTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTG 1260  
 T.ovisConsen TTTCCTTGATTCCTTTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTG 1260

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 T.ovis11-1 GTTAATTCCGTTAACGAACGAGACCTTAACCTGCTAAATAGGGTACGGGAATAAGCTTTT 1015  
 T.ovis10-16 GTTAATTCCGTTAACGAACGAGACCTTAACCTGCTAAATAGGGTACGGGAATAAGCTTTT 1291  
 T.ovis10-15 GTTAATTCCGTTAACGAACGAGACCTTAACCTGCTAAATAGGGTACGGGAATAAGCTTTT 1291  
 T.ovis11-11 GTTAATTCCGTTAACGAACGAGACCTTAACCTGCTAAATAGGGTACGGGAATAAGCTTTT 1015  
 T.ovis11-3 GTTAATTCCGTTAACGAACGAGACCTTAACCTGCTAAATAGGGTACGGGAATAAGCTTTT 1015  
 T.ovis9-21 GTTAATTCCGTTAACGAACGAGACCTTAACCTGCTAAATAGGGTACGGGAATAAGCTTTT 1291  
 T.ovis8 GTTAATTCCGTTAACGAACGAGACCTTAACCTGCTAAATAGGGTACGGGAATAAGCTTTT 1265  
 T.ovis8-24 GTTAATTCCGTTAACGAACGAGACCTTAACCTGCTAAATAGGGTACGGGAATAAGCTTTT 1320  
 T.ovisConsen GTTAATTCCGTTAACGAACGAGACCTTAACCTGCTAAATAGGGTACGGGAATAAGCTTTT 1320

T.ovis8-12 GCTGTCCCCTGATCGCTTCTTAGAGGGACTTTGCGGTTATAAATCGCAAGGAAGTTTAAG 1380  
 T.ovis11-1 GCTGTCCCCTGATCGCTTCTTAGAGGGACTTT----- 1047  
 T.ovis10-16 GCTGTCCCCTTATCGCTTCTTAGAGGGACTTTGCGGTTATAAATCGCAAGGAAGTTTAAG 1351  
 T.ovis10-15 GCTGTCCCCTTATCGCTTCTTAGAGGGACTTTGCGGTTATAAATCGCAAGGAAGTTTAAG 1351  
 T.ovis11-11 GCTGTCCCCTTATCGCTTCTTAGAGGGACTTT----- 1047  
 T.ovis11-3 GCTGTCCCCTGATCGCTTCTTAGAGGGACTTT----- 1047  
 T.ovis9-21 GCTGTCCCCTTATCGCTTCTTAGAGGGACTTTGCGGTTATAAATCGCAAGGAAGTTTAAG 1351  
 T.ovis8 GCTGTCCCCTGATCGCTTCTTAGAGGGACTTTGCGGTTATAAATCGCAAGGAAGTTTAAG 1325  
 T.ovis8-24 GCTGTCCCCTGATCGCTTCTTAGAGGGACTTTGCGGTTATAAATCGCAAGGAAGTTTAAG 1380  
 T.ovisConsen GCTGTCCCCTGATCGCTTCTTAGAGGGACTTTGCGGTTATAAATCGCAAGGAAGTTTAAG 1380

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 T.ovis11-1 -----  
 T.ovis10-16 GCAATAACAGGTCTGTGATGCCCTTAGATGTCCTGGGCTGCACGCGCGCTACACTGATGC 1411  
 T.ovis10-15 GCAATAACAGGTCTGTGATGCCCTTAGATGTCCTGGGCTGCACGCGCGCTACACTGATGC 1411  
 T.ovis11-11 -----  
 T.ovis11-3 -----  
 T.ovis9-21 GCAATAACAGGTCTGTGATGCCCTTAGATGTCCTGGGCTGCACGCGCGCTACACTGATGC 1411  
 T.ovis8 GCAATAACAGGTCTGTGATGCCCTTAGATGTCCTGGGCTGCACGCGCGCTACACTGATGC 1385  
 T.ovis8-24 GCAATAACAGGTCTGTGATGCCCTTAGATGCCCTGGGCTGCACGCGCGCTACACTGATGC 1440  
 T.ovisConsen GCAATAACAGGTCTGTGATGCCCTTAGATGTCCTGGGCTGCACGCGCGCTACACTGATGC 1440

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 T.ovis10-15 GTTCATCGAGTTTATCCTTGGCCGAGAGGCCTGGGTAATCTTTAGTACGCATCGTGATGG 1471  
 T.ovis11-11 -----  
 T.ovis11-3 -----  
 T.ovis9-21 GTTCATCGAGTTTATCCTTGGCCGAGAGGCCTGGGTAATCTTTAGTACGCATCGTGATGG 1471  
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 T.ovis8-24 GTTCATCGAGTTTATCCTTGGCCGAGAGGCCTGGGTAATCTTTAGTACGCATCGTGATGG 1500  
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 T.ovis10-15 GGATCGATTATTGCAATTATTAATCGTGAACGAGGAATGCCTAGTATGCGCAAGTCATCA 1531  
 T.ovis11-11 -----  
 T.ovis11-3 -----  
 T.ovis9-21 GGATCGATTATTGCAATTATTAATCGTGAACGAGGAATGCCTAGTATGCGCAAGTCATCA 1531  
 T.ovis8 GGATCGATTATTGCAATTATTAATCGTGAACGAGGAATGCCTAGTATGCGCAAGTCATCA 1505  
 T.ovis8-24 GGATCGATTATTGCAATTATTAATCGTGAACGAGGAATGCCTAGTATGCGCAAGTCATCA 1560  
 T.ovisConsen GGATCGATTATTGCAATTATTAATCGTGAACGAGGAATGCCTAGTATGCGCAAGTCATCA 1560

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 T.ovis11-1 -----  
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 T.ovis10-15 GCTTGTGCAGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTCCTACCGATCGAG 1591  
 T.ovis11-11 -----  
 T.ovis11-3 -----  
 T.ovis9-21 GCTTGTGCAGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTCCTACCGATCGAG 1591  
 T.ovis8 GCTTGTGCAGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTCCTACCGATCGAG 1565  
 T.ovis8-24 GCTTGTGCAGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCCCCCTACCGATCGAG 1620  
 T.ovisConsen GCTTGTGCAGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTCCTACCGATCGAG 1620

T.ovis8-12 TGATCCGGTGAATTATTCGGACCGTGATGTTCCCGTCAGGGAGCGTCTAGGGAAGTTTTG 1680  
 T.ovis11-1 -----  
 T.ovis10-16 TGATCCGGTGAATTATTCGGACCGTGATGTTCCCGTCAGGGAGCGTCTAGGGAAGTTTTG 1651  
 T.ovis10-15 TGATCCGGTGAATTATTCGGACCGTGATGTTCCCGTCAGGGAGCGTCTAGGGAAGTTTTG 1651  
 T.ovis11-11 -----  
 T.ovis11-3 -----  
 T.ovis9-21 TGATCCGGTGAATTATTCGGACCGTGATGTTCCCGTCAGGGAGCGTCTAGGGAAGTTTTG 1651  
 T.ovis8 TGATCCGGTGAATTATTCGGACCGTGATGTTCCCGTCAGGGAGCGT----- 1611  
 T.ovis8-24 TGATCCGGTGAATTATTCGGACCGTGATGTTCCCGTCAGGGAGCGTCTAGGGAAGTTTTG 1680  
 T.ovisConsen TGATCCGGTGAATTATTCGGACCGTGATGTTCCCGTCAGGGAGCGTCTAGGGAAGTTTTG 1680

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 T.ovis11-1 -----  
 T.ovis10-16 TGAACCTTATCACTTAAAGGAAGGAGAAGTCG----- 1683  
 T.ovis10-15 TGAACCTTATCACTTAAAGGAAGGAGAAGTCG----- 1683  
 T.ovis11-11 -----  
 T.ovis11-3 -----  
 T.ovis9-21 TGAACCTTATCACTTAAAGGAAGGAGAAGTCG----- 1683  
 T.ovis8 -----  
 T.ovis8-24 TGAACCTTATCACTTAAAGGAAGGAGAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCA 1740  
 T.ovisConsen TGAACCTTATCACTTAAAGGAAGGAGAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCA 1740

T.ovis8-12	GAAGGATC 1748
T.ovis11-1	-----
T.ovis10-16	-----
T.ovis10-15	-----
T.ovis11-11	-----
T.ovis11-3	-----
T.ovis9-21	-----
T.ovis8	-----
T.ovis8-24	GAAGGATC 1748
T.ovisConsen	GAAGGATC 1748

## APPENDIX 3

## ITS 1-5.8S-ITS 2 Gene Region Alignment

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TsIk_1      ----ATGTGCGCAAGTTGCGCCCCCGTCATCTTTTGATTTCATTAATACTAACTTGTGG 56
TbMi_14    -----
TsCh_1     -----
TbAr_20    -----
TsIk_2     ATGTGCGCAAGTTGCGCCCCGACATCTTTTGATTTCATTGTTTTAAATGCTAACTTGTGG 60
TbMi_3     -----
TsCh_4     -----
TsIk_7     ----ATGTGCGCAAGTTGCGCCCCCGTCATCTTTTGATTTCATTAATACTAACTTGTGG 56
TbTx_6     -----
TbAr_15    -----
TsIk_6     ----ATGTGCGCAAGTTGCGCCCCCGTCATCTTTTGATTTCATTAATACTAACTTGTGG 56
TbTx_11    -----
TbAr_25    -----
TsCh_5     -----
TsCh_2     -----
TbMi_5     -----
TbOk_10    -----
TbTx_5     -----
TsCh_3     -----
TbOk_9     -----
TbMi_15    -----
TbOk_8     -----
Tan5_8     -----
Tan7_7     -----
Tan1_3     -----
Tan2_12    -----
Tan3_9     -----
Tan3_3     -----
Tan5_7     -----
Tan3_8     -----
Tan6_11    -----
Tan7_18    -----
Tan1_2     -----
Tan5_13    -----
Tan2_3     -----
Tan2_11    -----
Tan6_18    -----
Tan6_24    -----
Tan1_13    -----
Tan7_13    -----
Tpar_U     -----
TmIn_10    -----
Tpar_AF    -----
TmIn_13    -----
TmIn_3     -----
Tan1_14    -----
Tan5_12    -----
Tan2_5     -----
Tan2_13    -----
Tan3_6     -----
Tan2_7     -----
TcerOkE_12 -----
TcerW2_9   -----
TcerCanE_10 -----
TcerCanE_7 -----
TcerW1_17 -----
TcerOkE_13 -----
TcerCanE_1 -----
TcerCanE_8 -----
TcerWisE   -----
Tcer183_8 -----
TcerOkE_11 -----
TcerInE_2  -----
Tcer181_1  -----

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TcerOkE\_10 -----  
 TcerW2\_10 -----  
 TcerCanE\_6 -----  
 TcerW3\_2 -----  
 Tcer181\_2 -----  
 TcerW1\_24 -----  
 Tcer183\_7 -----  
 TcerW2-3 -----  
 Tcer181\_10 -----  
 TcerW1\_16 -----  
 TcerW3\_8 -----  
 TcerInE\_1 -----  
 TcerW3\_7 -----  
 TcerInE\_3 -----  
 TcerCanE\_11 -----  
 Tcer183\_5 -----  
 ThDG\_10 -----  
 ThDG\_13 -----  
 ThDG\_12 -----  
 ThDG\_14 -----  
 ThDG\_11 -----  
 To8\_8 -----  
 To9\_13 -----  
 To9\_10 -----  
 To11\_5 -----  
 To9\_11 -----  
 To9\_12 -----  
 To11\_1 -----  
 To8\_4 -----  
 To8\_9 -----  
 To9\_14 -----  
 To11\_2 -----  
 Cfelis\_Tx -----  
 Olonga -----

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 TbMi\_14 -----  
 TsCh\_1 -----  
 TbAr\_20 -----  
 TsIk\_2 TAGCTTGTGCGCCCTTTTCCGAATGACACTTGACTTTCATTATGTGCCTGTCACGTAAAA 120  
 TbMi\_3 -----  
 TsCh\_4 -----  
 TsIk\_7 TAGCTTGTGCAACGCTTTTCCGAATGACACTTGACATTCAT-TGTGCCTGTCACGTAAAA 115  
 TbTx\_6 -----  
 TbAr\_15 -----  
 TsIk\_6 TAGCTTGTGCAACGCTTTTCCGAATGACACTTGACATTCAT-TGTGCCTGTCACGTAAAA 115  
 TbTx\_11 -----  
 TbAr\_25 -----  
 TsCh\_5 -----  
 TsCh\_2 -----  
 TbMi\_5 -----  
 TbOk\_10 -----  
 TbTx\_5 -----  
 TsCh\_3 -----  
 TbOk\_9 -----  
 TbMi\_15 -----  
 TbOk\_8 -----  
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 Tan7\_7 -----  
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 Tan7\_18 -----  
 Tan1\_2 -----  
 Tan5\_13 -----

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Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
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Tmln_10	-----
Tpar_AF	-----
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TcerWisE	-----
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TcerCanE_6	-----
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TcerW1_24	-----
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ThDG_11	-----
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To9_13	-----
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To11_5	-----
To9_11	-----
To9_12	-----
To11_1	-----
To8_4	-----
To8_9	-----
To9_14	-----
To11_2	-----
Cfelis_Tx	-----
Olonga	-----

TsIk_1	CACGTACAGGTGAAGGTGATTTAACAGTTTACTCATTGACTACTCGGGTCACCTGGGTGT 175
TbMi_14	-----
TsCh_1	-----



TbAr_20	-----
TsIk_2	CACGTACAGGTGACGGTGATATAACAGTTTACTCATTGACTCTTCGGGTCAACTGGGAGT 180
TbMi_3	-----
TsCh_4	-----
TsIk_7	CACGTACAGGTGAAGGTGATTTAACAGTTTACTCATTGACTACTCGGGTCACCTGGGTGT 175
TbTx_6	-----
TbAr_15	-----
TsIk_6	CACGTACAGGTGAAGGTGATTTAACAGTTTACTCATTGACTACTCGGGTCACCTGGGTGT 175
TbTx_11	-----
TbAr_25	-----
TsCh_5	-----
TsCh_2	-----
TbMi_5	-----
TbOk_10	-----
TbTx_5	-----
TsCh_3	-----
TbOk_9	-----
TbMi_15	-----
TbOk_8	-----
Tan5_8	-----
Tan7_7	-----
Tan1_3	-----
Tan2_12	-----
Tan3_9	-----
Tan3_3	-----
Tan5_7	-----
Tan3_8	-----
Tan6_11	-----
Tan7_18	-----
Tan1_2	-----
Tan5_13	-----
Tan2_3	-----
Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
Tmln_10	-----
Tpar_AF	-----
Tmln_13	-----
Tmln_3	-----
Tan1_14	-----
Tan5_12	-----
Tan2_5	-----
Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
TcerOkE_12	-----
TcerW2_9	-----
TcerCanE_10	-----
TcerCanE_7	-----
TcerW1_17	-----
TcerOkE_13	-----
TcerCanE_1	-----
TcerCanE_8	-----
TcerWisE	-----
Tcer183_8	-----
TcerOkE_11	-----
TcerInE_2	-----
Tcer181_1	-----
TcerOkE_10	-----
TcerW2_10	-----
TcerCanE_6	-----
TcerW3_2	-----
Tcer181_2	-----
TcerW1_24	-----
Tcer183_7	-----
TcerW2-3	-----
Tcer181_10	-----

TcerW1_16	-----
TcerW3_8	-----
TcerInE_1	-----
TcerW3_7	-----
TcerInE_3	-----
TcerCanE_11	-----
Tcer183_5	-----
ThDG_10	-----
ThDG_13	-----
ThDG_12	-----
ThDG_14	-----
ThDG_11	-----
To8_8	-----
To9_13	-----
To9_10	-----
To11_5	-----
To9_11	-----
To9_12	-----
To11_1	-----
To8_4	-----
To8_9	-----
To9_14	-----
To11_2	-----
Cfelis_Tx	-----
Olonga	-----
TsIk_1	CAAATTGTGCCACCGTCTCTGACACACCGTCATAAGTTACTCGTCGGTGTGTCAGGACTG 235
TbMi_14	-----
TsCh_1	-----
TbAr_20	-----
TsIk_2	CAAATTGTCCCACCGTCTCTGACATACCGTCATAAGTTACTCGTCGGTGTGTCAGGACTG 240
TbMi_3	-----
TsCh_4	-----
TsIk_7	CAAATTGTGCCACCGTCTCTGACATACCGTCATAAGTTACTCGTCGGTGTGTCAGGACTG 235
TbTx_6	-----
TbAr_15	-----
TsIk_6	CAAATTGTGCCACCGTCTCTGACACACCGTCATAAGTTACTCGTCGGTGTGTCAGGACTG 235
TbTx_11	-----
TbAr_25	-----
TsCh_5	-----
TsCh_2	-----
TbMi_5	-----
TbOk_10	-----
TbTx_5	-----
TsCh_3	-----
TbOk_9	-----
TbMi_15	-----
TbOk_8	-----
Tan5_8	-----
Tan7_7	-----
Tan1_3	-----
Tan2_12	-----
Tan3_9	-----
Tan3_3	-----
Tan5_7	-----
Tan3_8	-----
Tan6_11	-----
Tan7_18	-----
Tan1_2	-----
Tan5_13	-----
Tan2_3	-----
Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
Tmln_10	-----
Tpar_AF	-----
Tmln_13	-----

TmIn\_3 -----  
 Tan1\_14 -----  
 Tan5\_12 -----  
 Tan2\_5 -----  
 Tan2\_13 -----  
 Tan3\_6 -----  
 Tan2\_7 -----  
 TcerOkE\_12 -----  
 TcerW2\_9 -----  
 TcerCanE\_10 -----  
 TcerCanE\_7 -----  
 TcerW1\_17 -----  
 TcerOkE\_13 -----  
 TcerCanE\_1 -----  
 TcerCanE\_8 -----  
 TcerWisE -----  
 Tcer183\_8 -----  
 TcerOkE\_11 -----  
 TcerInE\_2 -----  
 Tcer181\_1 -----  
 TcerOkE\_10 -----  
 TcerW2\_10 -----  
 TcerCanE\_6 -----  
 TcerW3\_2 -----  
 Tcer181\_2 -----  
 TcerW1\_24 -----  
 Tcer183\_7 -----  
 TcerW2-3 -----  
 Tcer181\_10 -----  
 TcerW1\_16 -----  
 TcerW3\_8 -----  
 TcerInE\_1 -----  
 TcerW3\_7 -----  
 TcerInE\_3 -----  
 TcerCanE\_11 -----  
 Tcer183\_5 -----  
 ThDG\_10 -----  
 ThDG\_13 -----  
 ThDG\_12 -----  
 ThDG\_14 -----  
 ThDG\_11 -----  
 To8\_8 -----  
 To9\_13 -----  
 To9\_10 -----  
 To11\_5 -----  
 To9\_11 -----  
 To9\_12 -----  
 To11\_1 -----  
 To8\_4 -----  
 To8\_9 -----  
 To9\_14 -----  
 To11\_2 -----  
 Cfelis\_Tx -----  
 Olonga -----

TsIk\_1 GGGGCGGGTTTCTACCCAGGGAGTCGTGCGTCTAATCACTGGTCGACACATTTGTGTTTT 295  
 TbMi\_14 -----  
 TsCh\_1 -----  
 TbAr\_20 -----  
 TsIk\_2 GGGGCGGGTTTCTACCCAGGGAGTCGTGCGTCTAATCACTGGTCGACACATTTGTGTTTT 300  
 TbMi\_3 -----  
 TsCh\_4 -----  
 TsIk\_7 GGGGCGGGTTTCTACCCAGGGAGTCGTGCGTCTAATCACTGGTCGACACATTTGTGTTTT 295  
 TbTx\_6 -----  
 TbAr\_15 -----  
 TsIk\_6 GGGGCGGGTTTCTACCCAGGGAGTCGTGCGTCTAATCACTGGTCGACACATTTGTGTTTT 295  
 TbTx\_11 -----  
 TbAr\_25 -----  
 TsCh\_5 -----

TsCh_2	-----
TbMi_5	-----
TbOk_10	-----
TbTx_5	-----
TsCh_3	-----
TbOk_9	-----
TbMi_15	-----
TbOk_8	-----
Tan5_8	-----
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Tan1_3	-----
Tan2_12	-----
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Tan5_7	-----
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Tan7_18	-----
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Tan2_3	-----
Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
TmIn_3	-----
Tan1_14	-----
Tan5_12	-----
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Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
TcerOkE_12	-----
TcerW2_9	-----
TcerCanE_10	-----
TcerCanE_7	-----
TcerW1_17	-----
TcerOkE_13	-----
TcerCanE_1	-----
TcerCanE_8	-----
TcerWisE	-----
Tcer183_8	-----
TcerOkE_11	-----
TcerInE_2	-----
Tcer181_1	-----
TcerOkE_10	-----
TcerW2_10	-----
TcerCanE_6	-----
TcerW3_2	-----
Tcer181_2	-----
TcerW1_24	-----
Tcer183_7	-----
TcerW2-3	-----
Tcer181_10	-----
TcerW1_16	-----
TcerW3_8	-----
TcerInE_1	-----
TcerW3_7	-----
TcerInE_3	-----
TcerCanE_11	-----
Tcer183_5	-----
ThDG_10	-----
ThDG_13	-----
ThDG_12	-----
ThDG_14	-----

ThDG_11	-----
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To11_5	-----
To9_11	-----
To9_12	-----
To11_1	-----
To8_4	-----
To8_9	-----
To9_14	-----
To11_2	-----
Cfelis_Tx	-----
Olonga	-----
TsIk_1	AGGCAGCGACGAAGCATGACCGTTAACAAGACAGTGAGCGGTTCCACCTGGGTAAAAACC 355
TbMi_14	-----
TsCh_1	-----
TbAr_20	-----
TsIk_2	AGGCAGCGACGAAGCATGACCGTTAACAAGACAGTGAGCGGTTCCACCTGGGTAAAA-CC 359
TbMi_3	-----
TsCh_4	-----
TsIk_7	AGGCAGCGACGAAGCATGACCGTTAACAAGACAGTGAGCGGTTCCACCTGGGTAAAATCC 355
TbTx_6	-----
TbAr_15	-----
TsIk_6	AGGCAGCGACGAAGCATGACCGTTAACAAGACAGTGAGCGGTTCCACCTGGGTAAAATCC 355
TbTx_11	-----
TbAr_25	-----
TsCh_5	-----
TsCh_2	-----
TbMi_5	-----
TbOk_10	-----
TbTx_5	-----
TsCh_3	-----
TbOk_9	-----
TbMi_15	-----
TbOk_8	-----
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Tan2_3	-----
Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
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TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
TmIn_3	-----
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Tan2_5	-----
Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
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TcerCanE_10	-----

TcerCanE\_7 -----  
TcerW1\_17 -----  
TcerOkE\_13 -----  
TcerCanE\_1 -----  
TcerCanE\_8 -----  
TcerWisE -----  
Tcer183\_8 -----  
TcerOkE\_11 -----  
TcerInE\_2 -----  
Tcer181\_1 -----  
TcerOkE\_10 -----  
TcerW2\_10 -----  
TcerCanE\_6 -----  
TcerW3\_2 -----  
Tcer181\_2 -----  
TcerW1\_24 -----  
Tcer183\_7 -----  
TcerW2-3 -----  
Tcer181\_10 -----  
TcerW1\_16 -----  
TcerW3\_8 -----  
TcerInE\_1 -----  
TcerW3\_7 -----  
TcerInE\_3 -----  
TcerCanE\_11 -----  
Tcer183\_5 -----  
ThDG\_10 -----  
ThDG\_13 -----  
ThDG\_12 -----  
ThDG\_14 -----  
ThDG\_11 -----  
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To9\_10 -----  
To11\_5 -----  
To9\_11 -----  
To9\_12 -----  
To11\_1 -----  
To8\_4 -----  
To8\_9 -----  
To9\_14 -----  
To11\_2 -----  
Cfelis\_Tx -----  
Olonga -----

TsIk\_1 CAGAGGGTTGTAAGTTATGACAAACAGTGCAGCCTTTTCAAACGGCGGGGTTATGTGCC 415  
TbMi\_14 -----  
TsCh\_1 -----  
TbAr\_20 -----  
TsIk\_2 CAGAGGGTTGTAAGTTATGACAAACAGTGCAGCCTTTTCAAACGGCGGGGTTATGTGCC 419  
TbMi\_3 -----  
TsCh\_4 -----  
TsIk\_7 CAGAGGGTTCTAAGTTATGACAAACAGTGCAGCCTTTTCAAACGGCGAGGTTATGTGCC 415  
TbTx\_6 -----  
TbAr\_15 -----  
TsIk\_6 CAGAGGGTTCTAAGTTATGACAAACAGTGCAGCCTTTTCAAACGGCGAGGTTATGTGCC 415  
TbTx\_11 -----  
TbAr\_25 -----  
TsCh\_5 -----  
TsCh\_2 -----  
TbMi\_5 -----  
TbOk\_10 -----  
TbTx\_5 -----  
TsCh\_3 -----  
TbOk\_9 -----  
TbMi\_15 -----  
TbOk\_8 -----  
Tan5\_8 -----  
Tan7\_7 -----

Tan1_3	-----
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Tan3_8	-----
Tan6_11	-----
Tan7_18	-----
Tan1_2	-----
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Tan2_3	-----
Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
TmIn_3	-----
Tan1_14	-----
Tan5_12	-----
Tan2_5	-----
Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
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TcerW2_9	-----
TcerCanE_10	-----
TcerCanE_7	-----
TcerW1_17	-----
TcerOkE_13	-----
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TcerWisE	-----
Tcer183_8	-----
TcerOkE_11	-----
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Tcer181_1	-----
TcerOkE_10	-----
TcerW2_10	-----
TcerCanE_6	-----
TcerW3_2	-----
Tcer181_2	-----
TcerW1_24	-----
Tcer183_7	-----
TcerW2-3	-----
Tcer181_10	-----
TcerW1_16	-----
TcerW3_8	-----
TcerInE_1	-----
TcerW3_7	-----
TcerInE_3	-----
TcerCanE_11	-----
Tcer183_5	-----
ThDG_10	-----
ThDG_13	-----
ThDG_12	-----
ThDG_14	-----
ThDG_11	-----
To8_8	-----
To9_13	-----
To9_10	-----
To11_5	-----
To9_11	-----
To9_12	-----
To11_1	-----
To8_4	-----
To8_9	-----

To9_14	-----
To11_2	-----
Cfelis_Tx	-----
Olonga	-----
TsIk_1	TAAAAATCGTTTTGGACTTGGTTAGGTCGCCATGCTGATGTTTCGGGACCCCTAATGTTTAT 475
TbMi_14	-----
TsCh_1	-----
TbAr_20	-----
TsIk_2	TAAAAATCGTTTTGGACTTGGTTAGGTCGCCATGCTGATGTTTCGGGACCCCTAATGTTTAT 479
TbMi_3	-----
TsCh_4	-----
TsIk_7	TAAAAATCGTTTCGGACTTGGT-AGGTCGCCATGCTGATGTTTCGGGACCCCTAATGATGAG 474
TbTx_6	-----
TbAr_15	-----
TsIk_6	TAAAAATCGTTTCGGACTTGGT-AGGTCGCCATGCTGATGTTTCGGGACCCCTAATGATGAG 474
TbTx_11	-----
TbAr_25	-----
TsCh_5	-----
TsCh_2	-----
TbMi_5	-----
TbOk_10	-----
TbTx_5	-----
TsCh_3	-----
TbOk_9	-----
TbMi_15	-----
TbOk_8	-----
Tan5_8	-----
Tan7_7	-----
Tan1_3	-----
Tan2_12	-----
Tan3_9	-----
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Tan7_18	-----
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Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
TmIn_3	-----
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Tan5_12	-----
Tan2_5	-----
Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
TcerOkE_12	-----
TcerW2_9	-----
TcerCanE_10	-----
TcerCanE_7	-----
TcerW1_17	-----
TcerOkE_13	-----
TcerCanE_1	-----
TcerCanE_8	-----
TcerWisE	-----
Tcer183_8	-----
TcerOkE_11	-----
TcerInE_2	-----
Tcer181_1	-----
TcerOkE_10	-----



TcerW2\_10 -----  
 TcerCanE\_6 -----  
 TcerW3\_2 -----  
 Tcer181\_2 -----  
 TcerW1\_24 -----  
 Tcer183\_7 -----  
 TcerW2-3 -----  
 Tcer181\_10 -----  
 TcerW1\_16 -----  
 TcerW3\_8 -----  
 TcerInE\_1 -----  
 TcerW3\_7 -----  
 TcerInE\_3 -----  
 TcerCanE\_11 -----  
 Tcer183\_5 -----  
 ThDG\_10 -----  
 ThDG\_13 -----  
 ThDG\_12 -----  
 ThDG\_14 -----  
 ThDG\_11 -----  
 To8\_8 -----  
 To9\_13 -----  
 To9\_10 -----  
 To11\_5 -----  
 To9\_11 -----  
 To9\_12 -----  
 To11\_1 -----  
 To8\_4 -----  
 To8\_9 -----  
 To9\_14 -----  
 To11\_2 -----  
 Cfelis\_Tx -----  
 Olonga -----

TsIk\_1 ATGTGTGCAAGGCCGGCGTAGCCCAGGTGTAGACCGCGAAAGGCACGTTCCGGTTATTGTTT 535  
 TbMi\_14 -----  
 TsCh\_1 -----  
 TbAr\_20 -----  
 TsIk\_2 ATGTGTGCAAGGCCGGCGTAGCCCAGGTGTAGACCGCGAAAGGCACGTTCCGGTTATTGTTT 539  
 TbMi\_3 -----  
 TsCh\_4 -----  
 TsIk\_7 ATGTGTGCATGGCCGACGTAGCCCAGGTGTAGACCGCGAAAGGCACGTTCCGAAATTGTTT 534  
 TbTx\_6 -----  
 TbAr\_15 -----  
 TsIk\_6 ATGGTGCATGGCCGGCGTAGCCCAGGTGTAGACCGCGAAAGGCACGTTCCGGTTATTGTTT 534  
 TbTx\_11 -----  
 TbAr\_25 -----  
 TsCh\_5 -----  
 TsCh\_2 -----  
 TbMi\_5 -----  
 TbOk\_10 -----  
 TbTx\_5 -----  
 TsCh\_3 -----  
 TbOk\_9 -----  
 TbMi\_15 -----  
 TbOk\_8 -----  
 Tan5\_8 -----  
 Tan7\_7 -----  
 Tan1\_3 -----  
 Tan2\_12 -----  
 Tan3\_9 -----  
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 Tan5\_7 -----  
 Tan3\_8 -----  
 Tan6\_11 -----  
 Tan7\_18 -----  
 Tan1\_2 -----  
 Tan5\_13 -----  
 Tan2\_3 -----

Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
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Tan1_14	-----
Tan5_12	-----
Tan2_5	-----
Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
TcerOkE_12	-----
TcerW2_9	-----
TcerCanE_10	-----
TcerCanE_7	-----
TcerW1_17	-----
TcerOkE_13	-----
TcerCanE_1	-----
TcerCanE_8	-----
TcerWisE	-----
Tcer183_8	-----
TcerOkE_11	-----
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TcerOkE_10	-----
TcerW2_10	-----
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Tcer181_2	-----
TcerW1_24	-----
Tcer183_7	-----
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Tcer181_10	-----
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TcerW3_7	-----
TcerInE_3	-----
TcerCanE_11	-----
Tcer183_5	-----
ThDG_10	-----
ThDG_13	-----
ThDG_12	-----
ThDG_14	-----
ThDG_11	-----
To8_8	-----
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To9_10	-----
To11_5	-----
To9_11	-----
To9_12	-----
To11_1	-----
To8_4	-----
To8_9	-----
To9_14	-----
To11_2	-----
Cfelis_Tx	-----
Olonga	-----

TsIk_1	AGAAAGAATGTATTTTTACAGTGTAGAATGATACATGCAAAAGCAGTCCATTCTCTTAA 595
TbMi_14	-----
TsCh_1	-----
TbAr_20	-----
TsIk_2	AGAAAGAATGTATTTTTACAGTGTAGAATGATACATGCAAAAGCAGTCCATTCTCTTAA 599

TbMi\_3 -----  
TsCh\_4 -----  
Tslk\_7 AGAAAGACTGTATTTTTACAGTGTAGAACGTTACATGCATAAGCAGTCTTTTCCTCTTAG 594  
TbTx\_6 -----  
TbAr\_15 -----  
Tslk\_6 AGAAAGAATGTATTTTTACAGTGTAGAATGATACATGCAAAAGCAGTCCATTCTCTTAG 594  
TbTx\_11 -----  
TbAr\_25 -----  
TsCh\_5 -----  
TsCh\_2 -----  
TbMi\_5 -----  
TbOk\_10 -----  
TbTx\_5 -----  
TsCh\_3 -----  
TbOk\_9 -----  
TbMi\_15 -----  
TbOk\_8 -----  
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Tan7\_7 -----  
Tan1\_3 -----  
Tan2\_12 -----  
Tan3\_9 -----  
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Tan2\_3 -----  
Tan2\_11 -----  
Tan6\_18 -----  
Tan6\_24 -----  
Tan1\_13 -----  
Tan7\_13 -----  
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Tmln\_10 -----  
Tpar\_AF -----  
Tmln\_13 -----  
Tmln\_3 -----  
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Tan5\_12 -----  
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Tan3\_6 -----  
Tan2\_7 -----  
TcerOkE\_12 -----  
TcerW2\_9 -----  
TcerCanE\_10 -----  
TcerCanE\_7 -----  
TcerW1\_17 -----  
TcerOkE\_13 -----  
TcerCanE\_1 -----  
TcerCanE\_8 -----  
TcerWisE -----  
Tcer183\_8 -----  
TcerOkE\_11 -----  
TcerInE\_2 -----  
Tcer181\_1 -----  
TcerOkE\_10 -----  
TcerW2\_10 -----  
TcerCanE\_6 -----  
TcerW3\_2 -----  
Tcer181\_2 -----  
TcerW1\_24 -----  
Tcer183\_7 -----  
TcerW2-3 -----  
Tcer181\_10 -----  
TcerW1\_16 -----  
TcerW3\_8 -----

TcerInE_1	-----
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TcerInE_3	-----
TcerCanE_11	-----
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ThDG_10	-----
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ThDG_12	-----
ThDG_14	-----
ThDG_11	-----
To8_8	-----
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To11_5	-----
To9_11	-----
To9_12	-----
To11_1	-----
To8_4	-----
To8_9	-----
To9_14	-----
To11_2	-----
Cfelis_Tx	-----
Olonga	-----
TsIk_1	GCAGTCAATCTACTCTGTATGTGGGTGAAATCCCGGATTTCTGTGTGATGACCGTCCAGG 655
TbMi_14	-----
TsCh_1	-----
TbAr_20	-----
TsIk_2	GCAGTCAATCTACTCTGTATGTGGGTGAAATCCCGGATTTCTGTGTGATGACCGTCCAGG 659
TbMi_3	-----
TsCh_4	-----
TsIk_7	GCAGTCAATCTACTTTGTAGGTGGGTGAAATCCCGTATTTCTATGTGGTGACTGTCCAGG 654
TbTx_6	-----
TbAr_15	-----
TsIk_6	GCAGTCAATCTACTCTGTATGTGGGTGAAATCCCGTATTTCTGTGTGGTGACTGTCCAGG 654
TbTx_11	-----
TbAr_25	-----
TsCh_5	-----
TsCh_2	-----
TbMi_5	-----
TbOk_10	-----
TbTx_5	-----
TsCh_3	-----
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TbMi_15	-----
TbOk_8	-----
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Tan7_18	-----
Tan1_2	-----
Tan5_13	-----
Tan2_3	-----
Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
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TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
TmIn_3	-----

Tan1\_14 -----  
 Tan5\_12 -----  
 Tan2\_5 -----  
 Tan2\_13 -----  
 Tan3\_6 -----  
 Tan2\_7 -----  
 TcerOkE\_12 -----  
 TcerW2\_9 -----  
 TcerCanE\_10 -----  
 TcerCanE\_7 -----  
 TcerW1\_17 -----  
 TcerOkE\_13 -----  
 TcerCanE\_1 -----  
 TcerCanE\_8 -----  
 TcerWisE -----  
 Tcer183\_8 -----  
 TcerOkE\_11 -----  
 TcerInE\_2 -----  
 Tcer181\_1 -----  
 TcerOkE\_10 -----  
 TcerW2\_10 -----  
 TcerCanE\_6 -----  
 TcerW3\_2 -----  
 Tcer181\_2 -----  
 TcerW1\_24 -----  
 Tcer183\_7 -----  
 TcerW2-3 -----  
 Tcer181\_10 -----  
 TcerW1\_16 -----  
 TcerW3\_8 -----  
 TcerInE\_1 -----  
 TcerW3\_7 -----  
 TcerInE\_3 -----  
 TcerCanE\_11 -----  
 Tcer183\_5 -----  
 ThDG\_10 -----  
 ThDG\_13 -----  
 ThDG\_12 -----  
 ThDG\_14 -----  
 ThDG\_11 -----  
 To8\_8 -----  
 To9\_13 -----  
 To9\_10 -----  
 To11\_5 -----  
 To9\_11 -----  
 To9\_12 -----  
 To11\_1 -----  
 To8\_4 -----  
 To8\_9 -----  
 To9\_14 -----  
 To11\_2 -----  
 Cfelis\_Tx -----  
 Olonga -----

TsIk\_1 TTTTGTAACGGTCTGCCGGTTACATAACCCCCGTTGAAGCTGCATCGGCCAACATAACTA 715  
 TbMi\_14 -----  
 TsCh\_1 -----  
 TbAr\_20 -----  
 TsIk\_2 TTTTGTAACGGTCTGCCGGTTACATAACCCCCGTTGAAGCTGCATCGGCCAACATAACTA 719  
 TbMi\_3 -----  
 TsCh\_4 -----  
 TsIk\_7 TTTTGTAACGGTCTACCGGTTACATAACCCCCGTTGAAGCTGCATCGGCCATCATAACTA 714  
 TbTx\_6 -----  
 TbAr\_15 -----  
 TsIk\_6 TTTTGTAACGGTCTGCCGGTTACATAACCCCCGTTGAAGCTGCATCGGCCAACATAACTA 714  
 TbTx\_11 -----  
 TbAr\_25 -----  
 TsCh\_5 -----  
 TsCh\_2 -----

TbMi_5	-----
TbOk_10	-----
TbTx_5	-----
TsCh_3	-----
TbOk_9	-----
TbMi_15	-----
TbOk_8	-----
Tan5_8	-----
Tan7_7	-----
Tan1_3	-----
Tan2_12	-----
Tan3_9	-----
Tan3_3	-----
Tan5_7	-----
Tan3_8	-----
Tan6_11	-----
Tan7_18	-----
Tan1_2	-----
Tan5_13	-----
Tan2_3	-----
Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
TmIn_3	-----
Tan1_14	-----
Tan5_12	-----
Tan2_5	-----
Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
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TcerW2_9	-----
TcerCanE_10	-----
TcerCanE_7	-----
TcerW1_17	-----
TcerOkE_13	-----
TcerCanE_1	-----
TcerCanE_8	-----
TcerWisE	-----
Tcer183_8	-----
TcerOkE_11	-----
TcerInE_2	-----
Tcer181_1	-----
TcerOkE_10	-----
TcerW2_10	-----
TcerCanE_6	-----
TcerW3_2	-----
Tcer181_2	-----
TcerW1_24	-----
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TcerW2-3	-----
Tcer181_10	-----
TcerW1_16	-----
TcerW3_8	-----
TcerInE_1	-----
TcerW3_7	-----
TcerInE_3	-----
TcerCanE_11	-----
Tcer183_5	-----
ThDG_10	-----
ThDG_13	-----
ThDG_12	-----
ThDG_14	-----
ThDG_11	-----

To8_8	-----
To9_13	-----
To9_10	-----
To11_5	-----
To9_11	-----
To9_12	-----
To11_1	-----
To8_4	-----
To8_9	-----
To9_14	-----
To11_2	-----
Cfelis_Tx	-----
Olonga	-----
TsIk_1	TGTTCCCTCTTACTTCATGACCAGTGAGCATAGCACTATATAATCTTTAATTTTTGTCAA 775
TbMi_14	-----
TsCh_1	-----
TbAr_20	-----
TsIk_2	TGTTCCCTCTTACTTCATGACCAGTGAGCATAGCACTATATAATCTTTAATTTTTGTCAA 7-79
TbMi_3	-----
TsCh_4	-----
TsIk_7	TGTTCCCTCTCTCTTTATGACCAGTGAGCATAGCACTATATAATCTTTAATTTTTGTCAA 774
TbTx_6	-----
TbAr_15	-----
TsIk_6	TGTTCCCTCTTACTTCATGACCAGTGAGCATAGCACTATATAATCTTTAGTTTTGTCAA 774
TbTx_11	-----
TbAr_25	-----
TsCh_5	-----
TsCh_2	-----
TbMi_5	-----
TbOk_10	-----
TbTx_5	-----
TsCh_3	-----
TbOk_9	-----
TbMi_15	-----
TbOk_8	-----
Tan5_8	-----
Tan7_7	-----
Tan1_3	-----
Tan2_12	-----
Tan3_9	-----
Tan3_3	-----
Tan5_7	-----
Tan3_8	-----
Tan6_11	-----
Tan7_18	-----
Tan1_2	-----
Tan5_13	-----
Tan2_3	-----
Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
TmIn_3	-----
Tan1_14	-----
Tan5_12	-----
Tan2_5	-----
Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
TcerOkE_12	-----
TcerW2_9	-----
TcerCanE_10	-----
TcerCanE_7	-----

TcerW1\_17 -----  
 TcerOkE\_13 -----  
 TcerCanE\_1 -----  
 TcerCanE\_8 -----  
 TcerWisE -----  
 Tcer183\_8 -----  
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 TcerInE\_2 -----  
 Tcer181\_1 -----  
 TcerOkE\_10 -----  
 TcerW2\_10 -----  
 TcerCanE\_6 -----  
 TcerW3\_2 -----  
 Tcer181\_2 -----  
 TcerW1\_24 -----  
 Tcer183\_7 -----  
 TcerW2-3 -----  
 Tcer181\_10 -----  
 TcerW1\_16 -----  
 TcerW3\_8 -----  
 TcerInE\_1 -----  
 TcerW3\_7 -----  
 TcerInE\_3 -----  
 TcerCanE\_11 -----  
 Tcer183\_5 -----  
 ThDG\_10 -----  
 ThDG\_13 -----  
 ThDG\_12 -----  
 ThDG\_14 -----  
 ThDG\_11 -----  
 To8\_8 -----  
 To9\_13 -----  
 To9\_10 -----  
 To11\_5 -----  
 To9\_11 -----  
 To9\_12 -----  
 To11\_1 -----  
 To8\_4 -----  
 To8\_9 -----  
 To9\_14 -----  
 To11\_2 -----  
 Cfelis\_Tx -----  
 Olonga -----

TsIk\_1 CTTGGGATTAGCTGAGCCTGTAAGCAATTACTGGTTTTGCTAAATGATCGTTATTAATCC 835  
 TbMi\_14 -----  
 TsCh\_1 -----  
 TbAr\_20 -----  
 TsIk\_2 CTTGGGATTAGCTGAGCCTGTAAGCAATTACTGGTTTTGCTAAATGATCGTTATTAATCC 839  
 TbMi\_3 -----  
 TsCh\_4 -----  
 TsIk\_7 CTTGGGATTAGCTGAGCCTGTAAGCAATTACTGGTTTTGCTAAATGATCGTTATTAATCC 834  
 TbTx\_6 -----  
 TbAr\_15 -----  
 TsIk\_6 CTTGGGATTAGCTGAGCCTGTAAGCAATTACTGGTTTTGCTAAATGATCGTTATTAATCC 834  
 TbTx\_11 -----  
 TbAr\_25 -----  
 TsCh\_5 -----  
 TsCh\_2 -----  
 TbMi\_5 -----  
 TbOk\_10 -----  
 TbTx\_5 -----  
 TsCh\_3 -----  
 TbOk\_9 -----  
 TbMi\_15 -----  
 TbOk\_8 -----  
 Tan5\_8 -----  
 Tan7\_7 -----  
 Tan1\_3 -----



Tan2_12	-----
Tan3_9	-----
Tan3_3	-----
Tan5_7	-----
Tan3_8	-----
Tan6_11	-----
Tan7_18	-----
Tan1_2	-----
Tan5_13	-----
Tan2_3	-----
Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
TmIn_3	-----
Tan1_14	-----
Tan5_12	-----
Tan2_5	-----
Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
TcerOkE_12	-----
TcerW2_9	-----
TcerCanE_10	-----
TcerCanE_7	-----
TcerW1_17	-----
TcerOkE_13	-----
TcerCanE_1	-----
TcerCanE_8	-----
TcerWisE	-----
Tcer183_8	-----
TcerOkE_11	-----
TcerInE_2	-----
Tcer181_1	-----
TcerOkE_10	-----
TcerW2_10	-----
TcerCanE_6	-----
TcerW3_2	-----
Tcer181_2	-----
TcerW1_24	-----
Tcer183_7	-----
TcerW2-3	-----
Tcer181_10	-----
TcerW1_16	-----
TcerW3_8	-----
TcerInE_1	-----
TcerW3_7	-----
TcerInE_3	-----
TcerCanE_11	-----
Tcer183_5	-----
ThDG_10	-----
ThDG_13	-----
ThDG_12	-----
ThDG_14	-----
ThDG_11	-----
To8_8	-----
To9_13	-----
To9_10	-----
To11_5	-----
To9_11	-----
To9_12	-----
To11_1	-----
To8_4	-----
To8_9	-----
To9_14	-----

To11_2	-----
Cfelix_Tx	-----
Olonga	-----
TsIk_1	TGCTTTGTGGTGTGAATTAGTTTGATAACGCTAGTTTGGGTTAGTAATGGTTTAAAAAT 895
TbMi_14	-----
TsCh_1	-----
TbAr_20	-----
TsIk_2	TGCTTTGTGGTGTGAATTAGTTTGATAACGCTAGTTTGGGTTAGTAATGGTTTAAAAAT 899
TbMi_3	-----
TsCh_4	-----
TsIk_7	TGCTTAGTGGTGTGAATTAGTTTGATAACGCTAGTTTGGGTTAGTAATGGTTTAAAAAT 894
TbTx_6	-----
TbAr_15	-----
TsIk_6	TGCTTTGTGGTGTGAATTAGTTTGATAACGCTAGTTTGGGTTAGTAATGGTTTAAAAAT 894
TbTx_11	-----
TbAr_25	-----
TsCh_5	-----
TsCh_2	-----
TbMi_5	-----
TbOk_10	-----
TbTx_5	-----
TsCh_3	-----
TbOk_9	-----
TbMi_15	-----
TbOk_8	-----
Tan5_8	-----
Tan7_7	-----
Tan1_3	-----
Tan2_12	-----
Tan3_9	-----
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Tan5_7	-----
Tan3_8	-----
Tan6_11	-----
Tan7_18	-----
Tan1_2	-----
Tan5_13	-----
Tan2_3	-----
Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
TmIn_3	-----
Tan1_14	-----
Tan5_12	-----
Tan2_5	-----
Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
TcerOkE_12	-----
TcerW2_9	-----
TcerCanE_10	-----
TcerCanE_7	-----
TcerW1_17	-----
TcerOkE_13	-----
TcerCanE_1	-----
TcerCanE_8	-----
TcerWisE	-----
Tcer183_8	-----
TcerOkE_11	-----
TcerInE_2	-----
Tcer181_1	-----
TcerOkE_10	-----

TcerW2\_10 -----  
 TcerCanE\_6 -----  
 TcerW3\_2 -----  
 Tcer181\_2 -----  
 TcerW1\_24 -----  
 Tcer183\_7 -----  
 TcerW2-3 -----  
 Tcer181\_10 -----  
 TcerW1\_16 -----  
 TcerW3\_8 -----  
 TcerInE\_1 -----  
 TcerW3\_7 -----  
 TcerInE\_3 -----  
 TcerCanE\_11 -----  
 Tcer183\_5 -----  
 ThDG\_10 -----  
 ThDG\_13 -----  
 ThDG\_12 -----  
 ThDG\_14 -----  
 ThDG\_11 -----  
 To8\_8 ACGCTAAATTATTTAGGGTATGTGTTGTGATTAATCATGACATGTATCATTATGTGAGTG 60  
 To9\_13 ACGCTAAATTATTTAGGGTATGTGTTGTGATTAATCATGACATGTATCATTATGTGAGTG 60  
 To9\_10 ACGCTAAATTATTTAGGGTATGTGTTGTGATTAATCATGACATGTATCATTATGTGAGTG 60  
 To11\_5 ACGCTAAATTATTTAGGGTATGTGTTGTGATTAATCATGACATGTATCATTATGTGAGTG 60  
 To9\_11 ACGCTAAATTATTTAGGGTATGTGTTGTGATTAATCATGACATGTATCATTATGTGAGTG 60  
 To9\_12 ACGCTAAATTATTTAGGGTATGTGTTGTGATTAATCATGACATGTATCATTATGTGAGTG 60  
 To11\_1 ACGCTAAATTATTTAGGGTATGTGTTGTGATTAATCATGACATGTATCATTATGTGAGTG 60  
 To8\_4 ACGCTAAATTATTTAGGGTATGTGTTGTGATTAATCATGACATGTATCATTATGTGAGTG 60  
 To8\_9 ACGCTAAATTATTTAGGGTATGTGTTGTGATTAATCATGACATGTATCATTATGTGAGTG 60  
 To9\_14 ACGCTAAATTATTTAGGGTATGTGTTGTGATTAATCATGACATGTATCATTATGTGAGTG 60  
 To11\_2 ACGCTAAATTATTTAGGGTATGTGTTGTGATTAATCATGACATGTATCATTATGTGAGTG 60  
 Cfelis\_Tx -----  
 Olonga -----

TsIk\_1 TAGTGTCCCAAGTAAGTGCCTAACGGCCATTTTTAAACTGAAGACTTAATTTTAATTTT 955  
 TbMi\_14 -----  
 TsCh\_1 -----  
 TbAr\_20 -----  
 TsIk\_2 TAGTGTCCCAAGTAAGTGCCTAACGGCCATTTTTAAACTGAAGACTTAATTTTAATTTT 959  
 TbMi\_3 -----  
 TsCh\_4 -----  
 TsIk\_7 TAATGTCCCAAGTAAGTGCCTAACGGCCATTTTTAAACTTAAGACTTAATTTTAATATT 954  
 TbTx\_6 -----  
 TbAr\_15 -----  
 TsIk\_6 TAGTGTCCCAAGTAAGTGCCTAACGGCCATTTTTAAACTGGAGACTTAATTTTAATTTT 954  
 TbTx\_11 -----  
 TbAr\_25 -----  
 TsCh\_5 -----  
 TsCh\_2 -----  
 TbMi\_5 -----  
 TbOk\_10 -----  
 TbTx\_5 -----  
 TsCh\_3 -----  
 TbOk\_9 -----  
 TbMi\_15 -----  
 TbOk\_8 -----  
 Tan5\_8 -----  
 Tan7\_7 -----  
 Tan1\_3 -----  
 Tan2\_12 -----  
 Tan3\_9 -----  
 Tan3\_3 -----  
 Tan5\_7 -----  
 Tan3\_8 -----  
 Tan6\_11 -----  
 Tan7\_18 -----  
 Tan1\_2 -----  
 Tan5\_13 -----  
 Tan2\_3 -----

Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
TmIn_3	-----
Tan1_14	-----
Tan5_12	-----
Tan2_5	-----
Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
TcerOkE_12	-----
TcerW2_9	-----
TcerCanE_10	-----
TcerCanE_7	-----
TcerW1_17	-----
TcerOkE_13	-----
TcerCanE_1	-----
TcerCanE_8	-----
TcerWisE	-----
Tcer183_8	-----
TcerOkE_11	-----
TcerInE_2	-----
Tcer181_1	-----
TcerOkE_10	-----
TcerW2_10	-----
TcerCanE_6	-----
TcerW3_2	-----
Tcer181_2	-----
TcerW1_24	-----
Tcer183_7	-----
TcerW2-3	-----
Tcer181_10	-----
TcerW1_16	-----
TcerW3_8	-----
TcerInE_1	-----
TcerW3_7	-----
TcerInE_3	-----
TcerCanE_11	-----
Tcer183_5	-----
ThDG_10	-----
ThDG_13	-----
ThDG_12	-----
ThDG_14	-----
ThDG_11	-----
To8_8	TTTGGTTTCGGTTGTCCATTGATCGGGGTTGCTTTCGTATTTGTGACACTGGGGTGTGTC 120
To9_13	TTTGGTTTCGGTTGTCCATTGATCGGGGTTGCTTTCGTATTTGTGACACTGGGGTGTGTC 120
To9_10	TTTGGTTTCGGTTGTCCATTGATCGGGGTTGCTTTCGTATTTGTGACACTGGGGTGTGTC 120
To11_5	TTTGGTTTCGGTTGTCCATTGATCGGGGTTGCTTTCGTATTTGTGACACTGGGGTGTGTC 120
To9_11	TTTGGTTTCGGTTGTCCATTGATCGGGGTTGCTTTCGTATTTGTGACACTGGGGTGTGTC 120
To9_12	TTTGGTTTCGGTTGTCCATTGATCGGGGTTGCTTTCGTATTTGTGACACTGGGGTGTGTC 120
To11_1	TTTGGTTTCGGTTGTCCATTGATCGGGGTTGCTTTCGTATTTGTGACACTGGGGTGTGTC 120
To8_4	TTTGGTTTCGGTTGTCCATTGATCGGGGTTGCTTTCGTATTTGTGACACTGGGGTGTGTC 120
To8_9	TTTGGTTTCGGTTGTCCATTGATCGGGGTTGCTTTCGTATTTGTGACACTGGGGTGTGTC 120
To9_14	TTTGGTTTCGGTTGTCCATTGATCGGGGTTGCTTTCGTATTTGTGACACTGGGGTGTGTC 120
To11_2	TTTGGTTTCGGTTGTCCATTGATCGGGGTTGCTTTCGTATTTGTGACACTGGGGTGTGTC 120
Cfelis_Tx	-----
Olonga	-----
TsIk_1	TAATCCTTTAGATTTTAAAGGTAATATAGCTG-----GAAATTTAATCCT 1000
TbMi_14	-----GCAGCGCAA-CTT 12
TsCh_1	-----ACAGCGCAA-CTT 12
TbAr_20	-----ACAGCGCAA-TTT 12
TsIk_2	TAATCCTTTAGATTTTAAAGGTAATATAGCTG-----GAAATTTAATCCT 1004

TbMi\_3 -----GCAGCGCAA-CTT 12  
TsCh\_4 -----ACAGCGCAA-CTT 12  
TsIk\_7 TAATCCTCTAGATTTTAAAGGTAATATAGCTGGAAATTTAATCCTGGTTCGTCGG-GTT 1013  
TbTx\_6 -----ACAGCGTAA-CTT 12  
TbAr\_15 -----ACAGCGCAA-CTT 12  
TsIk\_6 TAATCCTTTAGATTTTAAAGGTAGTATAGCTGG-----AAATTTAAT-CCT 999  
TbTx\_11 -----ACAGCGCAG-CTT 12  
TbAr\_25 -----ACAGCGCAA-CTT 12  
TsCh\_5 -----ACAGCGCAA-CTT 12  
TsCh\_2 -----ACAGCGCAA-CTT 12  
TbMi\_5 -----GCAGCGCAA-CTT 12  
TbOk\_10 -----ACAGCGCAG-CTT 12  
TbTx\_5 -----ACAGCGCAG-CTT 12  
TsCh\_3 -----ACAGCGCAA-CTT 12  
TbOk\_9 -----ACAGCGCAG-CTT 12  
TbMi\_15 -----GCAGCGCAA-CTT 12  
TbOk\_8 -----ACAGCGCAG-CTT 12  
Tan5\_8 -----ACATTATA 8  
Tan7\_7 -----ACATTCTA 8  
Tan1\_3 -----ACATTCTA 8  
Tan2\_12 -----ACATTCT- 7  
Tan3\_9 -----ACATTC-- 6  
Tan3\_3 -----ACATTCTA 8  
Tan5\_7 -----ACATTCTA 8  
Tan3\_8 -----ACATTCTA 8  
Tan6\_11 -----ACATTA-A 7  
Tan7\_18 -----ACATT-A 7  
Tan1\_2 -----ACATTA 8  
Tan5\_13 -----ACATTCTA 8  
Tan2\_3 -----ACATTTTA 8  
Tan2\_11 -----ACATTCTA 8  
Tan6\_18 -----ACATTTTA 8  
Tan6\_24 -----ACATTCTA 8  
Tan1\_13 -----ACATTATA 8  
Tan7\_13 -----ACATTTTA 8  
Tpar\_U -----  
TmIn\_10 -----ACATTACCATCTA 13  
Tpar\_AF -----ATTACATTACCATCTA 17  
TmIn\_13 -----ACATTACCATCTA 13  
TmIn\_3 -----ACATTACCATCTA 13  
Tan1\_14 -----ACATTCTA 8  
Tan5\_12 -----ACATTCTA 8  
Tan2\_5 -----ACATTCTA 8  
Tan2\_13 -----ACATTA 6  
Tan3\_6 -----ACATTT 6  
Tan2\_7 -----ACATTCTA 8  
TcerOkE\_12 -----ACATTTTT 8  
TcerW2\_9 -----ACATTTTT 8  
TcerCanE\_10 -----ACATTA 8  
TcerCanE\_7 -----ACATTTTT 8  
TcerW1\_17 -----ACATTA 8  
TcerOkE\_13 -----ACATTA 8  
TcerCanE\_1 -----ACATTTTT 8  
TcerCanE\_8 -----ACATTA 8  
TcerWisE -----ACATTA 8  
Tcer183\_8 -----ACATTA 8  
TcerOkE\_11 -----ACATTA 8  
TcerInE\_2 -----ACATTA 8  
Tcer181\_1 -----ACATTA 8  
TcerOkE\_10 -----ACATTA 8  
TcerW2\_10 -----ACATTA 8  
TcerCanE\_6 -----ACATTTTT 8  
TcerW3\_2 -----ACATTTTT 8  
Tcer181\_2 -----ACATTA 8  
TcerW1\_24 -----ACATTA 8  
Tcer183\_7 -----ACATTA 8  
TcerW2-3 -----ACATTA 8  
Tcer181\_10 -----ACATTA 8  
TcerW1\_16 -----ACATTA 8  
TcerW3\_8 -----ACATTA 8

TcerInE\_1 -----ACATTA 8  
TcerW3\_7 -----ACATTA 8  
TcerInE\_3 -----ACATTA 8  
TcerCanE\_11 -----ATATTA 8  
Tcer183\_5 -----ACATTA 8  
ThDG\_10 -----  
ThDG\_13 -----  
ThDG\_12 -----  
ThDG\_14 -----  
ThDG\_11 -----  
To8\_8 ATGAGTATGGTGATATTTAGAGTTGAAAAGCCTCTTGATAGGCCAAGAGGGAGAGTGACC 180  
To9\_13 ATGAGTATGGTGATATTTAGAGTTGAAAAGCCTCTTGATAGGCCAAGAGGGAGAGTGACC 180  
To9\_10 ATGAGTATGGTGATATTTAGAGTTGAAAAGCCTCTTGATAGGCCAAGAGGGAGAGTGACC 180  
To11\_5 ATGAGTATGGTGATATTTAGAGTTGAAAAGCCTCTTGATAGGCCAAGAGGGAGAGTGACC 180  
To9\_11 ATGAGTATGGTGATATTTAGAGTTGAAAAGCCTCTTGATAGGCCAAGAGGGAGAGTGACC 180  
To9\_12 ATGAGTATGGTGATATTTAGAGTTGAAAAGCCTCTTGATAGGCCAAGAGGGAGAGTGACC 180  
To11\_1 ATGAGTATGGTGATATTTAGAGTTGAAAAGCCTCTTGATAGGCCAAGAGGGAGAGTGACC 180  
To8\_4 ATGAGTATGGTGATATTTAGAGTTGAAAAGCCTCTTGATAGGCCAAGAGGGAGAGTGACC 180  
To8\_9 ATGAGTATGGTGATATTTAGAGTTGAAAAGCCTCTTGATAGGCCAAGAGGGAGAGTGACC 180  
To9\_14 ATGAGTATGGTGATATTTAGAGTTGAAAAGCCTCTTGATAGGCCAAGAGGGAGAGTGACC 180  
To11\_2 ATGAGTATGGTGATATTTAGAGTTGAAAAGCCTCTTGATAGGCCAAGAGGGAGAGTGACC 180  
Cfelis\_Tx -----  
Olonga -----  
  
Tslk\_1 GGTTTCGTCGGGTTTTCCAGGACCGTGGCTGGATTTAAATGTGGCCGTCCAGCCCGGAA 1060  
TbMi\_14 GGCGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACGTTTAA 62  
TsCh\_1 GGTGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACG-ACAA 61  
TbAr\_20 GGCGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACGTTTAA 62  
Tslk\_2 GGTTTCGTCGGGTTTTCCAGGACCGTGGCTGGATTTAAATGTGGCCGTCCAGCCCGGAA 1064  
TbMi\_3 GGCGCAACCCAGCTGCTTT----TGAGGTTA---TTGAATGC--CTGCTCTACGTTTAA 62  
TsCh\_4 GGCGCAACCCAGCTGCTTT----TGAGGTTA---TTGAATGC--CTGCTCTACG-ACAA 61  
Tslk\_7 TTTCCAGGACCACCGTGGC----TGGAGTTA---A-GTGTGG--CCGTCCAGCCCGGAA 1062  
TbTx\_6 GGCGCAACCCAGCTGCTTT----TGAGGTTA---TTGAATGC--CTGCTCTACGTTTAA 62  
TbAr\_15 GGCGCAACCCAGCTGCTTT----TGAGGTTA---TTGAATGC--CTGCTCTACGTTTAA 62  
Tslk\_6 GGTTTCGTCGGGTTTTCCAGGACCGTGGCTGGATTTAAATGTGGCCGTCCAGCCCGGAA 1059  
TbTx\_11 GGCGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACGTTTAA 62  
TbAr\_25 GGCGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACGTTTAA 62  
TsCh\_5 GGCGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACG-ACAA 61  
TsCh\_2 GGCGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACG-ACAA 61  
TbMi\_5 GGCGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACGTTTAA 62  
TbOk\_10 GGCGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACGTTTAA 62  
TbTx\_5 GGCGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACGTTTAA 62  
TsCh\_3 GGCGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACGAC-AA 61  
TbOk\_9 GGCGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACGTTTAA 62  
TbMi\_15 GGCGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACGTTTAA 62  
TbOk\_8 GGCGCAACCCAGCTGCTTTTGA----GGTTA---TTGAATGC--CTGCTCTACGTTTAA 62  
Tan5\_8 AAATA-ACTGG--TACC-TTGG--GTACTG----TACTCAGATATCTTTGGGTATTT 56  
Tan7\_7 AAATA-ACTGG--TACCCTTGA---GTACTG----GT--TTAACTATAAT----- 46  
Tan1\_3 AAATA-ACTGG--TACCCTTGG---GTACTG----TAACTCAGATATCTTTGGGTATTT 57  
Tan2\_12 AATTA-ACTAG--TACCCTTGG---GTACTG----TAACTCAGATATCTTTGGGTATTT 56  
Tan3\_9 AATTA-ACC-G--TATCTTGG---GTACTG----TACTCAGATATCTTTGGGTATTT 54  
Tan3\_3 AAATA-TCTGG--TACCTTAGG---GTACTGTACTATAACTCAGATATCTTTGGGTATTT 62  
Tan5\_7 AAATA-ACTAG--TATCTTGG---GTACTGTACTATAACTCAGATATCTTTGGGTATTT 62  
Tan3\_8 AAATA-TCTGG--TACCTTAGG---GTACTGTACTATAACTCAGATATCTTTGGGTATTT 62  
Tan6\_11 AATA--ACTGG--TATCGTATG--ATA-TT---GGTGA-----ACCTTTAGGGTTTT 49  
Tan7\_18 AATTT-ACTAG--TACCTTGG---GTACTT---GATTACTCAGATATCTTTGGGTATTT 58  
Tan1\_2 ATAT--ACTGG--TATCTTATG--ATATTG-----GTTTAACTATTG-----ATTT 48  
Tan5\_13 AAATT-ACTGG--TATCCTTGG---GTACTA-----TAACTCAGATATCTTTGGGTATTT 57  
Tan2\_3 AATTACACTGG--TATC-TTGA---GTA-----TATGTGGTGTACCTTTAGGGTTTT 54  
Tan2\_11 A-TTA-ACTAG--TACCCTTGG---GTACTG----TAACTCAGATATCTTTGGGTATTT 56  
Tan6\_18 AAATA-ACTGG--TACCCTAGG---GTACTGTACTATAACTCAGATATCTTTAGGGTTTT 62  
Tan6\_24 AAATA-ACTGG--TACCCTTGG---GTATTG---GTGA-----ACCTTTAGGGTTTT 51  
Tan1\_13 AATTT-ACTAG--TATCCTTGG---GTACTG----TACTCAGATATCTTTGGGTATTT 57  
Tan7\_13 ATTGA-ACTGG--TATCGTATG--ATATTG----GTG-----AACCTTTAGGGTCTT 51  
Tpar\_U -----ATTACATTATC---ACACAG----TT--TT---CGACTACAGAGTTGA 37  
TmIn\_10 GGTCC-TCTGGACCACCTCGTA---ACAGAG----TT--TTA--TGGCTACAGAGTTTT 60  
Tpar\_AF GGTCC-TCTGGACCACATTGTA---ACAGAG----TTGATTGAGTGACTACACTGGTAG 68  
TmIn\_13 GGTCC-TCTGGACCACCTCGTA---ACAGAG----TT--TTA--TGGCTACAGAGTTTT 60  
TmIn\_3 GGTCC-TCTGGACCACCTCGTA---ACAGAG----TT--TTA--TGGCTACAGAGTTTT 60

Tan1\_14 TAATA-ACTAG--TACCCTTGG--GTACTGTACTGTAACCTAGATATCTTTGGGTATTT 62  
 Tan5\_12 AAATA-ACTAG--TATCTTGAG--GTACTGTACTATAACTCAGATATCTTTGGGTATTT 62  
 Tan2\_5 AAATT-AATTG--AACCTTTGG--GTACTGT-----TACTCAGATATCTTTGGGTATTT 57  
 Tan2\_13 AATAT-ACCGG--TACCCTTGG--GTACTGTACTGTTACTCAGATATCTTTAGGTATTT 60  
 Tan3\_6 AAATA-ACTGG--TATCGTATG--ATATTAG-----GTGAACCTTTAGG-GTTT 49  
 Tan2\_7 AAATT-AATTG--AACCTTTGG--GTACTGT-----TACTCAGATATCTTTGGGTATTT 57  
 TcerOkE\_12 CAGTATTCGGAGTTTTCGGA--TTTTTTTCCAATAACTTTTGGT-TCCAATCCTAAA 65  
 TcerW2\_9 CAGTATTCGGAGTTTACTCGGG--CAAT----CTGATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerCanE\_10 TAAATTCGGAGTTTACTCGGG--CTATCT----CTGATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerCanE\_7 CAGTATTCGGAGTTTACTCGGA--TTTTTTC-CCAATAACTTTTGGT-TCCAATTTAAT 64  
 TcerW1\_17 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerOkE\_13 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerCanE\_1 CAGTATTCGGAGTTTACTCGGA--TTTTTTC-CCAATAACTTTTGGT-TCCAATTTAAT 64  
 TcerCanE\_8 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerWisE TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 Tcer183\_8 TAAATTCGGAGTTTACTCGGG--CAATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerOkE\_11 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerInE\_2 TACATTCGGAGTTTACTCGGG--CAATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 Tcer181\_1 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerOkE\_10 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerW2\_10 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerCanE\_6 CAGTATTCGGAGTTTACTCGGA--TTTTTTC-CCAATAACTTTTGGT-TCCAATTTAAT 64  
 TcerW3\_2 CAGTATTCGGAGTTTACTCGGG--CAATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 Tcer181\_2 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerW1\_24 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 Tcer183\_7 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerW2-3 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 Tcer181\_10 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerW1\_16 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerW3\_8 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerInE\_1 TACATTCGGAGTTTACTCGGG--CAATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerW3\_7 TAAATTCGGAGTTTACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerInE\_3 TACATTCGGAGTTTACTCGGG--CAATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 TcerCanE\_11 TAAATTCGGAGTT-ACTCGGG--CTATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 60  
 Tcer183\_5 TACATTCGGAGTTTACTCGGG--CAATCT----GATAGCTTTTGGT-TCCAGTCTCTGA 61  
 ThDG\_10 -----  
 ThDG\_13 -----  
 ThDG\_12 -----  
 ThDG\_14 -----  
 ThDG\_11 -----  
 To8\_8 CAGATTGATTACCTTACGCTTG--TGACGGGACGGTTGGGTTTTAAAAATTC AATCGTCAA 238  
 To9\_13 CAGATTGATTACCTTACGCTTG--TGACGGGACGGTTGGGTTTTAAAAATTC AATCGTCAA 238  
 To9\_10 CAGATTGATTACCTTACGCTTG--TGACGGGACGGTTGGGTTTTAAAAATTC AATCGTCAA 238  
 To11\_5 CAGATTGATTACCTTACGCTTG--TGACGGGACGGTTGGGTTTTAAAAATTC AATCGTCAA 238  
 To9\_11 CAGATTGATTACCTTACGCTTG--TGACGGGACGGTTGGGTTTTAAAAATTC AATCGTCAA 238  
 To9\_12 CAGATTGATTACCTTACGCTTG--TGACGGGACGGTTGGGTTTTAAAAATTC AATCGTCAA 238  
 To11\_1 CAGATTGATTACCTTACGCTTG--TGACGGGACGGTTGGGTTTTAAAAATTC AATCGTCAA 238  
 To8\_4 CAGATTGATTACCTTACGCTTG--TGACGGGACGGTTGGGTTTTAAAAATTC AATCGTCAA 238  
 To8\_9 CAGATTGATTACCTTACGCTTG--TGACGGGACGGTTGGGTTTTAAAAATTC AATCGTCAA 238  
 To9\_14 CAGATTGATTACCTTACGCTTG--TGACGGGACGGTTGGGTTTTAAAAATTC AATCGTCAA 238  
 To11\_2 CAGATTGATTACCTTACGCTTG--TGACGGGACGGTTGGGTTTTAAAAATTC AATCGTCAA 238  
 Cfelis\_Tx -----  
 Olonga -----  
  
 Tslk\_1 CTGTTA--TGCTCACCCGAAT-TAGT---GTCTGTTGACTGTCATTACGGACTGTTGGC 1114  
 TbMi\_14 CAGTGG--TACACGATCGCG---ATT---GTCTGACGGCTGCCGTTATGGGATCGA-GAT 113  
 TsCh\_1 CAGTGG--TACACGATCGCG---ATT---GTCTGACGGCTGCCGTTATGGGATCGT-GAT 112  
 TbAr\_20 CAGTGG--TACACGATCGCG---ATT---GTCTGACGGCTGCCGTTATGGGATCGA-GAT 113  
 Tslk\_2 CTGTTA--TGCTCACCCGAAT-TAGT---GTCTGTTGACTGTCATTACGGACTGTTGGT 1118  
 TbMi\_3 CAGTGG--TACACGATCG--C-GATT---GTCTGACGGCTGCCGTTATGGGATCGA-GAT 113  
 TsCh\_4 CAGTGG--TACACGATCG--C-GATT---GTCTGGCGGGCTGCCGTTATGGGATCGT-GAT 112  
 Tslk\_7 CTGTTA--TGCTCACCCG--A-AATTAGTGTCTGTCGACTGTCATTATGGACTGTTGGT 117  
 TbTx\_6 CAGTGG--TACACGATCG--C-GATT---GTCTGACGGCTGCCGTTATGGGATCGT-GAT 113  
 TbAr\_15 CAGTGG--TACACGATCG--C-GATT---GTCTGACGGCTGCCGTTATGGGATCGA-GAT 113  
 Tslk\_6 CTGTTA--TGCTCACCCGAAT-TAGT---GTCTGTTGACTGTCATTACGGACTGTTGGT 1113  
 TbTx\_11 CAGTGG--TACACGATCGCG---ATT---GTCTGACGGCTGCCGTTATGGGAACGT-GAT 113  
 TbAr\_25 CAGTGG--TACACGATCGCG---ATT---GTCTGACGGCTGCCGTTATGGGATCGA-GAT 113  
 TsCh\_5 CAGTGG--TACACGATCGCG---ATT---GTCTGACGGCTGCCGTTATGGGATCGT-GAT 112  
 TsCh\_2 CAGTGG--TACACGATCGCG---ATT---GTCTGACGGCTGCCGTTATGGGATCGT-GAT 112

TbMi\_5 CAGTGG--TACACGATCGCG---ATT---GTCTGACGGCTGCCGTTATGGGATCGT-GAT 113  
 TbOk\_10 CAGTGG--TACACGATCGCG---ATT---GTCTGACGGCTGCCGTTATGGGATCGT-GAT 113  
 TbTx\_5 CAGTGG--TACACGATTGCG---ATT---GTCTGACGGCTGCCGTTATGGGATCGT-GAT 113  
 TsCh\_3 CAGTGG--TACACGATCGCG---ATT---GTCTGACGGCTGCCGTTATGGGATCGT-GAT 112  
 TbOk\_9 CAGTGG--TACACGATCGCG---ATT---GTCTGACGGCTGCCGTTATGGGATCGT-GAT 113  
 TbMi\_15 CAGTGG--TACACGATCGCG---ATT---GTCTGACGGCTGCCGTTATGGGATCGA-GAT 113  
 TbOk\_8 CAGTGG--TACACGATCGCG---ATT---GTCTGACGGCTGCCGTTATGGGATCGT-GAT 113  
 Tan5\_8 GGGTT---TGGGAGTTTACTC-CATT----CCCAA-GCTTCTGGTAATCCAATTGATCCA 107  
 Tan7\_7 ---TT---TGGGAGTTTACTC-CATT----CCTAG-ACTTCTGGTAATCCAATTGATCCA 94  
 Tan1\_3 GGGTT---TGGGAGTTTACTC-CATT----CCCAG-ACTTCTGGTAATCCAATTGATCCA 108  
 Tan2\_12 GGGTT---TAGGAGTTTACTC-CATT----CCCGG-ACTTCTGGTAATCCAATTGATCCA 107  
 Tan3\_9 GGGTT---TGGGAGTTTACTC-CATT----CCCAG-GCTTCTGGTAATCCAATTGATCCA 105  
 Tan3\_3 GGGTT---TGGGAGTTTACTC-CATT----CCCAG-ACTTTTGGTAATCCAATTGATCCA 113  
 Tan5\_7 GGGTT---TTGGAGTTTACTC-CATT----CCCGG-ACTTCTGGTAATCCAATTGATCCA 113  
 Tan3\_8 GGGTT---TGGGAGTTTACTC-CATT----CCCAG-ACTTTTGGTAATCCAATTGATCCA 113  
 Tan6\_11 GTTTT---G-GGAGTTTACTC-CATT----CCCAG-ACTTCTGGTAATCCAATTGATCCA 99  
 Tan7\_18 GGGTT---T-GGAGTTTACTC-CATT----CCCAG-GCTTCTGGTAATCCAATTGATCCA 108  
 Tan1\_2 GGTAG---TAGCTAGTACTC-CATT----CCCAG-ACTTCTGGTAATCCAATTGATCCA 99  
 Tan5\_13 GGGTT---TGGGAGTTTACTC-CATT----CCCAA-ACTTCTGGTAATCCAATTGATCCA 108  
 Tan2\_3 A--TT---TGGGAGTTTACTC-CATT----CCAGCACTTCTGGTAATCCAATTGATCCA 104  
 Tan2\_11 GGGTT---TAGGAGTTTACTC-CATT----CCCGG-ACTTCTGGTAATCCAATTGATCCA 107  
 Tan6\_18 T--GT---TGAGAGTTTACTC-CATT----CCTAG-ACTTCTGGTAATCCAATTGATCCA 111  
 Tan6\_24 A--TT---TGGGAGTTTACTC-CATT----CCCAG-ACTTCTGGTAATCCAATTGATCCA 100  
 Tan1\_13 GGGTT---TGGGAGTTTACTC-CATT----CCTAG-ACTTCTGGTAATCCAATTGATCC- 107  
 Tan7\_13 A--TT---TGGGAGTTTACTC-CATT----CCCAG-ACTTTTGGTAATCCAATTGATCC- 99  
 Tpar\_U TTGA----GTGACTACACGG--AGT-----AG-TTACA-----TACTATATTCT 75  
 TmIn\_10 GTAGTACTGTGACTACACTGGTAGT----CTGGG-TTCCAGAGGGAACACTATTTCCT 115  
 Tpar\_AF TTACTACCTATCATTAACACTACAGAGT---TG TAG-TTACAT-----TACCTTATTCT 117  
 TmIn\_13 GTAGTACTGTGACTACACTGGTAGT----CTGGG-TTCCAGAGGGAACACTATTTCCT 115  
 TmIn\_3 GTAGTACTGTGACTACACTGGTAGT----CTGGG-TTCCAGAGGGAACACTATTTCCT 115  
 Tan1\_14 GGGTT---TGGGAGTTTACTC-CATT----CCCAG-ACTTCTGGTAATCCAATTGATCCA 113  
 Tan5\_12 GGGTT---TTGGAGTTTACTC-CATT----CCCGG-ACTTCTGGTAATCCAATTGATCCA 113  
 Tan2\_5 GGGTT---TGGGAGTTTACTC-CATT----CCCAG-GCTTCTGGTAATCCAATTGATCCA 108  
 Tan2\_13 GGGTT---TAGGAGTTTACTC-CATT----CCCAG-ACTTCTGGTAATCCAATTGATCCA 111  
 Tan3\_6 TGTTT---TGGGAGTTTACTC-CATT----CCCAG-ACTTCTGGTAATCCAATTGATCCA 100  
 Tan2\_7 GGGTT---TGGGAGTTTACTC-CATT----CCCAG-GCTTCTGGTAATCCAATTGATCCA 108  
 TeerOkE\_12 CTATATTTT--TGGTATA---T-----ATAAAGATTA----- 92  
 TeerW2\_9 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 TeerCanE\_10 CTATATCTTTCATGGCATAAECTCT-----TCAGGAGTGGTCTTTGTTCTCTGATTCAG 113  
 TeerCanE\_7 CTATATTTT--TGGTATA-----TATAA 85  
 TeerW1\_17 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 TeerOkE\_13 CTATATCATAATGGTATAAECTCT-----TCAGGAGTGGTCTTTGTTCTCTGATTCAG 113  
 TeerCanE\_1 CTATATTTT--TGGTATA-----TATAA 85  
 TeerCanE\_8 CTATATCTTTCATGGTATAAECTCT-----TCAGGAGTGGTCTTTGTTCTCTGATTCAG 113  
 TeerWisE CTATATCTTTCATGGTATAAECTCT-----TCAGGAGTGGTCTTTGTTCTCTGATTCAG 113  
 Teer183\_8 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 TeerOkE\_11 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 TeerInE\_2 CTATATCTTTCATGGTATAAECTCT-----TCAGGAGTGGTCTTTGTTCTCTGATTCAG 113  
 Teer181\_1 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 TeerOkE\_10 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 TeerW2\_10 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 TeerCanE\_6 CTATATTTT--TGGTATA-----TATAA 85  
 TeerW3\_2 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 Teer181\_2 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 TeerW1\_24 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 Teer183\_7 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 TeerW2-3 CTATATCATAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 Teer181\_10 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 TeerW1\_16 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 TeerW3\_8 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 TeerInE\_1 CTATATCTTTCATGGTATAAECTCT-----TCAGGAGTGGTCTTTGTTCTCTGATTCAG 113  
 TeerW3\_7 CTATATCTTAATGGTATAAECTCT-----TCAGGAGTTGTCTTTAGTCTCTGATTCAG 113  
 TeerInE\_3 CTATATCTTTCATGGTATAAECTCT-----TCGGGAGTGGTCTTTGTTCTCTGATTCAG 113  
 TeerCanE\_11 CTATATCTTTCATGGTATAAECTCT-----TCAGGAGTGGTCTTTGTTCTCTGATTCAG 112  
 Teer183\_5 CTATATCTTTCATGGTATAAECTCT-----TCAGGAGTGGTCTTTGTTCTCTGATTCAG 113  
 ThDG\_10 -----  
 ThDG\_13 -----  
 ThDG\_12 -----  
 ThDG\_14 -----  
 ThDG\_11 -----



To8\_8 CCCTCACTGTCTGGCTTAGTGTCAAG-----CTTTGAGGGCGTTACACCCACCCCTCTGA 293  
 To9\_13 CCCTCACTGTCTGGCTTAGTGTCAAG-----CTTTGAGGGCGTTACACCCACCCCTCTGA 293  
 To9\_10 CCCTCACTGTCTGGCTTAGTGTCAAG-----CTTTGAGGGCGTTACACCCACCCCTCTGA 293  
 To11\_5 CCCTCACTGTCTGGCTTAGTGTCAAG-----CTTTGAGGGCGTTACACCCACCCCTCTGA 293  
 To9\_11 CCCTCACTGTCTGGCTTAGTGTCAAG-----CTTTGAGGGCGTTACACCCACCCCTCTGA 293  
 To9\_12 CCCTCACTGTCTGGCTTAGTGTCAAG-----CTTTGAGGGCGTTACACCCACCCCTCTGA 293  
 To11\_1 CCCTCACTGTCTGGCTTAGTGTCAAG-----CTTTGAGGGCGTTACACCCACCCCTCTGA 293  
 To8\_4 CCCTCACTGTCTGGCTTAGTGTCAAG-----CTTTGAGGGCGTTACACCCACCCCTCTGA 293  
 To8\_9 CCCTCACTGTCTGGCTTAGTGTCAAG-----CTTTGAGGGCGTTACACCCACCCCTCTGA 293  
 To9\_14 CCCTCACTGTCTGGCTTAGTGTCAAG-----CTTTGAGGGCGTTACACCCACCCCTCTGA 293  
 To11\_2 CCCTCACTGTCTGGCTTAGTGTCAAG-----CTTTGAGGGCGTTACACCCACCCCTCTGA 293  
 Cfelis\_Tx -----ACATGAAATAATTATTACATGAG 24  
 Olonga -----ACACTAATCCAACACTACTCAACCAAGCCTTCAGTTGCAGCCGAGGTGTTCCG 53

Tslk\_1 TGGCACTCGGCCACTTTGGTTGAGCTTAAGTAAGGCTTGTTTTATAAGGTGTCGGGACT 1174  
 TbMi\_14 CGAGCCTGTGCCGCTTCGGCTAGAGTTGAGCTGTAATAAGCCTTAGAAGGAGTTGGAAAC 173  
 TsCh\_1 CGGCACGTTGCCGCTTTGGCTAGAGTTGAGCTGTAAGTAACCTTAGAAGGAGTTGGAAAC 172  
 TbAr\_20 CGAGCCTGTGCCGCTTCGGCTAGAGTTGAGCTGTAATAAACCTTAGAAGGAGTTGGAAAC 173  
 Tslk\_2 TGGCACTCGGCCACTTTGGTTGAGCTTAAGTAAGGCTTGTTTTATAAGGTGTCGGGACT 1178  
 TbMi\_3 CGAGCCTGTGCCGCTTCGGCTAGAGTTGAGCTGTAATAAACCTTAGAAGGAGTTGGAAAC 173  
 TsCh\_4 CGGCACGTTGCCGCTTTGGCTAGAGTTGAGCTGTAAGTAACCTTAGAAGGAGTTGGAAAC 172  
 Tslk\_7 AGGCACTAGGCCACTTTGGTTGAGCTTATGGAAGACGTTTTTTATAAGATGTCGGGACT 1177  
 TbTx\_6 CGAGCCTGTGCCGCTTCGGCTAGAGTTGAGCTGTAATAAACCTTAGAAGGAGTTGGAAAC 173  
 TbAr\_15 CGAGCCTGTGCCGCTTCGGCTAGAGTTGAGCTGTAATAAACCTTAGAAGGAGTTGGAAAC 173  
 Tslk\_6 TGGCACTCGGCCACTTTGGTTGAGCTTAAGTAAGGCTTGTTTTATAAGGTGTCGGGACT 1173  
 TbTx\_11 CGAGCCTGTGCCGCTTCGGCTAGAGTTGAGCTGTAATAAACCTTAGAAGGAGTTGGAAAC 173  
 TbAr\_25 CGAGCCTGTGCCGCTTCGGCTAGAGTTGAGCTGTAATAAACCTTAGAAGGAGTTGGAAAC 173  
 TsCh\_5 CGGCACGTTGCCGCTTTGGCTAGAGTTGAGCTGTAAGTAACCTTAGAAGGAGTTGGAAAC 172  
 TsCh\_2 CGGCACGTTGCCGCTTTGGCTAGAGTTGAGCTGTAAGTAACCTTAGAAGGGGTTGGAAAC 172  
 TbMi\_5 CGAGCCTGTGCCGCTTCGGCTAGAGTTGAGCTGTAATAAACCTTAGAAGGAGTTGGAAAC 173  
 TbOk\_10 CGAGCCTGTGCCGCTTCGGCTAGAGTTGAGCTGTAATAAACCTTAGAAGGAGTTGGAAAC 173  
 TbTx\_5 CGAGCCTGTGCCGCTTCGGCTAGAGTTGAGCTGTAATAAACCTTAGAAGGAGTTGGAAAC 173  
 TsCh\_3 CGGCACGTTGCCGCTTTGGCTAGAGTTGAGCTGTAAGTAACCTTAGAAGGAGTTGGAAAC 172  
 TbOk\_9 CGAGCCTGTGCCGCTTCGGCTAGAGTTGAGCTGTAATAAACCTTAGAAGGAGTTGGAAAC 173  
 TbMi\_15 CGAGCCTGTGCCGCTTCGGCTAGAGTTGAGCTGTAATAAACCTTAGAAGGAGTTGGAAAC 173  
 TbOk\_8 CGAGCCTGTGCCGCTTCGGCTAGAGTTGAGCTGTAATAAACCTTAGAAGGAGTTGGAAAC 173  
 Tan5\_8 TC-GATCAAATT-GATCCATATGGATGAAGTGATTGCTAGTTGTTTGGGAAACGATGTGAC 165  
 Tan7\_7 TC-GATCCTATT-GATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 152  
 Tan1\_3 TC-GATCCTTTT-GATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 166  
 Tan2\_12 TC-GATCCTATT-GATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 165  
 Tan3\_9 TCAGATCCTTTT-GATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAACGATGTGAC 164  
 Tan3\_3 TC-GATCCTATTTGATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 172  
 Tan5\_7 TC-GATCCTATT-GATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 171  
 Tan3\_8 TC-GATCCTATTTGATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 172  
 Tan6\_11 TC-GATCCTTTT-GATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 157  
 Tan7\_18 TC-GATCCAAATT-GATCCATATGGATGAAGTGATTGCTAGTTGTTTGGGAAACGATGTGAC 166  
 Tan1\_2 TC-GATCCTTTT-GATCAATATGGATGAAGTGATTGCTAGTTTGGGAAAGATGTGAC 157  
 Tan5\_13 TC-GATCCTATT-GATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAACGATGTGAC 166  
 Tan2\_3 TC-AAATCCTATT-GATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAACGATGTGAC 162  
 Tan2\_11 TC-GATCCTATT-GATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 165  
 Tan6\_18 TC-GATCCTATTTGATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 170  
 Tan6\_24 TC-GATCCTATTTGATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 159  
 Tan1\_13 ATCGATCCTATTGATCCA-TATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 166  
 Tan7\_13 ATCGATCCTATTGATCAA-TATGGGTGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 158  
 Tpar\_U GCTAAGGCTGGTGTCTAGTTTTAGTGGGAAGATG--TGACGGGACGGTA--GAAA-ATC 130  
 Tmln\_10 GCTAAGACTGGTGTCTAGTTTTAGTGGGAAGATG--TGACGGGACGGTAAAGAAA-ATC 172  
 Tpar\_AF GCTAAGACTGGTGTCTAGTTTTAGTGGGAAGATG--TGACGGGACGGTAAAGAAA-ATC 174  
 Tmln\_13 GCTAAGACTGGTGTCTAGTTTTAGTGGGAAGATG--TGACGGGACGGTAAAGAAA-ATC 172  
 Tmln\_3 GCTAAGGCTGGTGTCTAGTTTTAGTGGGAAGATG--TGACGGGACGGTAAAGAAA-ATC 172  
 Tan1\_14 TC-GATCCTTTT-GATCAATATGGATGAAGCGATTGCTAGTTCTTTGGGAAACGATGTGAC 171  
 Tan5\_12 TC-GATCCTATT-GATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 171  
 Tan2\_5 TC-GATCCATTTT-GATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAACGATGTGAC 167  
 Tan2\_13 TC-GATCCATTT-GATCCATATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 169  
 Tan3\_6 TC-GATCCTATT-GATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAAGATGTGAC 158  
 Tan2\_7 TC-GATCCATTTT-GATCAATATGGATGAAGTGATTGCTAGTTGTTTGGGAAACGATGTGAC 167  
 TcerOkE\_12 ----AGGGTATAGTTTTAGAAAATTTGGTTCTAGA---AGTTGTTTGGATCATTAGTGAC 144  
 TcerW2\_9 AGGCGGGGGTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATT-GGATACT--GTGAC 167  
 TcerCanE\_10 AGGCGGGGGTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATT-GGATACT--GTGAC 167  
 TcerCanE\_7 AGACAAAAGTATAGCTTTAGAGATTGGTTCTAGA---AGTTGTTGGATCATTTTGTGAC 142

TcerW1\_17 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerOkE\_13 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerCanE\_1 AGACAAAAGTATAGCTTTAGAGATTGGTTCTAGA---AGTTGTTGGATCATTTTGTGAC 142  
 TcerCanE\_8 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerWisE AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 Tcer183\_8 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerOkE\_11 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerInE\_2 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 Tcer181\_1 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerOkE\_10 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerW2\_10 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerCanE\_6 AGACAAAAGTATAGCTTTAGAGATTGGTTCTAGA---AGTTGTTGGATCATTTTGTGAC 142  
 TcerW3\_2 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 Tcer181\_2 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerW1\_24 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 Tcer183\_7 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerW2\_3 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 Tcer181\_10 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerW1\_16 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerW3\_8 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerInE\_1 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerW3\_7 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerInE\_3 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 TcerCanE\_11 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 166  
 Tcer183\_5 AGGCGGGGCTCTTCGCCTGTTGAGTTGGTTCTAGG---AGTTATTGGAT---ACTGTGAC 167  
 ThDG\_10 -----  
 ThDG\_13 -----  
 ThDG\_12 -----  
 ThDG\_14 -----  
 ThDG\_11 -----  
 To8\_8 GCTTCGTCGCGTTAACTTCCCATGGTACCCATTAG---CGTTAGTCGGT-----AGGGTA 345  
 To9\_13 GCTTCGTCGCGTTAACTTCCCATGGTACCCATTAG---CGTTAGTCGGT-----AGGGTA 345  
 To9\_10 GCTTCGTCGCGTTAACTTCCCATGGTACCCATTAG---CGTTAGTCGGT-----AGGGTA 345  
 To11\_5 GCTTCGTCGCGTTAACTTCCCATGGTACCCATTAG---CGTTAGTCGGT-----AGGGTA 345  
 To9\_11 GCTTCGTCGCGTTAACTTCCCATGGTACCCATTAG---CGTTAGTCGGT-----AGGGTA 345  
 To9\_12 GCTTCGTCGCGTTAACTTCCCATGGTACCCATTAG---CGTTAGTCGGT-----AGGGTA 345  
 To11\_1 GCTTCGTCGCGTTAACTTCCCATGGTACCCATTAG---CGTTAGTCGGT-----GGGTA 345  
 To8\_4 GCTTCGTCGCGTTAACTTCCCATGGTACCCATTAG---CGTTAGTCGGT-----GGGTA 345  
 To8\_9 GCTTCGTCGCGTTAACTTCCCATGGTACCCATTAG---CGTTAGTCGGT-----GGGTA 345  
 To9\_14 GCTTCGTCGCGTTAACTTCCCATGGTACCCATTAG---CGTTAGTCGGT-----GGGTA 345  
 To11\_2 GCTTCGTCGCGTTAACTTCCCATGGTACCCATTAG---CGTTAGTCGGT-----GGGTA 345  
 Cfelis\_Tx TGAGGGAAGTCGATGACGAAGTCAGTGACGCAGAGCGAAGCGAAGTTATG-----AAA 77  
 Olonga CGTCAGGCAGCCGCCACAGCAGCAACCACAACAACCTAATCATTCAAAG-GACTTTAAC 112

Tslk\_1 TC-GCGACTCCGGTG----TTTACTAGGCGTGATA---AGCCGGTT-TACTGTTGGGCTT 1224  
 TbMi\_14 ACAGCGGCTTTGCGG----GTTATGGCTGGACATT---AATCAGTTGTAAACCGGGGCTC 225  
 TsCh\_1 A--GCGGCTTTGCGG----GTTATGGCTGGCAG----AAACAGTTGTAAACCGGGGCTC 220  
 TbAr\_20 ACAGCGGCTTTGCGG----GTTATGGCTGGACATT---AATCAGTTGTAAACCGGGGCTC 225  
 Tslk\_2 TC-GCGACTCCGGTG----TTTACTAGGCGTGATA---AGCCGGTT-TACTGTTGGGCTT 1228  
 TbMi\_3 ACAGCGGCTTTGCGG----GTTATGGCTGGACATT---AATCAGTTGTAAACCGGGGCTC 225  
 TsCh\_4 A--GCGGCTTTGCGG----GTTATGGCTGGCAG----AAACAGTTGTAAACCGGGGCTC 220  
 Tslk\_7 TC-GCGACTCCGGTG----TTTACTAGGCGTGATA---AGCCGGTT-TACTGTTGGGCTT 1227  
 TbTx\_6 A--GCGGCTTTGCGG----GTTATGGCTGGACATT---AATCAGTTGTAAACCGGGGCTC 223  
 TbAr\_15 ACAGCGGCTTTGCGG----GTTATGGCTGGACATT---AATCAGTTGTAAACCGGGGCTC 225  
 Tslk\_6 TC-GCGACTCCGGTG----TTTACTAGGCGTGATA---AGCCGGTT-TACTGTTGGGCTT 1223  
 TbTx\_11 A--GCGGCTTTGCGG----GTTATGGCTGGACATT---AATCAGTTGTAAACCGGGGCTC 223  
 TbAr\_25 AC-AGCGGCTTTGCGG----GTTATGGCTGGACATT---AATCAGTTGTAAACCGGGGCTC 224  
 TsCh\_5 A--GCGGCTTTGCGG----GTTATGGCTGGCAG----AAACAGTTGTAAACCGGGGCTC 220  
 TsCh\_2 A--GCGGCTTTGCGG----GTTATGGCTGGCAG----AAACAGTTGTAAACCGGGGCTC 220  
 TbMi\_5 A--GCGGCTTTGCGG----GTTATGGCTGGACATT---AATCAGTTGTAAACCGGGGCTC 223  
 TbOk\_10 A--GCGGCTTTGCGG----GTTATGGCTGGACATT---AATCAGTTGTAAACCGGGGCTC 223  
 TbTx\_5 A--GCGGCTTTGCGG----GTTATGGCTGGACATT---AATCAGTTGTAAACCGGGGCTC 223  
 TsCh\_3 A--GCGGCTTTGCGG----GTTATGGCTGGCAG----AAACAGTTGTAAACCGGGGCTC 220  
 TbOk\_9 A--GCGGCTTTGCGG----GTTATGGCTGGACATT---AATCAGTTGTAAACCGGGGCTC 223  
 TbMi\_15 ACAGCGGCTTTGCGG----GTTATGGCTGGATATT---AATCAGTTGTAAACCGGGGCTC 225  
 TbOk\_8 ---AGCGGCTTTGCGG----GTTATGGCTGGACATT---AATCAGTTGTAAACCGGGGCTC 223  
 Tan5\_8 GGGACGGTTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGA-TATGCTTCTGAGGC 220  
 Tan7\_7 GGGACGGTTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGG-TATGCTTCTGAGGC 207  
 Tan1\_3 GGGACGGTTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGA-TATGCTTCTGAGGC 221

Tan2\_12 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGG-TATGCTTCTGAGGC 220  
 Tan3\_9 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGG-TATGCTTCTGAGGC 219  
 Tan3\_3 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGA-TATGCTTCTGAGGC 227  
 Tan5\_7 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGA-TATGCTTCTGAGGC 226  
 Tan3\_8 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGA-TATGCTTCTGAGGC 227  
 Tan6\_11 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGA-TATGCTTCTGAGGC 212  
 Tan7\_18 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGG-TATGCTTCTGAGGC 221  
 Tan1\_2 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGA-TATGCTTCTGAGGC 212  
 Tan5\_13 GGGACGGTTTTAATAAAAATCGTCATCCCTC-AGGTC---ATTTGA-TATGCTTCTGAGGC 221  
 Tan2\_3 GGGACGGTTTTAATAAAAATCGTCATCCCTC-TGGTC---ATTTGA-TATGCTTCTGAGGC 217  
 Tan2\_11 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGG-TATGCTTCTGAGGC 220  
 Tan6\_18 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGA-TATGCTTCTGAGGC 225  
 Tan6\_24 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGG-TATGCTTCTGAGGC 214  
 Tan1\_13 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GAGTC---ATTTGG-TATGCTTCTGAGGC 221  
 Tan7\_13 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGG-TGTGCTTCTGAGGC 213  
 Tpar\_U CATATGGGTTTGCTTA--TCGTCATCCCTCAGGGTC---AGCTGGCTGAGCGATAGAGGC 185  
 TmIn\_10 CATTCCGGTTTGCTTA--TCGTCATCCCTCAGGGTC---AGCTGGCTAAGCGATAGAGGC 227  
 Tpar\_AF CACATGGGTTTGCTTA--TCGTCATCCCTCAGGGTC---AGCTGGCTGAGCGATAGAGGC 229  
 TmIn\_13 CATTCCGGTTTGCTTA--TCGTCATCCCTCAGGGTC---AGCTGGCTAAGCGATAGAGGC 227  
 TmIn\_3 CATTCCGGTTTGCTTA--TCGTCATCCCTCAGGGTC---AGCTGGCTAAGCGATAGAGGC 227  
 Tan1\_14 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGA-TATGCTTCTGAGGC 226  
 Tan5\_12 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGA-TATGCTTCTGAGGC 226  
 Tan2\_5 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGG-TATGCTTCTGAGGC 222  
 Tan2\_13 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGA-TATGCTTCTGAGGC 224  
 Tan3\_6 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGG-TATGCTTCTGAGGC 213  
 Tan2\_7 GGGACGGTTTTAATAAAAATCGTCATCCCTC-GGGTC---ATTTGG-TATGCTTCTGAGGC 222  
 TeerOkE\_12 GGGACGGTTGAGTTTCAATCGTCAACCCTCGAGATCTGGTTAGCTCTAGACT-CGAGGGC 203  
 TeerW2\_9 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerCanE\_10 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerCanE\_7 GGGACGGTTGAGTTTCAATCGTCAACCCTCGAGATCTGGTTAGCTCTAGACT-CGAGGGC 201  
 TeerW1\_17 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerOkE\_13 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerCanE\_1 GGGACGGTTGAGTTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 201  
 TeerCanE\_8 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerWisE GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 Teer183\_8 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerOkE\_11 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerInE\_2 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 Teer181\_1 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerOkE\_10 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerW2\_10 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerCanE\_6 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 201  
 TeerW3\_2 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 Teer181\_2 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerW1\_24 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 Teer183\_7 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerW2-3 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 Teer181\_10 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerW1\_16 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerW3\_8 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerInE\_1 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerW3\_7 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerInE\_3 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 TeerCanE\_11 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 226  
 Teer183\_5 GGGACGGTTGAATTTCAATCGTCAACCCTCGCAGTCCGGCTCCGGCTGGGCTACGAGGGC 227  
 ThDG\_10 -----ACATTTAATATTTTC-TGTTCCAG-CTATTCTGGTCTATCTCCACGGGGAT 48  
 ThDG\_13 -----ACATTTAATATTTTT-TGCTCCAG-CTATTCTGGTCTGTCTCTACGGGGAT 48  
 ThDG\_12 -----ACATTTAATATTTTT-TGCTCCAG-CTATTCTGGTCTGTCTCTACGGGGAT 48  
 ThDG\_14 -----ACATTAACAATCTTTTCTTCCAG-CTCTTCTGGTCTATCTCCACGGGGAT 52  
 ThDG\_11 -----ACATTTAATATTTTC-TGTTCCAG-CTATTCTGGTCTATCTCCACGGGGAT 48  
 To8\_8 TACACTATTGACTCTCGTTAGCAAAGTCTT-TGGATGGTCTGGAGGTTTTTCCTCACCAT 404  
 To9\_13 TACACTATTGACTCTCGTTAGCAAAGTCTT-TGGATGGTCTGGAGGTTTTTCCTCACCAT 404  
 To9\_10 TACACTATTGACTCTCGTTAGCAAAGTCTT-TGGATGGTCTGGAGGTTTTTCCTCACCAT 404  
 To11\_5 TACACTATTGACTCTCGTTAGCAAAGTCTT-TGGATGGTCTGGAGGTTTTTCCTCACCAT 404  
 To9\_11 TACACTATTGACTCTCGTTAGCAAAGTCTT-TGGATGGTCTGGAGGTTTTTCCTTACCAT 404  
 To9\_12 TACACTATTGACTCTCGTTAGCAAAGTCTT-TGGATGGTCTGGAGGTTTTTCCTCACCAT 404  
 To11\_1 TACACTATTGACTCTCGTTAGCAAAGTCTTTGGATG-GTCTGGAGGTTTTTCCTCACCAT 404  
 To8\_4 TACACTATTGACTCTCGTTAGCAAAGTCTTTGGATG-GTCTGGAGGTTTTTCCTCACCAT 404  
 To8\_9 TACACTATTGACTCTCGTTAGCAAAGTCTTTGGATG-GTCTGGAGGTTTTTCCTCACCAT 404  
 To9\_14 TACACTATTGACTCTCGTTAGCAAAGTCTTTGGATG-GTCTGGAGGTTTTTCCTCACCAT 404

To11\_2 TGC ACTATTGACTCTCGTTAGCAAAGTCTTTGGATG-GTCTGGAGGTTTTTCCTACCAT 404  
Cfelis\_Tx TCACTGATGTCAGAGACGTAGTCAATGACTGATGTGATGAATGAAGTAACGACCCGAGGTC 137  
Olonga TAAGCCTTTCAACAAAA---CCAAATTCTCAACGATGGATATCTTGGTTCCCATACGAT 169

TsIk\_1 TCGGGGTGCCAAAGTGGCCACCCCGGGAGTTTGTGCGACCTTTTTTACCCTCCGGCAT 1284  
TbMi\_14 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 279  
TsCh\_1 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 274  
TbAr\_20 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 279  
TsIk\_2 TCGGGGTGCCAAAGTGGCCACCCCGGGAGTTTGTGCGACCTTTTTTACCCTCCGGCAT 1288  
TbMi\_3 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCC---CTACCCCTCCGGCAT 279  
TsCh\_4 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCC---CTACCCCTCCGGCAT 274  
TsIk\_7 TCGGGGTGCCAAAGTGGCCACCCCGGGAGTTTGTGCGACCTTTTACCCTCCGGCAT 1286  
TbTx\_6 TCGGGAGCCTATAGCAAGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 277  
TbAr\_15 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 279  
TbTx\_6 TCGGGGTGCCAAAGTGGCCACCCCGGGAGTTTGTGCGACCTTTTTTACCCTCCGGCAT 1283  
TbTx\_11 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 277  
TbAr\_25 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 278  
TsCh\_5 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 274  
TsCh\_2 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 274  
TbMi\_5 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 277  
TbOk\_10 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 277  
TbTx\_5 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 277  
TsCh\_3 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 274  
TbOk\_9 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 277  
TbMi\_15 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 279  
TbOk\_8 TCGGGAGCCTATAGCAGGT-GTCCCGAGAGTC-GTCGCGCCCT---ACCCCTCCGGCAT 277

Tan5\_8 G---CAGTTCAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGA-AT 267  
Tan7\_7 G---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 254  
Tan1\_3 A---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 268  
Tan2\_12 A---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 267  
Tan3\_9 G---CAGCATAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 266  
Tan3\_3 A---CAGTATAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 274  
Tan5\_7 A---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 273  
Tan3\_8 G---CAGTATAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 274  
Tan6\_11 A---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 259  
Tan7\_18 A---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 268  
Tan1\_2 A---CAGCATAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 259  
Tan5\_13 A---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 268  
Tan2\_3 G---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 264  
Tan2\_11 A---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 267  
Tan6\_18 A---CAGCATAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 272  
Tan6\_24 G---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 261  
Tan1\_13 G---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 268  
Tan7\_13 A---CAGCATAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 260  
Tpar\_U AAT-CAATTGGT--CGGTTGACTTTGAGGGC--GTTACACCCT---ACCCCGCCGG-AT 235  
TmIn\_10 AAT-CAATTGGT--CGGTTGACTTTGAGGGC--GTTACACCCT---ACCCCGCCGG-AT 277  
Tpar\_AF AAT-CGGTTGGT--CAGTTGACTTTGAGGGC--GTTACACCCT---ACCCCGCCGG-AT 279  
TmIn\_13 AAT-CAATTGGT--CGGTTGACTTTGAGGGC--GTTACACCCT---ACCCCGCCGG-AT 277  
TmIn\_3 AAT-CAATTGGT--CGGTTGACTTTGAGGGC--GTTACACCCT---ACCCCGCCGG-AT 277  
Tan1\_14 A---CAGCATAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 273  
Tan5\_12 A---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 273  
Tan2\_5 A---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 269  
Tan2\_13 G---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 271  
Tan3\_6 G---CAGCATAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 260  
Tan2\_7 A---CAGCTTAT--CACTTGGCTC-GAGGGC--GTTACACACT---ACCCCGCCGG-AT 269

TcerOkE\_12 GTTACACCCACCCCTCCTGTA---GATGACCT-TTTCATCTTA-ATCAGTAGTTTCTAC 258  
TcerW2\_9 GTTACACCCACCCCTCCTG---GATGGTCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
TcerCanE\_10 GTTACACCCACCCCTCCTG---GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
TcerCanE\_7 GTTACACCCACCCCTCCTGTA---GATGACCT-TTTCATCTTA-ATCAGTAGTTTCTAC 256  
TcerW1\_17 GTTACACCCACCCCTCCTG---GATGGCTGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
TcerOkE\_13 GTTACACCCACCCCTCCTG---GATGGTCGGTTTCTTCTTA-ATCAGTAGTTGACTT 281  
TcerCanE\_1 GTTACACCCACCCCTCCTGTA---GATGACCT-TTTCATCTTA-ATCAGTAGTTTCTAC 256  
TcerCanE\_8 GTTACACCCACCCCTCCTG---GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
TcerWisE GTTACACCCACCCCTCCTG---GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
Tcer183\_8 GTTACACCCACCCCTCCTG---GATGGTCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
TcerOkE\_11 GTTACACCCACCCCTCCTG---GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
TcerInE\_2 GTTACACCCACCCCTCCTG---GATTGTCGGTTTCTTCTTA-ATCAGTAGTTGACTT 281  
Tcer181\_1 GTTACACCCACCCCTCCTG---GATGGCTGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
TcerOkE\_10 GTTACACCCACCCCTCCTG---GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281

TcerW2\_10 GTTACACCCTACCCCTCCTG----GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
 TcerCanE\_6 GTTACACCCACCCCTCCTGTA---GATGACCT-TTTCATCTTA-ATCAGTAGTTTCTAC 256  
 TcerW3\_2 GTTACACCCTACCCCTCCTG----GATGGTCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
 Tcer181\_2 GTTACACCCTACCCCTCCTG----GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
 TcerW1\_24 GTTACACCCTACCCCTCCTG----GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
 Tcer183\_7 GTTACACCCTACCCCTCCTG----GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
 TcerW2-3 GTTACACCCTACCCCTCCTG----GATGGTCGGTTTCTTCTTA-ATCAGTAGTTGACTT 281  
 Tcer181\_10 GTTACACCCTACCCCTCCTG----GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
 TcerW1\_16 GTTACACCCTACCCCTCCTG----GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
 TcerW3\_8 GTTACACCCTACCCCTCCTG----GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
 TcerInE\_1 GTTACACCCTACCCCTCCTG----GATTGTCGGTTTCTTCTTA-ATCAGTAGTTGACTT 281  
 TcerW3\_7 GTTACACCCTACCCCTCCTG----GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
 TcerInE\_3 GTTACACCCTACCCCTCCTG----GATTGTCGGTTTCTTCTTA-ATCAGTAGTTGACTT 281  
 TcerCanE\_11 GTTACACCCTACCCCTCCTG----GATGACCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 280  
 Tcer183\_5 GTTACACCCTACCCCTCCTG----GATGGCCGGTTTCTTCTTA-ATCAGTAGTTGGCTT 281  
 ThDG\_10 GTTCTAGTTTAGTTGGGCATGT---GACGGGACGGTTGATTCA-ATC-GTCGTTCCCTC 103  
 ThDG\_13 GTTCTAGTTTAGTTGGGCATGT---GACGGGACGGTTGATTCA-ATC-GTCGTTCCCTC 103  
 ThDG\_12 GTTCTAGTTTAGTTGGGCATGT---GACGGGACGGTTGATTCA-ATC-GTCGTTCCCTC 103  
 ThDG\_14 GTTCTAGTTTAGTTGGGCATGT---GACGGGACGGTTGATTCA-ATC-GTCGTTCCCTC 107  
 ThDG\_11 GTTCTAGTTTAGTTGGGCATGT---GACGGGACGGTTGATTCA-ATC-GTCGTTCCCTC 103  
 To8\_8 TTCAGTCTAGGATTCTCTAGA---GAGTGTGCGGCGCGCTTAAG-ACACCTCTTTGATT 460  
 To9\_13 TTCAGCCCCTAGGATTCTCTAGA---GAGTGTGCGGCGCGCTTAAG-ACACCTCTTTGATT 460  
 To9\_10 TTTAGCCCCTAGGATTCTCTAGA---GAGTGTGCGGCGCGCTTAAG-ACACCTCTTTGATT 460  
 To11\_5 TTCAGCCCCTAGGATTCTCTAGA---GAGTGTGCGGCGCGCTTAAG-ACACCTCTTTGATT 460  
 To9\_11 TTCAGCCCCTAGGATTCTCTAGA---GAGTGTGCGGCGCGCTTAAG-ACACCTCTTTGATT 460  
 To9\_12 TTCAGCCCCTAGGATTCTCTAGA---GAGTGTGCGGCGCGCTTAAG-ACACCTCTTTGATT 460  
 To11\_1 TTCAGCCCCTAGGATTCTCTAGA---GAGTGTG-GGCGCGCTTAAGACACCTCTTTGATT 460  
 To8\_4 TTCAGCCCCTAGGATTCTCTAGA---GAGTGTG-GGCGCGCTTAAGACACCTCTTTGATT 460  
 To8\_9 TTCAGCCCCTAGGATTCTCTAGA---GAGTGTG-GGCGCGCTTAAGACACCTCTTTGATT 460  
 To9\_14 TTCAGCCCCTAGGATTCTCTAGA---GAGTGTG-GGCGCGCTTAAGACACCTCTTTGATT 460  
 To11\_2 TTCAGCCCCTAGGATTCTCTAGA---GAGTGTG-GGCGCGCTTAAGACACCTCTTTGATT 460  
 Cfelis\_Tx GTGATTGTCTTATAACTGAGAT--AATAACAACTTCAAACCTAACTTCATAACCTACTT 195  
 Olonga GAAGAACGCAGCGAAGTGCATAAGCAATGCGAATTGCAGAACC-GTGAGTCATCAGATT 228

TsIk\_1 TCAAGCGTGATATTGCATTAGTACGGCGTGGTG-CGGTACCT--GGCTCAATG--CCTG 1338  
 TbMi\_14 TCAAGCGTGATGCTACTGTATTGTCTG-----CGGTACT---GTGCAAC---TGCG 324  
 TsCh\_1 TCAAGCGTGATGCTACTGTATTGT-----CGGTACT---GTGCAAC---CGCG 316  
 TbAr\_20 TCAAGCGTGATGCTACTGTATTGTCTG-----CGGTACT---GTGCAAC---TGCG 324  
 TsIk\_2 TCAAGCGTGATATTGCATTAGTACGGCGTGGTG-CGGTACCT--GGCTCAATG--CCTG 1342  
 TbMi\_3 TCAAGCGTGATGCTACTGTATTGTCTG-----CGGTACT---GTGCAAC---GC-G 324  
 TsCh\_4 TCAAGCGTGATGCTACTGTATTGT-----CGGTACT---GTGCAAC---CGCG 316  
 TsIk\_7 TCAAGCGTGATATTGCATTAGTACGGCGTGGTG-CGGTACCT--GGCTCAATG--CCTG 1340  
 TbTx\_6 TCAAGCGTGATGCTACTGTATTGTCTG-----CGGTACT---GTGCAAC---TGCG 322  
 TbAr\_15 TCGAGCGTGATGCTACTGTATTGTCTG-----CGGTACA---GTGCAAC---TGCG 324  
 TsIk\_6 TCAAGCGTGATATTGCATTAGTACGGCGTGGTG-CGGTACTT--GGCTCAATG--CCTG 1337  
 TbTx\_11 TCAAGCGTGATGCTACTGTATTGTCTG-----CGGTACT---GTGCAAC---TGCG 322  
 TbAr\_25 TCAAGCGTGATGCTACTGTATTGTCTG-----CGGTACT---GTGCAAC---TGCG 323  
 TsCh\_5 TCAAGCGTGATGCTGCGGTATTGT-----CAATAC---GTGCAACT---CGCG 316  
 TsCh\_2 TCAAGCGTGATGCTGCGGTATTGT-----CAATAC---GTGCACT---CGCG 316  
 TbMi\_5 TCAAGCGTGATGCTACTGTATTGTCTG-----CGGTACT---GTGCAAC---TGCG 322  
 TbOk\_10 TCAAGCGTGATGCTACTGTATTGTCTG-----CGGTACT---GTGCAAC---TGCG 322  
 TbTx\_5 TCAAGCGTGATGCTACTGTATTGTCTG-----CGGTACT---GTGCAAC---TGCG 322  
 TsCh\_3 TCAAGCGTGATGCTGCGGTATTGTCA-----ATAC---GTGCAACT---CGCG 316  
 TbOk\_9 TCAAGCGTGATGCTACTGTATTGTCTG-----CGGTACT---GTGCAACT---GCG 322  
 TbMi\_15 TCAAGCGTGATGCTACTGTATTGTCTG-----CGGTACT---GTGCAAC---TGCG 324  
 TbOk\_8 TCAAGCGTGATGCTACTGTATTGTCTG-----CGGTACT---GTGCAAC---TGCG 322  
 Tan5\_8 CCAGATCCCAGACTAGTCTAGGCT-----GGCTTGG--GGCTGGAGT--TCCC 311  
 Tan7\_7 CCAGATCCCAGACTAGTCTAGGCT-----T-CTTGG--GACTGGAGT--TCCC 297  
 Tan1\_3 CCATATCCCAGACTAGTCTAGGCT-----GGCTTGG--GGCTGGAGT--TCCC 312  
 Tan2\_12 CCAGATCCCAGACTAGTCTAGGCT-----GGCTTGG--GACTGGAGT--TCCC 311  
 Tan3\_9 CCAGATCCCAGACTAGTCTAGGCT-----GGCTTGG--GACTGGAGT--TCCC 310  
 Tan3\_3 CCAGATCCCAGACTAGTCTAGGCT-----GGCTTGG--GGCTGGAGT--TCCC 318  
 Tan5\_7 CCAGATCCCAGACTAGTCTAGGCT-----GGCTTGG--GACTGGAGT--TCCC 317  
 Tan3\_8 CCAGATCCCAGACTAGTCTAGGCT-----GGCTTGG--GGCTGGAGT--TCCC 318  
 Tan6\_11 CCAGATCCCAGACTAGTCTAGGCT-----GGCTTGG--GAATGGAGT--TCCC 303  
 Tan7\_18 CCAGATCCCAGACTAGTCTAGGCT-----GGCTTGG--GACTGGAGT--TCCC 312  
 Tan1\_2 CCAGATCCCAGACTAGTCTAGGCT-----GGCTTGG--GACTGGAGT--TCCC 303  
 Tan5\_13 CCATATCCCAGACTAGTCTAGGCT-----GGCTTGG--GAATGGAGT--TCCC 312  
 Tan2\_3 CCAGATCCCAGACTAGTCTAGGCT-----GGCTTGG--GGCTGGAGT--TCCC 308

Tan2\_11 CCAGATCCCAACTAGTCCTAGGCT-----GGCTTGG--GACTGGAGT---TCCC 311  
 Tan6\_18 CCAGATCCCAACTAGTCCTAGGCT-----GGCTTGG--GAATGGAGT---TCCC 316  
 Tan6\_24 CCAGATCCCAACTAGTCCTAGGCT-----GGCTTGG--GACTGGAGT---TCCC 305  
 Tan1\_13 CCAGATCCCAACTAGTCCTAGGCT-----GGCTTGG--GGCTGGAGT---TCCC 312  
 Tan7\_13 CCAGATCCCAACTAGTCCTAGGCT-----GGCTTGG--GGCTGGAGT---TCCC 304  
 Tpar\_U CCTCATTCTACTAGTTACTAGT-----AGTTTGG--AG---AGT---ACCC 273  
 TmIn\_10 CCTCATTCTACTAGTTACTAGT-----AGTTTGA--AG---AGT---ACCC 315  
 Tpar\_AF CCTCAATCTACTAGTTACTAGT-----AGTTTGA--AG---AGT---ACCC 330  
 TmIn\_13 CCTCGTTCTACTAGTTACTAGT-----AGTTTGA--AG---AGT---ACCC 315  
 TmIn\_3 CCTCATTCTACTAGTTACTAGT-----AGTTTGA--AG---AGT---ACCC 315  
 Tan1\_14 CCAGATCCCAACTAGTCCTAGGCT-----GGCTTGG--GACTGGAGT---TCCC 317  
 Tan5\_12 CCAGATCCCAACTAGTCCTAGGCT-----GGCTTGG--GACTGGAGT---TCCC 317  
 Tan2\_5 CCAGATCCCAACTAGTCCTAGGCT-----GGCTTGG--GTCTGGAGT---TCCC 313  
 Tan2\_13 CCAGATCCCAACTAGTCCTAGGCT-----GGCTTGG--GAATGGAGT---TCCC 315  
 Tan3\_6 CCAGATCCCAACTAGTCCTAGGCT-----GGCTTGG--GACTGGAGT---TCCC 304  
 Tan2\_7 CCAGATCCCAACTAGTCCTAGGCT-----GGCTTGG--GTCTGGAGT---TCCC 313  
 TcerOkE\_12 ACGCG-----TTAGGTAATTTGCTGGGAGATGAACTGTGG--CATCCAAG--GGTTAC 307  
 TcerW2\_9 -----CTGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerCanE\_10 A-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerCanE\_7 ACGCG-----TTAGGTAATTTGCTGGGAGATGAACTGTGG--CATCCAAG--GGTTAC 305  
 TcerW1\_17 -----CTGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerOkE\_13 -----TTGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerCanE\_1 ACGCG-----TTAGGTAATTTGCTGGGAGATGAACTGTGG--CATCCAAG--GGTTAC 305  
 TcerCanE\_8 ATG-----GTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerWisE ATG-----GTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 Tcer183\_8 CTG-----GTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerOkE\_11 A-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerInE\_2 C-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 Tcer181\_1 C-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerOkE\_10 A-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerW2\_10 A-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerCanE\_6 ACGCG-----TTAGGTAATTTGCTGGGAGATGAACTGTGG--CATCCAAG--GGTTAC 305  
 TcerW3\_2 -----CTGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 Tcer181\_2 A-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerW1\_24 A-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 Tcer183\_7 A-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerW2-3 C-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 Tcer181\_10 A-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerW1\_16 A-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerW3\_8 A-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerInE\_1 C-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerW3\_7 A-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerInE\_3 C-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 TcerCanE\_11 A-----TGGTCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 323  
 Tcer183\_5 C-----TGGCCAATTTTCTGGGAGAAGGGAC-TAA--CATCCAAG--GGTTAC 324  
 ThDG\_10 G-----GTCGGCACCTGGTGCTGGA--CTTGAGGG--CGTTAC 138  
 ThDG\_13 G-----GTCGGCACCTGGTGCTGGA--CTTGAGGG--CGTTAC 138  
 ThDG\_12 G-----GTCGGCACCTGGTGCTGGA--CTTGAGGG--CGTTAC 138  
 ThDG\_14 G-----GTCGGCACCTGGTGCTGGA--CTTGAGGG--CGTTAC 142  
 ThDG\_11 G-----GTCGGCACCTGGTGCTGGA--CTTGAGGG--CGTTAC 138  
 To8\_8 CATTGACACACTGTGGGAGGGTGACGAAAGCTCGGGTCATGC--CTCTCAAGTAGGTTTA 518  
 To9\_13 CATTGACACACTGTGGGAGGGTGACGAAAGCTCGGGTCATGC--CTCTCAAGTAGGTTTA 518  
 To9\_10 CATTGACACACTGTGGGAGGGTGACGAAAGCTCGGGTCATGC--CTCTCAAGTAGGTTTA 518  
 To11\_5 CATTGACACACTGTGGGAGGGTGACGAAAGCTCGGGTCATGC--CTCTCAAGTAGGTTTA 518  
 To9\_11 CATTGACACACTGTGAGAGGGTGACGAAAGCTCGGGTCATGC--CTCTCAAGTAGGTTTA 518  
 To9\_12 CATTGACACACTGTGGGAGGGTGACGAAAGCTCGGGTCATGC--CTCTCAAGTAGGTTTA 518  
 To11\_1 CATTGACACACTGTGGGAGGGTGACGAAAGCTCGGGTCATGC--CTCTCAAGTAGGTTTA 518  
 To8\_4 CATTGACACACTGTGGGAGGGTGACGAAAGCTCGGGTCATGC--CTCTCAAGTAGGTTTA 518  
 To8\_9 CATTGACACACTGTGGGAGGGTGACGAAAGCTCGGGTCATGC--CTCTCAAGTAGGTTTA 518  
 To9\_14 CATTGACACACTGTGGGAGGGTGACGAAAGCTCGGGTCATGC--CTCTCAAGTAGGTTTA 518  
 To11\_2 CATTGACACACTGTGGGAGGGTGACGAAAGCTCGGGTCATGC--CTCTCAAGTAGGTTTA 518  
 Cfelis\_Tx CAACCTAACGTACATAACTATCTCCCTTACCTGTAATTTTCG--TAACGTTGTTTATCA 253  
 Olonga TTTGAACGCAACTGGCGCTGGTTGGTTATCCAGCCAGCATGCTTGTTTCAGTGTCTCTTT 288  
  
 Tslk\_1 TGTGAGCACGCCGGCGCTG----T-AGTGTTACGCCAATGCCAGGGTCACGCCTCTCACC 1393  
 TbMi\_14 CCGTATCGTGACGGTACT----T-AGTGATACGCCAATGCCAGGGTTACGCCTCTCATC 378  
 TsCh\_1 CGGTATCGTGACGACTG----TGAGTGCTACGCCAATGCCAGGGTTACGCCTCTCATC 372  
 TbAr\_20 CCGTATCGTGACGGTACT----T-AGTGATACGCCAATGCCAGGGTTACGCCTCTCATC 378  
 Tslk\_2 TGTGAGCACGCCGGCGCTG----T-AGTGTTACGCCAATGCCAGGGTCACGCCTCTCACC 1397

TbMi\_3 CCGTATCGTGACGGTACT----T-AGTGATACGCCAATGCCAGGGTTACGCCTCTCATC 378  
 TsCh\_4 CCGTATCCTGACGGTACTG----TGAGTGCTACGCCAATGCCAGGGTTACGCCTCTCATC 372  
 TsIk\_7 TGTGAGCACGCCGGCGCTG----T-AGTGTTACGCCAATGCCAGGGTTACGCCTCTCATC 1395  
 TbTx\_6 CCGTATCGTGACGGTACT----T-AGTGATACGCCAATGCCAGGGTTACGCCTCTCATC 376  
 TbAr\_15 CCGTATCGTGACGGTACT----T-AGTGATACGCCAATGCCAGGGTTACGCCTCTCATC 378  
 TsIk\_6 TGTGAGCACGCCGGCGCTG----T-AGTGTTACGCCAATGCCAGGGTTACGCCTCTCATC 1392  
 TbTx\_11 CCGTATCGTGACGGTACT----T-AGTGATACGCCAATGCCAGGGTTACGCCTCTCATC 376  
 TbAr\_25 CCGTATCGTGACGGTACT----T-AGTGATACGCCAATGCCAGGGTTACGCCTCTCATC 377  
 TsCh\_5 CCGTATCCTGACAGTGCTG----TGAGTGCTACGCCAATGCCAGGGTTACGCCTCTCATC 372  
 TsCh\_2 CCGTATCCTGACAGTGCTG----TGAGTGCTACGCCAATGCCAGGGTTACGCCTCTCATC 372  
 TbMi\_5 CCGTATCGTGACGGTACT----T-AGTGATACGCCAATGCCAGGGTTACGCCTCTCATC 376  
 TbOk\_10 CCGTATCGTGACGGTACT----T-AGTGATACGCCAATGCCAGGGTTACGCCTCTCATC 376  
 TbTx\_5 CCGTATCGTGACGGTACT----T-AGTGATACGCCAATGCCAGGGTTACGCCTCTCATC 376  
 TsCh\_3 CCGTATCCTGACAGTGCTG----TGAGTGCTACGCCAATGCCAGGGTTACGCCTCTCATC 372  
 TbOk\_9 CCGTATCGTGACGGTACT----TAGTGATACGCCAATGCCAGGGTTACGCCTCTCATC 376  
 TbMi\_15 CCGTATCGTGACGGTACT----TAGTGATACGCCAATGCCAGGGTTACGCCTCTCATC 378  
 TbOk\_8 CCGTATCGTGACGGTACT----TAGTGATACGCCAATGCCAGGGTTACGCCTCTCATC 376  
 Tan5\_8 GGGTATGCACACAGTCATC---TCAATCTTTCTACATTT-----TGTGGAATT 356  
 Tan7\_7 GGGTATGCACACAGTCATC---TCAATGTGTCTACATTT-----TGTGGAATT 342  
 Tan1\_3 GGGTATGCACACAGTCATC---TCAATCTGTCTACATTT-----TGTGGAATT 357  
 Tan2\_12 GGGTATGCACACAGTCATC---TCAATGTTTCTACATTA-----TGTGGAATT 356  
 Tan3\_9 GGGTATGCACACAGTCATC---TCAATCTTTCTACATTT-----TGTGGAATT 355  
 Tan3\_3 GGGTATGCACACAGTCATC---TCAATCTTTCTACATTT-----TTTGAATT 363  
 Tan5\_7 GGGTATGCACATAGTCATC---TCAATCTTTCTACATTT-----TTTGAATT 362  
 Tan3\_8 GGGTATGCACACAGTCATC---TCAATCTTTCTACATTT-----TTTGAATT 363  
 Tan6\_11 GGGTATGCACATAGTCATC---TCAATCTTTCTACATTT-----TGTGGAATT 348  
 Tan7\_18 GGGTATGCACACAGTCATC---TCAATCTTTCTACATTT-----TGTGGAATT 357  
 Tan1\_2 GGGTATGCACATAGTCATC---TCAATGTTTCTACATTT-----TGTGGAATT 348  
 Tan5\_13 GGGTATGCACACAGTCATC---TCAATGTGTCTACATTT-----TGTGGAATT 357  
 Tan2\_3 GGGTATGCACACAGTCATC---TCAATCTTTCTACATTT-----TGTGGAATT 353  
 Tan2\_11 GGGTATGCACACAGTCATC---TCAATGTTTCTACATTA-----TGTGGAATT 356  
 Tan6\_18 GGGTATGCACACAGTCATC---TCAATCTT---ACATTT-----TGTGGAATT 358  
 Tan6\_24 GGGTATGCACACAGTCATC---TCAATGTTTCTACATTT-----TGTGGAATT 350  
 Tan1\_13 GGGTATGCACACAGTCATC---TCAATCTTTCTACATTT-----TGTGGAATT 357  
 Tan7\_13 GGGTATGCACACAGTCATC---TCAATCTGTCTACATTT-----TGTGGAATT 349  
 Tpar\_U GGGTAAGCCCATGCCACAAAGTGATAGTATGTGTAGGATTAGGGTTTTGGGTTTTAGAAA 333  
 TmIn\_10 GGGTAAGCCCATGCCAATGCGGATCAGTATGTGGAGGATT--GTTTAGGGTTTTGGGTT 372  
 Tpar\_AF GGGTAAGCCCATATTCACAAGTGGCAGTATGTAGTGGATTGGGTTTTACGGTTTTAGCGTT 390  
 TmIn\_13 GGGTAAGCCCATGCCAATGCGGATCAGTATGTGGAGGATT--GTTTAGGGTTTTGGGTT 372  
 TmIn\_3 GGGTAAGCCCATGCCAATGCGGATCAGTATGTGGAGGATT--GTTTAGGGTTTTGGGTT 372  
 Tan1\_14 GGGTATGCACACAGTCATC---TCAATCTTTCTACATTT-----TGTGGAATT 362  
 Tan5\_12 GGGTATGCACATAGTCATC---TCAATCTTTCTACATTT-----TTTGAATT 362  
 Tan2\_5 GGGTATGCACACAGTCATC---TCA---TGTCTATATTT-----TGTGGAATT 355  
 Tan2\_13 GGGTATGCACACAGTCATC---TCAATCTTTCTACATTT-----TGTGGAATT 360  
 Tan3\_6 GGGTATGCGCACAGTCATC---TCAATGTGTCTACATTT-----TGTGGAATT 349  
 Tan2\_7 GGGTATGCACACAGTCATC---TCA---TGTCTATATTT-----TGTGGAATT 355  
 TcerOkE\_12 GCCTCAC--TACTGACTTCGATAGCTCTGTTCTGCGG-----GTAA 347  
 TcerW2\_9 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerCanE\_10 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerCanE\_7 GCCTCAC--TACTGACTTCGATGGCTCTGTTCTGCGG-----GTAA 345  
 TcerW1\_17 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerOkE\_13 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerCanE\_1 GCCTCAC--TACTGACTTCGATGGCTCTGTTCTGCGG-----GTAA 345  
 TcerCanE\_8 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerWisE GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 Tcer183\_8 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerOkE\_11 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerInE\_2 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 Tcer181\_1 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerOkE\_10 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerW2\_10 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerCanE\_6 GCCTCAC--TACTGACTTCGATGGCTCTGTTCTGCGG-----GTAA 345  
 TcerW3\_2 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 Tcer181\_2 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerW1\_24 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 Tcer183\_7 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerW2-3 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 Tcer181\_10 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerW1\_16 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerW3\_8 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357

TcerInE\_1 GCCTCTA--TTCAGGTTCCCTAGAGCTCT-GTCCTGT----- 357  
 TcerW3\_7 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 TcerInE\_3 GCCTCTA--TTCAGGTTCCCTAGAGCTCT-GTCCTGT----- 357  
 TcerCanE\_11 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 356  
 Tcer183\_5 GCCTCTA--TTCAGGTTCCGAGAGCTCT-TTCCTGT----- 357  
 ThDG\_10 ACCCCTA--CCCCGCCGGCATTGACGTCACTACCCT----- 172  
 ThDG\_13 ACCCCTA--CCCCGCCGGCATTGACGTCACTACCCT----- 172  
 ThDG\_12 ACCCCTA--CCCCGCCGGCATTGACGTCACTACCCT----- 172  
 ThDG\_14 ACCCCTA--CCCCGCCGGCATTGACGTCACTACCCT----- 176  
 ThDG\_11 ACCCCTA--CCCCGCCGGCATTGACGTCACTACCCT----- 172  
 To8\_8 TCTGTAGATTGAGATTTCCGAAAAGGTGATTGATTGAGTTTTATTAGAAAACCTTCTGATCA 578  
 To9\_13 TCTGTAGATTGAGATTTCCGAAAAGGTGATTGATTGAGTTTT-----ATTA 565  
 To9\_10 TCTGTAGATTGAGATTTCCGAAAAGGTGATTGATTGAGTTTT-----ATTA 565  
 To11\_5 TCTGTAGATTGAGATTTCCGAAAAGGTGATTGATTGAGTTTTATTAGAAAACCTTCTGATCA 578  
 To9\_11 TCTGTAGATTGAGATTTCCGAAAAGGTGATTGATT-----GAGTTTTTATTG 565  
 To9\_12 TCTGTAGATTGAGATTTCCGAAAAGGTGATTGAGTTTTATTAG----AAACTTCTGATCA 574  
 To11\_1 TCTGTAGATTGAGATTTCCGAAAAGGTGATTGATTGAGTTTTATTAGAAAACCTTCTGATCA 578  
 To8\_4 TCTGTAGATTGAGATTTCCGAAAAGGTGATTGATTGAGTTTTATTAGAAAACCTTCTGATCA 578  
 To8\_9 TCTGTAGATTGAGATTTCCGAAAAGGTGATTGATTGAGTTTTATTAGAAAACCTTCTGATCA 577  
 To9\_14 TCTGTAGATTGAGATTTCCGAAAAGGTGATTGATTGAGTTTTATTAGAAAACCTTCTGATCA 578  
 To11\_2 TCTGTAGATTGAGATTTCCGAAAAGGTGATTGATTGAGTTTTATTAGAAAACCTTCTGATCA 578  
 Cfelis\_Tx TAGAGTAAACGCTTCCTCCGGAAAAACGTTACATTACCA-----C 294  
 Olonga ATCCCTCACCTAAATCTTAATGCGAGAGATACCCTTCTCTCGTTAA-----GCAAGAAA 343

Tslk\_1 AAGTTGTCGTTGGTATATTGCTTACCAGTTTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 1452  
 TbMi\_14 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 437  
 TsCh\_1 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 431  
 TbAr\_20 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 437  
 Tslk\_2 AAGTTGTCGTTGGTATATTGCTTACCAGTTTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 1456  
 TbMi\_3 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 437  
 TsCh\_4 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 431  
 Tslk\_7 AAGTTGTCGTTGGTATATTGCTTACCAGTTTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 1454  
 TbTx\_6 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 435  
 TbAr\_15 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 437  
 Tslk\_6 AAGTTGTCGTTGGTATATTGCTTACCAGTTTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 1451  
 TbTx\_11 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 435  
 TbAr\_25 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 436  
 TsCh\_5 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 431  
 TsCh\_2 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 431  
 TbMi\_5 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 435  
 TbOk\_10 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 435  
 TbTx\_5 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 435  
 TsCh\_3 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 431  
 TbOk\_9 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 435  
 TbMi\_15 AAGTTGTTGCCGGCGCCTCGTGTTCGGTCTC-CGCTTGTTGAGAGGATGCCTTTTGCGG 437  
 TbOk\_8 AAGTTGTTGCCGGCGCCTCATGTTCCGGTCCC-CGCTTGTTGAGAGGATGCCTTTTGCGG 435  
 Tan5\_8 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 389  
 Tan7\_7 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 375  
 Tan1\_3 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 390  
 Tan2\_12 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 389  
 Tan3\_9 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 388  
 Tan3\_3 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 396  
 Tan5\_7 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 395  
 Tan3\_8 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 396  
 Tan6\_11 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 381  
 Tan7\_18 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 390  
 Tan1\_2 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 381  
 Tan5\_13 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 390  
 Tan2\_3 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 386  
 Tan2\_11 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 389  
 Tan6\_18 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 391  
 Tan6\_24 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAG----G 383  
 Tan1\_13 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 390  
 Tan7\_13 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 382  
 Tpar\_U CCCTTAG-GGTTAATTTTATACTTTATT-AA-CTAGATCCTTTTGCATACTGTTCCCGT 390  
 TmIn\_10 AATTTATT-AACCTAT--TATACTTTAT--AT-CTTAATCCTTTTGCATACTGT-CCACG 425  
 Tpar\_AF AATTTATTAAACCTAT--TATACTTTAT--AA-CTAAATCCTTTTGCATACTGTTCCACG 446  
 TmIn\_13 AATTTATT-AACCTAT--TATACTTTAT--AT-CTTAATCCTTTTGCATACTGT-CCACG 425  
 TmIn\_3 AATTTATT-AACCTAT--TATACTTTAT--AT-CTTAATCCTTTTGCATACTGT-CCACG 425



Tan1\_14 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 395  
 Tan5\_12 GATTT----GTCTGTGTGATGCTCTAA-----CGATACTAT----G 395  
 Tan2\_5 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 388  
 Tan2\_13 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 393  
 Tan3\_6 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 382  
 Tan2\_7 GATTT----GTCTGTGTGATGCTCTAA-----GGATACTAT----G 388  
 TeerOkE\_12 TAATAAAGGGGGGCTTGAGGAAGGAGGTTTT-----GAGGATGTCTAGTGTGCG 395  
 TeerW2\_9 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerCanE\_10 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerCanE\_7 TAATAAAGGGGGGCTTGAGGAAGGAGGTTTT-----GAGGATGTCTAGTGTGCG 393  
 TeerW1\_17 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerOkE\_13 ---TTCAGGGGGGTTCTGGGAGTTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerCanE\_1 TAATAAAGGGGGGCTTGAGGAAGGAGGTTTT-----GAGGATGTCTAGTGTGCG 393  
 TeerCanE\_8 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerWisE ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 Teer183\_8 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerOkE\_11 ---TTCAGGAGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerInE\_2 ---TTCAGGGGGGTTCTGGGAGTTGGAGG-----GAGGATACCCT-TAACG 400  
 Teer181\_1 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerOkE\_10 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerW2\_10 ---TTCAGGGGGG-TTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 399  
 TeerCanE\_6 TAATAAAGGGGGGCTTGAGGAAGGAGGTTTT-----GAGGATGTCTAGTGTGCG 393  
 TeerW3\_2 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 Teer181\_2 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerW1\_24 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 Teer183\_7 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerW2-3 ---TTTAGGGGGGTTCTGGGAGTTGGAGG-----GAGGATACCCT-TAACG 400  
 Teer181\_10 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerW1\_16 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerW3\_8 ---TTCAGGGGGGTTTGAAGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerInE\_1 ---TTCAGGGGGGTTCTGGGAGTTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerW3\_7 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerInE\_3 ---TTCAGGGGGGTTCTGGGAGTTGGAGG-----GAGGATACCCT-TAACG 400  
 TeerCanE\_11 ---TTCAGGGGGGTTTGAGGAGTCTGGAGG-----GAGGATACCCT-TAACG 399  
 Teer183\_5 ---TTCAGGGGGGTTCTGGGAGTTGGAGG-----GAGGATACCCT-TAACG 400  
 ThDG\_10 -----AGGGTGTGGGCAATGCTCGGG-----TTACGCCTT----G 203  
 ThDG\_13 -----AGGGTGTGGGCAATGCTCGGG-----TTACGCCTT----G 203  
 ThDG\_12 -----AGGGTGTGGGCAATGCTCGGG-----TTACGCCTT----G 203  
 ThDG\_14 -----AGGGTGTGGGCAATGCTCGGG-----TTACGCCTT----G 207  
 ThDG\_11 -----AGGGTGTGGGCAATGCTCGGG-----TTACGCCTT----G 203  
 To8\_8 GTTATCGAGTACGTTTTGATGCTGCAAGGATTCTTGCTTGGAGGATGCCTCATCAGT 638  
 To9\_13 GTCATCGAGTACGTTTTGATGCTGCAAGGATTCTTGCTTGGAGGATGCCTCATCAGT 625  
 To9\_10 GTCATCGAGTACGTTTTGATGCTGCAAGGATTCTTGCTTGGAGGATGCCTCATCAGT 625  
 To11\_5 GTTATCGAGTACGTTTTGATGCTGCAAGGATTCTTGCTTGGAGGATGCCTCATCAGT 638  
 To9\_11 GTCATCGAGTACGTTTTGATGCTGCAAGGATTCTTGCTTGGAGGATGCCTCATCAGT 625  
 To9\_12 GTTATCGAGTACGTTTTGATGCTGCAAGGATTCTTGCTTGGAGGATGCCTCATCGGT 634  
 To11\_1 GTTATCGAGTACGTTTTGATGCTGCAAGGATTCTTGCTTGGAGGATGCCTCATCAGT 638  
 To8\_4 GTTATCGAGTACGTTTTGATGCTGCAAGGATTCTTGCTTGGAGGATGCCTCATCAGT 638  
 To8\_9 GTTATCGAGTACGTTTTGATGCTGCAAGGATTCTTGCTTGGAGGATGCCTCATCAGT 637  
 To9\_14 GTTATCGAGTACGTTTTGATGCTGCAAGGATTCTTGCTTGGAGGATGCCTCATCAGT 638  
 To11\_2 GTCATCGAGTACGTTTTGATGCTGCAAGGATTCTTGCTTGGAGGATGCCTCATCAGT 638  
 Cfelis\_Tx CCCTCCATGTGATTTAAATCACTTGGGTT-----ATGTTGCACT--GAGA 338  
 Olonga GCGCTCTGCGCTCTGCGAGCGGCTTCGACTCG-----TTCGAGGTGCGACT-CAATG 394  
  
 TsIk\_1 CGCATTGATGTACCCTTTGGGCGCTAC-TCTGTAGCTCATACAAACACATGTAACGAC 1511  
 TbMi\_14 CGCATTGATGCTCCGCTCGAGGCGCTACGTCAGTGGCTTTTGCAAACACATGTGACGAC 497  
 TsCh\_1 CGCATTGATGCTCCGCTCGAGGCGCTACGTAAGTGGCTTTTGCAAACACATGTGACGAC 491  
 TbAr\_20 CGCATTGATGCTCCGCTCGAGGCGCTACGTCAGTGGCTTTTGCAAACACATGTGACGAC 497  
 TsIk\_2 CGCATTGATGTACCCTTTGGGCGCTAC-TCTGTAGCTCATACAAACACATGTAACGAC 1515  
 TbMi\_3 CGCATTGATGCTCCGCTCGAGGCGCTACGTCAGTGGCTTTTGCAAACACATGTGACGAC 497  
 TsCh\_4 CGCATTGATGCTCCGCTCGAGGCGCTACGTAAGTGGCTTTTGCAAACACATGTGACGAC 491  
 TsIk\_7 CGCATTGATGTACCCTTTGGGCGCTAC-TCTGTAGCTCATACAAACACATGTGACGAC 1513  
 TbTx\_6 CGCATTGATGCTCCGCTCGAGGCGCTACGTCAGTGGCTTTTGCAAACACATGTGACGAC 495  
 TbAr\_15 CGCATTGATGCTCCGCTCGAGGCGCTACGTCAGTGGCTTTTGCAAACACATGTGACGAC 497  
 TsIk\_6 CGCATTGATGTACCCTTTGGGCGCTAC-TCTGTAGCTCATACAAACACATGTAACGAC 1510  
 TbTx\_11 CGCATTGATGCTCCGCTCGAGGCGCTACGTCAGTGGCTTTTGCAAACACATGTGACGAC 495  
 TbAr\_25 CGCATTGATGCTCCGCTCGAGGCGCTACGTCAGTGGCTTTTGCAAACACATGTGACGAC 496  
 TsCh\_5 CGCATTGATGCTCCGCTCGAGGCGCTACGTAAGTGGCTTTTGCAAACACATGTGACGAC 491  
 TsCh\_2 CGCATTGATGCTCCGCTCGAGGCGCTACGTAAGTGGCTTTTGCAAACACATGTGACGAC 491

TbMi\_5 CGCATTGACGCTCCGCTCGAGGGCGTACGTCAGTGGCTTTTGCAAACACATGTGACGAC 495  
 TbOk\_10 CGCATTGATGCTCCGCTCGAGGGCGTACGTCAGTGGCTTTTGCAAACACATGTGACGAC 495  
 TbTx\_5 CGCATTGATGCTCCGCTCGAGGGCGTACGTCAGTGGCTTTTGCAAACACATGTGACGAC 495  
 TsCh\_3 CGCATTGATGCTCCGCTCGAGGGCGTACGTAAGTGGCTTTTGCAAACACATGTGACGAC 491  
 TbOk\_9 CGCATTGATGCTCCGCTCGAGGGCGTACGTCAGTGGCTTTTGCAAACACATGTGACGAC 495  
 TbMi\_15 CGCATTGATGCTCCGCTCGAGGGCGTACGTCAGTGGCTTTTGCAAACACATGTGACGAC 497  
 TbOk\_8 CGCATTGATGCTCCGCTCGAGGGCGTACGTCAGTGGCTTTTGCAAACACATGTGACGAC 495  
 Tan5\_8 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 433  
 Tan7\_7 TAGAATTAGAGCTTTCCATATGG-A----TTTGTGAAATACAAGGGTTC----- 419  
 Tan1\_3 TAGAATTAGAGCTTTCCATATGG-A----TTTGTGAAATACAAGAGTTC----- 434  
 Tan2\_12 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 433  
 Tan3\_9 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 432  
 Tan3\_3 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 440  
 Tan5\_7 TAGAATTAGAGCTTTCCATTTGG-A----TTT-GAAATACAAGAGTTC----- 437  
 Tan3\_8 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 440  
 Tan6\_11 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 425  
 Tan7\_18 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 434  
 Tan1\_2 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 425  
 Tan5\_13 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 434  
 Tan2\_3 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 430  
 Tan2\_11 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 433  
 Tan6\_18 TAGGATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 435  
 Tan6\_24 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 427  
 Tan1\_13 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 434  
 Tan7\_13 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 426  
 Tpar\_U TGGTTATGGGATGTTT-TTATGATA----CTTGGTAGATTAAGGAGCTTTATCATCTTG 444  
 TmIn\_10 TGGTTATGGGATGTTTCTTATGATA----CTTGGTAGATTAAGGAGCTTTATCAT---G 477  
 Tpar\_AF TGGTTATGGGATGTTTCTTATGATA----CTTGGTAGATTAAGGAGCTTTATCAT---G 498  
 TmIn\_13 TGGTTATGGGATGTTTCTTATGATA----CTTGGTAGATTAAGGAGCTTTATCAT---G 477  
 TmIn\_3 TGGTTATGGGATGTTTCTTATGATA----CTTGGTAGATTAAGGAGCTTTATCAT---G 477  
 Tan1\_14 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 439  
 Tan5\_12 TAGAATTAGAGCTTTCCATTTGG-A----TTT-GAAATACAAGAGTTC----- 437  
 Tan2\_5 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 432  
 Tan2\_13 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 437  
 Tan3\_6 TAGAATTAGAGCTTTCCAATTGG-A----TTTGTGAAATACAAGAGTTC----- 426  
 Tan2\_7 TAGAATTAGAGCTTTCCATTTGG-A----TTTGTGAAATACAAGAGTTC----- 432  
 TeerOkE\_12 GACATTTGATG-TTCGCGTAGGCCCT--CCGTTGATCATGCTAGCTGGTTCG----- 442  
 TeerW2\_9 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACTATGCTAGCTAGTTCG----- 449  
 TeerCanE\_10 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGAC--TGCTAGTTAGTTCG----- 447  
 TeerCanE\_7 GACATTTGATG-TTCGCGTAGGCCCT--CCGTTGATCATGCTAGCTGGTTCG----- 440  
 TeerW1\_17 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGAC--TGCTAGTTAGTTCG----- 447  
 TeerOkE\_13 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACTATGCTAGCTAGTTCG----- 449  
 TeerCanE\_1 GACATTTGATG-TTCGCGTAGGCCCT--CCGTTGATCATGCTAGCTGGTTCG----- 440  
 TeerCanE\_8 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGAC--TGCTAGTTAGTTCG----- 447  
 TeerWisE TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGAC--TGCTAGTTAGTTCG----- 447  
 Teer183\_8 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGAC--TGCTAGTTAGTTCG----- 447  
 TeerOkE\_11 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACT--GCTAGTTAGTTCG----- 447  
 TeerInE\_2 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACTATGCTGGCTAGTTCG----- 449  
 Teer181\_1 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACT--GCTAGTTAGTTCG----- 447  
 TeerOkE\_10 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACT--GCTAGTTAGTTCG----- 447  
 TeerW2\_10 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACT--GCTAGTTAGTTCG----- 446  
 TeerCanE\_6 GACATTTGATG-TTCGCGTAGGCCCT--CCGTTGATCATGCTAGCTGGTTCG----- 440  
 TeerW3\_2 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACTATGCTAGCTAGTTCG----- 449  
 Teer181\_2 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGAC--TGTTAGTTAGTTCG----- 447  
 TeerW1\_24 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGAC--TGCTAGTTAGTTCG----- 447  
 Teer183\_7 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACT--GCTAGTTAGTTCG----- 447  
 TeerW2-3 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACTATGCTAGCTAGTTCG----- 449  
 Teer181\_10 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACT--GCTAGTTAGTTCG----- 447  
 TeerW1\_16 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACT--GCTAGTTAGTTCG----- 447  
 TeerW3\_8 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACT--GCTAGTTAGTTCG----- 447  
 TeerInE\_1 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACTATGCTAGCTAGTTCG----- 449  
 TeerW3\_7 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGAC--TGCTAGTTAGTTCG----- 447  
 TeerInE\_3 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACTATGCTAGCTAGTTCG----- 449  
 TeerCanE\_11 TTCATTTGATG-GGCGTTAAGGGGTTGCTATTGACT--GCTAGTTAGTTCG----- 446  
 Teer183\_5 TTCATTTGATG-GGCGTTAAGGGGTTGCTATCGACTATGCTAGCTAGTTCG----- 449  
 ThDG\_10 CTGATCC--TG-GGTTAGCAGGGATACCGACCTGGTTCAC-ATTTGATGT----- 249  
 ThDG\_13 CTGATCC--TG-GGTTAGCAGGGATACCGACCTGGTTCAC-ATTTAATGT----- 249  
 ThDG\_12 CTGATCC--TG-GGTTAGCAGGGATACCGACCTGGTTCAC-ATTTAATGT----- 249  
 ThDG\_14 CTGATCC--TG-GGTTAGCAGGGATACCGACCTGGTTCAC-ATTTGATGT----- 253  
 ThDG\_11 CTGATCC--TG-GGTTAGCAGGGATACCGACCTGGTTCAC-ATTTGATGT----- 249

To8\_8 CGCATTTGATGTGATAAGAAAGGAGGATAGGCTAGAGTTTAAGGCAGTAC----- 688  
 To9\_13 CGCATTTGATGTGATATGAAAGGAGGATAGGCTAGAGTTTAAGGCAGTAC----- 675  
 To9\_10 CGCATTTGATGTGATATGAAAGGAGGATAGGCTAGAGTTTAAGGCAGTAC----- 675  
 To11\_5 CGCATTTGATGTGATATGAAAGGAGGATAGGCTAGAGTTTAAGGCAGTAC----- 688  
 To9\_11 CGCATTTGATGTGATATGAAAGGAGGATGGGCTAGAGTTTAAGGCAGTAC----- 675  
 To9\_12 CGCATTTGATGTGATATGAAAGGAGGATAGGCTAGAGTTTAAGGCAGTAC----- 684  
 To11\_1 CGCATTTGATGTGATATGAAAGGAGGATAGGCTAGAGTTTAAGGCAGTAC----- 688  
 To8\_4 CGCATTTGATGTGATATGAAAGGAGGATAGGCTAGAGTTTAAGGCAGTAC----- 688  
 To8\_9 CGCATTTGATGTGATATGAAAGGAGGATAGGCTAGAGTTTAAGGCAGTAC----- 687  
 To9\_14 CGCATTTGATGTGATATGAAAGGAGGATAGGCTAGAGTTTAAGGCAGTAC----- 688  
 To11\_2 CGCATTTGATGTGATATGAAAGGAGGATAGGCTAGAGTTTAAGGCAGTAC----- 688  
 Cfelis\_Tx TTCATTGCAAATGTAATTAATAGAGTAATTGCTAAT-TCTCTATTAGTTG----- 387  
 Olonga CAGCGGTCACATTGTTCCACAATGTGAACTCATTGAGAGTAGAGGCAGTGTAGTTTCGACT 454

Tslk\_1 CGTCTGTT-----TTACCTGGTGTGTTTGTTTTTAGTGGGTTGCTTGCAACAA----G 1560  
 TbMi\_14 CGTTGTTTGTGCGGCTCGTTTGTCTGCTTGTGTTTTCCGGTACACGTATAACATCGCCTA 557  
 TsCh\_1 CGTTGTTTATCGGCTCGTTTGTCT-CTTGTTGTTTTAGTACACGTATAACATGGCCTA 550  
 TbAr\_20 CGTTGTTTGTGCGGCTCGTTTGTCTGCTTGTGTTTTCCGGTACACGTATAACATCGCCTA 557  
 Tslk\_2 CGTCTGTT-----TTACCTGGTGTGTTTGTTTTTAGTGGGTTGCTTGCAACAA----G 1564  
 TbMi\_3 CGTTGTTTGTGCGGCTCGTTTGTCTGCTTGTGTTTTCCGGTACACGTATAACATCGCCTA 557  
 TsCh\_4 CGTTGTTTATCGGCTCGTTTGTCT-CTTGTTGTTTTAGTACACGTATAACATGGCCTA 550  
 Tslk\_7 CGTCTGTT-----TTACCTGGTGTGTTTGTTTTTAGTGGGTTGCTTGCAACAA----G 1562  
 TbTx\_6 CGTTGTTTGTGCGGCTCGTTTGTCTGCTTGTGTTTTCCGGTACACGTATAACATCGCCTA 555  
 TbAr\_15 CGTTGTTTGTGCGGCTCGTTTGTCTGCTTGTGTTTTCCGGTACACGTATAACATCGCCTA 557  
 Tslk\_6 CGTCTGTT-----TTACCTGGTGTGTTTGTTTTTAGTGGGTTGCTTGCAACAA----G 1559  
 TbTx\_11 CGTTGTTTGTGCGGCTCGTTTGTCTGCTTGTGTTTTCCGGTACACGTATAACATCGCCTA 555  
 TbAr\_25 CGTTGTTTGTGCGGCTCGTTTGTCTGCTTGTGTTTTCCGGTACACGTATAACATCGCCTA 556  
 TsCh\_5 CGTTGTTTATCGGCTCGTTTGTCT-CTTGTTGTTTTAGTACACGTATAACATGGCCTA 547  
 TsCh\_2 CGTTGTTTATCGGCTCGTTTGTCT-CTTGTTGTTTTAGTACACGTATAACATGGCCTA 547  
 TbMi\_5 CGTTGTTTGTGCGGCTCGTTTGTCTGCTTGTGTTTTCCGGTACACGTATAACATCGCCTA 555  
 TbOk\_10 CGTTGTTTGTGCGGCTCGTTTGTCTGCTTGTGTTTTCCGGTACACGTATAACATCGCCTA 555  
 TbTx\_5 CGTTGTTTATCGGCTCGTTTGTCTGTT-CTTGTTGTTTTCCGGTACACGTATAACATCGCCTA 555  
 TsCh\_3 CGTTGTTTATCGGCTCGTTTGTCTGTT-CTTGTTGTTTTCCGGTACACGTATAACATGGCCTA 547  
 TbOk\_9 CGTTGTTTGTGCGGCTCGTTTGTCTGCTTGTGTTTTCCGGTACACGTATAACATCGCCTA 555  
 TbMi\_15 CGTTGTTTGTGCGGCTCGTTTGTCTGCTTGTGTTTTCCGGTACACGTATAACATCGCCTA 557  
 TbOk\_8 CGTTGTTTGTGCGGCTCGTTTGTCTGCTTGTGTTTTCCGGTACACGTATAACATCGCCTA 555  
 Tan5\_8 -----AAGGACTGGAACC-----T-GGGTTTCCAAATTTGGTAACCTA 470  
 Tan7\_7 -----AAGGACGGGAAC-----GGTTTCCAGATCTTGGAAATCCA 454  
 Tan1\_3 -----AAGGA-GGGAAC-----GGGTTTCCAGATCTTGGAAATCCA 469  
 Tan2\_12 -----AAGGACTTGAAC-----T-GGGTTTCCAGATCTGGTAACCTA 469  
 Tan3\_9 -----AAGGACTGAACC-----T-AGGTTTCCAGATTTGGTAACCTA 469  
 Tan3\_3 -----AAGGACTGGAAC-----TGGTTTCCAGATCTTGGAAATCCA 475  
 Tan5\_7 -----AAGGGCGGGTAC-----CTGC----- 453  
 Tan3\_8 -----AAGGACTGGAAC-----TGGTTTCCAGATCTTGGAAATCCA 475  
 Tan6\_11 -----AAGGAC-GGAAC-----T-GAGTTTCCAAATTTGGTATCCTA 460  
 Tan7\_18 -----AAGGACTGGAAC-----T-CGGTTTCCAAATTTGGAAGCCTA 470  
 Tan1\_2 -----AAGGACAGGAA-----T-GGGTTTCCAAATCTGGTAACCTA 460  
 Tan5\_13 -----AAGGACGGGAAC-----T-GGGTTTCCAAATTTGGTAACCTA 470  
 Tan2\_3 -----AAGGACTAGAAC-----CTCT 446  
 Tan2\_11 -----AAGGACTTGAAC-----T-GGGTTTCCAGATCTGGTAACCTA 469  
 Tan6\_18 -----AAGGACGGATAC-----C-TG-----CGGG----- 454  
 Tan6\_24 -----AAGGACTGGAAC-----T-CGGTTTCCAAATATGGGATCCCA 463  
 Tan1\_13 -----AAGGACTGGAAC-----TAGGTTTCCAAATTTGGGAATCCA 471  
 Tan7\_13 -----AAGGACTGGAGC-----AGGGTTTCCAAATTTGGGAATCCTA 463  
 Tpar\_U GTAACATGTTTTACATATTACCTG----GTGATCTA-GTGAAAAACGTGTACCAATG 498  
 Tmln\_10 GGAAACCCTTATTAGGGGCTACCGTGAT-CCGTGAAAAACGTGCCAAACTGGTTACTCTG 536  
 Tpar\_AF GGAAACCC---TTAGGGACTACCATGAT-CCGTAAAAAACTTGCCAAACTGGTTACTCTG 554  
 Tmln\_13 GGAAACCCTTATTAGGGGCTACCGTGAT-CCGTGAAAAACGTGCCAAACTGGTTACTCTG 536  
 Tmln\_3 GGAAACCCTTATTAGGGGCTACCGTGAT-CCGTGAAAAACGTGCCAAACTGGTTACTCTG 536  
 Tan1\_14 -----AAGGACTAGAAC-----GGGTTTCCAAATTTGGGAACCTA 475  
 Tan5\_12 -----AAGGGC-----GGGTACCTG 452  
 Tan2\_5 -----AAGGACGGAACCT-----GGGTTTCCAGATTTGGTAGCCTA 468  
 Tan2\_13 -----AAGGGCTGGAACC-----GG-TTTCCAGATCTGGAATCCTA 472  
 Tan3\_6 -----AAGGACTGGAACG-----GGGTTTCCAAATTTGTGAAACCCA 462  
 Tan2\_7 -----AAGGACGGAACCT-----GGGTTTCCAGATTTGGTAGCCTA 468  
 TcerOkE\_12 -----ATGTTTCTTGA-----CAAATAC-----CGTCTGTTT 469  
 TcerW2\_9 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTTT 476  
 TcerCanE\_10 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTTT 474  
 TcerCanE\_7 -----ATGTTTCTGTA-----CAAATAC-----CGTCTGTTT 467

TcerW1\_17 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 TcerOkE\_13 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 476  
 TcerCanE\_1 -----ATGTTTCGTGA-----CAAATAC-----CGTCTGTT 467  
 TcerCanE\_8 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 TcerWisE -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 Tcer183\_8 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 TcerOkE\_11 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 TcerInE\_2 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 476  
 Tcer181\_1 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 TcerOkE\_10 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 TcerW2\_10 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 473  
 TcerCanE\_6 -----ATGTTTCGTGA-----CAAATAC-----CGTCTGTT 467  
 TcerW3\_2 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 476  
 Tcer181\_2 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 TcerW1\_24 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 Tcer183\_7 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 TcerW2-3 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 476  
 Tcer181\_10 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 TcerW1\_16 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 TcerW3\_8 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 TcerInE\_1 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 476  
 TcerW3\_7 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 474  
 TcerInE\_3 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 476  
 TcerCanE\_11 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 473  
 Tcer183\_5 -----ATAGTTTGTA-----GAAACAC-----CGTCTTTT 476  
 ThDG\_10 -----GGATCTCGTTG-----GACAC-----TTGATTC 272  
 ThDG\_13 -----GGATCTCGTTG-----GACTC-----TTGATTC 272  
 ThDG\_12 -----GGATCTCGTTG-----GACTC-----TTGATTC 272  
 ThDG\_14 -----GGATCTCGTTG-----GACAC-----TTGATTC 276  
 ThDG\_11 -----GGATCTCGTTG-----GACTC-----TTGATTC 272  
 To8\_8 -----TAGCATTGAAA-----GACATCCA-----TGTTGTGTT 716  
 To9\_13 -----TAGCATTGAAA-----GACATCCA-----TGTTGTGTT 703  
 To9\_10 -----TAGCATTGAAA-----GACATCCA-----TGTTGTGTT 703  
 To11\_5 -----TAGCATTGAAA-----GACATCCA-----CGTTGTGTT 716  
 To9\_11 -----TAGCATTGAAA-----GACATCCA-----TGTTGTGTT 703  
 To9\_12 -----TAGCATTGAAA-----GACATCCA-----TGTTGTGTT 712  
 To11\_1 -----TAGCATTGAAA-----GACATCCATGTTGTGTTTCATT 721  
 To8\_4 -----TAGCATTGAAA-----GACATCCATGTTGTGTTTCATT 721  
 To8\_9 -----TAGCATTGAAA-----GACATCCATGTTGTGTTTCATT 720  
 To9\_14 -----TAGCATTGAAA-----GACATCCATGTTGTGTTTCATT 721  
 To11\_2 -----TAGCATTGAAA-----GACATCCATGTTGTGTTTCATT 721  
 Cfelis\_Tx -----CTGGATATTAAT-----TATCC-----TTCTTTCTTT 414  
 Olonga ACCAGCGCTT--AGGCACTCAAACCTTTTCTGTATCTGAAAT-CAAGCAGGACCACCCG 510

Tslk\_1 TAGTTGTG-----AAAACACCAAACGGATA---ACAAACAACCAGTAAGACG 1604  
 TbMi\_14 CGGCCGTGCTATCGTGGCCTGAGATCGACGAGTGCGGA---CAGACCCGTCGAATAAACG 614  
 TsCh\_1 CGGCCGTGGTA-CGTGGCCTGGGATCGACGAGTG--AA--CAGACCCGTCGACGAAACG 604  
 TbAr\_20 CGGCCGTGCTATCGTGGCCTGAGATCGACGAGTGCGGA---CAGACCCGTCGAATAAACG 614  
 Tslk\_2 TAGTTGTG-----AAAACACCAAACGGATA---ACAAACAACCAGTAAGACG 1608  
 TbMi\_3 CGGCCGTGCTATCGTGGCCTGAGATCGACGAGTGCGGA---CAGACCCGTCGAATAAACG 614  
 TsCh\_4 CGGCCGCGGTA-CGTGGCCTGGGATCGACGAGTGAACA----GACCCGTCGACGAAACG 604  
 Tslk\_7 TAGTTGTG-----AAAACACCAA--ACGGATAACAAACA-ACCAGTAAGACG 1606  
 TbTx\_6 CGGCCGTGCTATCGTGGCCTGAGATCAGCGAGTATAAACGACAAAACCTGTTGACAAAACG 615  
 TbAr\_15 CGGCCGTGCTATCGTGGCCTGAGATCGACGAGTGCGGA---CAGACCCGTCGAATAAACG 614  
 Tslk\_6 TAGTTGTG-----AAAACACCAA--ACGGATAACAAACA-ACCAGTAAGACG 1603  
 TbTx\_11 CGGCCGTGCTATCGTGGCCTGAGATCAGCGAGTATAAACGACAAAACCTGTTGACAAAACG 615  
 TbAr\_25 CGGCCGTGCTATCGTGGCCTGAGATCGACGAGTGCGG---ACAGACCCGTCGAATAAACG 613  
 TsCh\_5 CGGCCGTGGTA-CGTGGCCTGGGATCGACGAGTGAACA----GACCCGTCGACGAAACG 601  
 TsCh\_2 CGGCCGTGGTA-CGTGGCCTGGGATCGACGAGTGAACA----GACCCGTCGACGAAACG 601  
 TbMi\_5 CGGCCGTGCTATCGTGGCCTGAGATCAGCGAGTATAAACGACAAAACCTGTTGACAAAACG 615  
 TbOk\_10 CGGCCGTGCTATCGTGGCCTGAGATCAGCGAGTATAAACGACAAAACCTGTTGACAAAACG 615  
 TbTx\_5 CGGCCGTGCTATCGTGGCCTGAGATCAGCGAGTATAAACGACAAAACCTGTTGACAAAACG 615  
 TsCh\_3 CGGCCGTGGTA-CGTGGCCTGGGATCGACGAGTG----AACAGACCCGTCGACGAAACG 601  
 TbOk\_9 CGGCCGTGCTATCGTGGCCTGAGATCAGCGAGTATAAACGACAAAACCTGTTGACAAAACG 615  
 TbMi\_15 CGGCCGTGCTATCGTGGCCTGAGATCGACGAGTGCG---GACAGACCCGTCGAATAAACG 614  
 TbOk\_8 CGGCCGTGCTATCGTGGCCTGAGATCAGCGAGTATAAACGACAAAACCTGTTGACAAAACG 615  
 Tan5\_8 CAGT-----TTCT-----GTTCT 484  
 Tan7\_7 ATGT-----T-CT---GGTCCT 467  
 Tan1\_3 AGGT-----T-CT---GGTCCT 482

Tan2\_12 CAGT-----TTC----TGATCT 482  
 Tan3\_9 TAGT-----TTCC----TGTTCC 483  
 Tan3\_3 AGGT-----TCT----GTTCC 488  
 Tan5\_7 -GGG-----TCC----GGTCCT 465  
 Tan3\_8 AGGT-----TCT----GTTCC 488  
 Tan6\_11 CGGT-----TTG----GTCC 472  
 Tan7\_18 -GGT-----TCT----ATCCC 481  
 Tan1\_2 -----TGC---GGTTCT 469  
 Tan5\_13 AAGG-----TTCT---ATTCC 484  
 Tan2\_3 TGG-----TTTC---TAGCCT 459  
 Tan2\_11 CAG-----TTTC---TGATCT 482  
 Tan6\_18 -----TTC---TTTTCC 463  
 Tan6\_24 AAG-----TTTC---TTTTCC 476  
 Tan1\_13 GGTT-----CTGG----TCCT 483  
 Tan7\_13 TAGT-----TTCT----AGCC 475  
 Tpar\_U TAA-----AGTGGATTA-----A-TCTAC---ATACAC 522  
 TmIn\_10 TAATTACG-----TAATTACTTC-----A-ATTATTGTAATTCCA 570  
 Tpar\_AF TAATTACA-----TAATTACTTT-----A-ATTATTGTAATTCCA 588  
 TmIn\_13 TAATTACG-----TAATTACTTC-----A-ATTATTGTAATTCCA 570  
 TmIn\_3 TAATTACG-----TAATTACTTC-----A-ATTATTGTAATTCCA 570  
 Tan1\_14 AAGG-----TTCT---GGCCCT 489  
 Tan5\_12 CGGG-----T-CC---GGTCCT 465  
 Tan2\_5 CAGT-----TTCT---AGGTCC 482  
 Tan2\_13 CAGT-----TTCT---AGTCCT 486  
 Tan3\_6 C-----CT---GGTCCA 471  
 Tan2\_7 CAGT-----TTCT---AGGTCC 482  
 TcerOkE\_12 CCGA-----GGCGCTTAAGTATTAGGAAAC 494  
 TcerW2\_9 C-----GGCATTATGCCT--GAAACT 496  
 TcerCanE\_10 C-----GGCATTATTGTC--GAAACT 494  
 TcerCanE\_7 CCGG-----GGCGCATAAGTATTAGGAAAC 492  
 TcerW1\_17 CGG-----CATTTATTGTCGAAACT 494  
 TcerOkE\_13 CGG-----CATTTATGCTCGAAACT 496  
 TcerCanE\_1 CCGA-----GGCGCATAAGTATTAGGAAAC 492  
 TcerCanE\_8 CGG-----CATTTATTGTCGAAACT 494  
 TcerWisE CGG-----CATTTATTGTCGAAACT 494  
 Tcer183\_8 CGG-----CATTTATGCTCGAAACT 494  
 TcerOkE\_11 CGG-----CATTTGT--CGAAACT 491  
 TcerInE\_2 CGG-----CATTTATGCTCGAAACT 496  
 Tcer181\_1 CGG-----CATTTATTGTCGAAACT 494  
 TcerOkE\_10 CGG-----CATT--TGTCGAAACT 491  
 TcerW2\_10 CGG-----CATTTATTGTCGAAACT 493  
 TcerCanE\_6 CCGA-----GGCGCATAAGTATTAGGAAAC 492  
 TcerW3\_2 CGG-----CATTTATGCCTGAAACT 496  
 Tcer181\_2 CGG-----CATTTATTGTCGAAACT 494  
 TcerW1\_24 CGG-----CATTTATTGTCGAAACT 494  
 Tcer183\_7 CGG-----CATTTATTGTCGAAACT 494  
 TcerW2-3 CGG-----CATTTATGCTCGAAACT 496  
 Tcer181\_10 CGG-----CATTTATTGTCGAAACT 494  
 TcerW1\_16 CGG-----CATTTATTGTCGAAACT 494  
 TcerW3\_8 CGG-----CATTTATTGTCGAAACT 494  
 TcerInE\_1 CGG-----CATTTATGCTCGAAACT 496  
 TcerW3\_7 CGG-----CATTTATTGTCGAAACT 494  
 TcerInE\_3 CGG-----CATTTATGCTCGAAACT 496  
 TcerCanE\_11 CGG-----CATTTATTGTCGAAACT 493  
 Tcer183\_5 CGG-----CATTTATGCTCGAAACT 496  
 ThDG\_10 CAA-----ACACTCGTCCTTG----T 289  
 ThDG\_13 CAA-----ACACACGTCCA-A----T 288  
 ThDG\_12 CAA-----ACACACGTCTTG----T 289  
 ThDG\_14 CAA-----ACACACGTCCATG----T 293  
 ThDG\_11 CAA-----ACACACGTCC-TG----T 288  
 To8\_8 CAT-----TTTTTGATTAAAAATGAT 738  
 To9\_13 CAT-----TTTTTGATTAAAAATGAT 725  
 To9\_10 CAT-----TTTTTGATTAAAAATGAT 725  
 To11\_5 CAT-----TTTTTGATTAAAAATGAT 738  
 To9\_11 CAT-----TTTTTGATTATAAAATGAT 725  
 To9\_12 CAT-----TTTTTGATTAAAAATGAT 734  
 To11\_1 -----TTTTGATTAAAAATGAT 738  
 To8\_4 -----TTTTGATTAAAAATGAT 738  
 To8\_9 T-----TTTGATTAAAAATGAT 737  
 To9\_14 T-----TTTGATTAAAAATGAT 738

Tol1\_2 T-----TTTGATTA AAAATGAT 738  
 Cfelis\_Tx CATA-----CAACTACATGAGAT 432  
 Olonga CTGA-----ACTTAAGCATATCAMT 530

TsIk\_1 GCGGAGCGTTAA-ATA-TACCAAG--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 1660  
 TbMi\_14 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 671  
 TsCh\_1 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 661  
 TbAr\_20 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 671  
 TsIk\_2 GCGGAGCGTTAA-ATA-TACCAAG--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 1664  
 TbMi\_3 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 671  
 TsCh\_4 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 661  
 TsIk\_7 GCGGAGCGTTAA-ATA-TACCAAG--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 1662  
 TbTx\_6 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 672  
 TbAr\_15 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 671  
 TsIk\_6 GCGGAGCGTTAA-ATA-TACCAAG--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 1659  
 TbTx\_11 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 672  
 TbAr\_25 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 670  
 TsCh\_5 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 658  
 TsCh\_2 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 658  
 TbMi\_5 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 672  
 TbOk\_10 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 672  
 TbTx\_5 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 672  
 TsCh\_3 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 658  
 TbOk\_9 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 672  
 TbMi\_15 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 671  
 TbOk\_8 ATGGAACGTCAAGATT-TACTACA--TTTTACACTTTTAGCGGTGGATGTCTTGGCTCAC 672  
 Tan5\_8 TGGTAACT-C-GGAT----TTAAT--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 536  
 Tan7\_7 TAGTAACT-CAGGAT----TTAAT--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 520  
 Tan1\_3 TAGTAACT-CAGGAT----TTAAT--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 535  
 Tan2\_12 TGGTAACT-CAGGAT----TTAAT--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 535  
 Tan3\_9 TAGTAACT-C-GGAT----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 535  
 Tan3\_3 TGGTAACT-CAGGAT----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 541  
 Tan5\_7 TAGTAACT-CGGATT----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 518  
 Tan3\_8 TGGTAACT-CAGGAT----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 541  
 Tan6\_11 TAGTAACT-CGGGAT----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 525  
 Tan7\_18 TAGTAACT-CAGGAT----TTAAT--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 534  
 Tan1\_2 TAGTAACT-CAGGAT----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 522  
 Tan5\_13 TGGTAACT-CAG-AT----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 536  
 Tan2\_3 TGGTAACT-CAGGAT----TTAAT--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 512  
 Tan2\_11 TGGTAACT-CAGGAT----TTAAT--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 535  
 Tan6\_18 TGGTAACT-CGGAAT----TTAAT--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 516  
 Tan6\_24 TAGTAACT-CGGA-T----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 528  
 Tan1\_13 TGGTAACT-CAGGAT----TTAAT--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 536  
 Tan7\_13 TGGTAACT-C-GGGT----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 527  
 Tpar\_U TGGTAACT-CAGGAT----TTAAT--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 573  
 TmIn\_10 TTGTAATCACTTGGTTACTTCAAAA--TTTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 628  
 Tpar\_AF TTGTAATCACTTGGTTACTTCAAAA--TTTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 648  
 TmIn\_13 TTGTAATCACTTGGTTACTTCAAAA--TTTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 628  
 TmIn\_3 TTGTAATCACTTGGTTACTTCAAAA--TTTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 628  
 Tan1\_14 TAGTAACT-CAGGAT----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 542  
 Tan5\_12 TAGTAACT-CGGATT----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 518  
 Tan2\_5 TGGTAACT-CAGGAT----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 535  
 Tan2\_13 TGGTAACT-CAGGAT----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 539  
 Tan3\_6 TGGTAACT-C-GGAT----TTAAT--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 523  
 Tan2\_7 TGGTAACT-CAGGAT----TTAAA--ATTTAAACTTTTCAGCGGTGGATGTCTTGGCTCAC 535  
 TcerOkE\_12 GCACAAGACT--TGG----TTTTACACTTAAAACCTTTTCAGCGGTGGATGTCTCGGCTCAT 548  
 TcerW2\_9 GGACAA-----TGG----TAAAAGATTTAAA--CTTTCAGCGGTGGATGTCTCGGCTCAT 545  
 TcerCanE\_10 GGACAA-----TGG----TAAAAGATTTAAA--CTTTCAGCGGTGGATGTCTCGGCTCAT 543  
 TcerCanE\_7 GCACAAGACT--TGG----TTTTACACTTAAAACCTTTTCAGCGGTGGATGTCTCGGCTCAT 546  
 TcerW1\_17 GGACAA-----TGG----TAAAAGATTTAAA--CTTTCAGCGGTGGATGTCTCGGCTCAT 544  
 TcerOkE\_13 GGACAA-----TGG----TAA-AAGATTTAAA--CTTTCAGCGGTGGATGTCTCGGCTCAT 545  
 TcerCanE\_1 GGACAA-----TGG----TTTTACACTTAAAACCTTTTCAGCGGTGGATGTCTCGGCTCAT 546  
 TcerCanE\_8 GGACAA-----TGG----TAAAAGATTTAAA--CTTTCAGCGGTGGATGTCTCGGCTCAT 543  
 TcerWisE GGACAA-----TGG----TAAAAGATTTAAA--CTTTCAGCGGTGGATGTCTCGGCTCAT 543  
 Tcer183\_8 GGACAA-----TGG----TAAAAGATTTAAA--CTTTCAGCGGTGGATGTCTCGGCTCAT 543  
 TcerOkE\_11 GGACAA-----TGG----TAAAAGATTTAAA--CTTTCAGCGGTGGATGTCTCGGCTCAT 541  
 TcerInE\_2 GGACAA-----TGG----TAAAAGATTTAAA--CTTTCAGCGGTGGATGTCTCGGCTCAT 545  
 Tcer181\_1 GGACAA-----TGG----TAAAAGATTTAAA--CTTTCAGCGGTGGATGTCTCGGCTCAT 544  
 TcerOkE\_10 GGACAA-----TGG----TAAAAGATTTAAA--CTTTCAGCGGTGGATGTCTCGGCTCAT 541

TcerW2\_10 GGACAA-----TGG---TAAAAAGATTTAAACTTTCAGCGGTGGATGTCTCGGCTCAT 543  
 TcerCanE\_6 GCACAAGACT--TGG----TTTTACACTTAAAACTTTCAGCGGTGGATGTCTCGGCTCGT 546  
 TcerW3\_2 GGACAA-----TGG---TAAAAAGATTTAAA-CTTTCAGCGGTGGATGTCTCGGCTCAT 545  
 Tcer181\_2 GGACAA-----TGG---TAAAAAGATTTAAACTTTCAGCGGTGGATGTCTCGGCTCAT 544  
 TcerW1\_24 GGACAA-----TGG---TAAAAAGATTTAAACTTTCAGCGGTGGATGTCTCGGCTCAT 544  
 Tcer183\_7 GGACAA-----TGG---TAAAAAGATTTAAACTTTCAGCGGTGGATGTCTCGGCTCAT 544  
 TcerW2-3 GGACAA-----TGG---TAAAA-GATTTAAACTTTCAGCGGTGGATGTCTCGGCTCAT 545  
 Tcer181\_10 GGACAA-----TGG---TAAAAAGATTTAAACTTTCAGCGGTGGATGTCTCGGCTCAT 544  
 TcerW1\_16 GGACAA-----TGG---TAAAAAGATTTAAACTTTCAGCGGTGGATGTCTCGGCTCAT 544  
 TcerW3\_8 GGACAA-----TGG---TAAAAAGATTTAAACTTTCAGCGGTGGATGTCTCGGCTCAT 544  
 TcerInE\_1 GGACAA-----TGG---TAAAA-GATTTAAACTTTCAGCGGTGGATGTCTCGGCTCAT 545  
 TcerW3\_7 GGACAA-----TGG---TAAAAAGATTTAAACTTTCAGCGGTGGATGTCTCGGCTCAT 544  
 TcerInE\_3 GGACAA-----TGG---TAAAA-GATTTAAACTTTCAGCGGTGGATGTCTCGGCTCAT 545  
 TcerCanE\_11 GGACAA-----TGG---TAAAA-GATTTAAACTTTCAGCGGTGGATGTCTCGGCTCAT 542  
 Tcer183\_5 GGACAA-----TGG---TAAAA-GATTTAAACTTTCAGCGGTGGATGTCTCGGCTCAT 545  
 ThDG\_10 GGACAA-----TATTACCTTTTAAACTGTCAGCGGTGGATGTCTGGCTCAC 336  
 ThDG\_13 GGACTA-----TGTTACCATTTAAACTGTCAGCGGTGGATGTCTGGCTCAC 335  
 ThDG\_12 GGACAA-----TATTACCCTTAAACTGTCAGCGGTGGATGTCTGGCTCAC 336  
 ThDG\_14 GGACAA-----TGTTACCCTTAAACTGTCAGCGGTGGATGTCTGGCTCAC 340  
 ThDG\_11 GGACAA-----TATTACCTTTTAAACTGTCAGCGGTGGATGTCTGGCTCAC 335  
 To8\_8 GAACGACTTGGAGAA----TTTTAAAATTTAAACTTATAGCGGTGGATGTCTCGGCTCAT 794  
 To9\_13 GAACGACTTGGAGAA----TTTTAAAATTTAAACTTATAGCGGTGGATGTCTCGGCTCAT 781  
 To9\_10 GAACGACTTGGAGAA----TTTTAAAATTTAAACTTATAGCGGTGGATGTCTCGGCTCAT 781  
 To11\_5 GAACGACTTGGAGAA----TTTTAAAATTTAAACTTATAGCGGTGGATGTCTCGGCTCAT 794  
 To9\_11 GAACGACTTGGAGAA----TTTTAAAATTTAAACTTATAGCGGTGGATGTCTCGGCTCAT 781  
 To9\_12 GAACGACTTGGAGAA----TTTTAAAATTTAAACTTATAGCGGTGGATGTCTCGGCTCAT 790  
 To11\_1 GAACGACTTGGAGAA----TTTTAAAATTTAAACTTATAGCGGTGGATGTCTCGGCTCAT 794  
 To8\_4 GAACGACTTGGAGAA----TTTTAAAATTTAAACTTATAGCGGTGGATGTCTCGGCTCAT 794  
 To8\_9 GAACGACTTGGAGAA----TTTTAAAATTTAAACTTATAGCGGTGGATGTCTCGGCTCAT 793  
 To9\_14 GAACGACTTGGAGAA----TTTTAAAATTTAAACTTATAGCGGTGGATGTCTCGGCTCAT 794  
 To11\_2 GAACGACTTGGAGAA----TTTTAAAATTTAAACTTATAGCGGTGGATGTCTCGGCTCAT 794  
 Cfelis\_Tx GTTTCATCTCAACACA---TTTAT--TTATAAACTTTCAGCGATGGATGTCTTGGCTCAC 487  
 Olonga AAGCGGAGGAGAAGAA-ATTAAGTAAAGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAAA 589

TsIk\_1 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 1717  
 TbMi\_14 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 728  
 TsCh\_1 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 718  
 TbAr\_20 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 728  
 TsIk\_2 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 1721  
 TbMi\_3 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 728  
 TsCh\_4 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 718  
 TsIk\_7 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 1719  
 TbTx\_6 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 729  
 TbAr\_15 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 728  
 TsIk\_6 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 1716  
 TbTx\_11 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 729  
 TbAr\_25 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 727  
 TsCh\_5 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 715  
 TsCh\_2 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 715  
 TbMi\_5 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 729  
 TbOk\_10 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 729  
 TbTx\_5 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 729  
 TsCh\_3 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 715  
 TbOk\_9 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 729  
 TbMi\_15 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 728  
 TbOk\_8 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 729  
 Tan5\_8 ACAACGATGAAGGACGCAGCGAAGTGC---ATAAGCATTGTGACTTGCAGACTTCTGCG 593  
 Tan7\_7 ACAACGATGAAGGACGCAGCGAAGTGC---ATAAGCATTGTGACTTGCAGACTTCTGCG 577  
 Tan1\_3 ACAACGATGAAGGACGCAGCGAAGTGC---ATAAGCATTGTGACTTGCAGACTTCTGCG 592  
 Tan2\_12 ACAACGATGAAGGACGCAGCGAAGTGC---ATATGCATTGTGACTTGCAGACTTCTGCG 592  
 Tan3\_9 ACAACGATGAAGGACGCAGCGAAGTGC---ATAAGCATTGTGACTTGCAGACTTCTGCG 592  
 Tan3\_3 ACAACGATGAAGGACGCAGCGAAGTGC---ATAAGCATTGTGACTTGCAGACTTCTGCG 598  
 Tan5\_7 ACAACGATGAAGGACGCAGCGAAGTGC---ATAAGCATTGTGACTTGCAGACTTCTGCG 575  
 Tan3\_8 ACAACGATGAAGGACGCAGCGAAGTGC---ATAAGCATTGTGACTTGCAGACTTCTGCG 598  
 Tan6\_11 ACAACGATGAAGGACGCAGCGAAGTGC---ATAAGCATTGTGACTTGCAGACTTCTGCG 582  
 Tan7\_18 ACAACGATGAAGGACGCAGCGAAGTGC---ATAAGCATTGTGACTTGCAGACTTCTGCG 591  
 Tan1\_2 ACAACGATGAAGGACGCAGCGAAGTGC---ATAAGCATTGTGACTTGCAGACTTCTGCG 579  
 Tan5\_13 ACAACGATGAAGGACGCAGCGAAGTGC---ATAAGCATTGTGACTTGCAGACTTCTGCG 593  
 Tan2\_3 ACAACGATGAAGGACGCAGCGAAGTGC---ATAAGCATTGTGACTTGCAGACTTCTGCG 569

Tan2\_11 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 592  
 Tan6\_18 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 573  
 Tan6\_24 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 585  
 Tan1\_13 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 593  
 Tan7\_13 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 584  
 Tpar\_U ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 630  
 TmIn\_10 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 685  
 Tpar\_AF ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 705  
 TmIn\_13 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 685  
 TmIn\_3 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 685  
 Tan1\_14 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 599  
 Tan5\_12 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 575  
 Tan2\_5 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGAAGACTTCTGCG 592  
 Tan2\_13 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 596  
 Tan3\_6 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 580  
 Tan2\_7 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 592  
 TeerOkE\_12 ACAGCGATGAAGGACGCAGCGAATTGCG---ATATGCATTGTGATCTGTACACTTCTGCG 605  
 TeerW2\_9 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 602  
 TeerCanE\_10 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 600  
 TeerCanE\_7 ACAGCGATGAAGGACGCAGCGAATTGCG---ATATGCATTGTGATCTGCACACTTCTGCG 603  
 TeerW1\_17 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 601  
 TeerOkE\_13 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 602  
 TeerCanE\_1 ACAGCGATGAAGGACGCAGCGAATTGCG---ATATGCATTGTGATCTGCACACTTCTGCG 603  
 TeerCanE\_8 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 600  
 TeerWisE ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 600  
 Teer183\_8 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 600  
 TeerOkE\_11 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 598  
 TeerInE\_2 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 602  
 Teer181\_1 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 601  
 TeerOkE\_10 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 598  
 TeerW2\_10 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 600  
 TeerCanE\_6 ACAGCGATGAAGGACGCAGCGAATTGCG---ATATGCATTGTGATCTGCACACTTCTGCG 603  
 TeerW3\_2 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 602  
 Teer181\_2 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 601  
 TeerW1\_24 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 601  
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 TeerW2-3 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 602  
 Teer181\_10 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 601  
 TeerW1\_16 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 601  
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 TeerW3\_7 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 601  
 TeerInE\_3 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 602  
 TeerCanE\_11 ACAACGATGAAGGACGCAGTGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 599  
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 ThDG\_12 ACAACGATGAAGGACGCAGCGAAGTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 393  
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 To9\_13 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 838  
 To9\_10 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 838  
 To11\_5 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 851  
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 To11\_1 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 851  
 To8\_4 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 851  
 To8\_9 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 850  
 To9\_14 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 851  
 To11\_2 ACAACGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 851  
 Cfelis\_Tx ACATCGATGAAGGACGCAGCGAATTGCG---ATAAGCATTGTGACTTGCAGACTTCTGCG 544  
 Olonga GCCCAAAATGGAAATCTTGTGCACTACGTGTACACGAATTGTAATCTAGAGATAGT--CC 647

Tslk\_1 AATCAACAGATTTCTGAACGTATTAGACACACCACC-CTTTT-----GTGGTACTCCCA 1770  
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 TbAr\_20 AATCAACAGATTTCTGAACGTGTTAGACACACCACC-TCTGCTTGCACGTGGTACTCCCA 787  
 Tslk\_2 AATCAACAGATTTCTGAACGTATTAGACACACCACC-CTTTT-----GTGGTACTCCCA 1774



TbMi\_3 AATCAACAGATTTCTGAACGTATTAGACACACCACC-TCTGCTTGCACGTGGTACTCCCA 787  
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 Tslk\_7 AATCAACAGATTTCTGAACGTATTAGACACACCACC-TCTT-----GTGGTACTCCCA 1772  
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 TbAr\_15 AATCAACAGATTTCTGAACGTATTAGACACACCACC-TCTGCTTGCACGTGGTACTCCCA 787  
 Tslk\_6 AATCAACAGATTTCTGAACGTATTAGACACACCACC-TCTT-----GTGGTACTCCCA 1769  
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 TbMi\_15 AATCAACAGATTTCTGAACGTATTAGACACACCACC-TCTGCTTGCACGTGGTACTCCCA 787  
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 Tan5\_8 AATCAACAGATTTCTGAACGTATTAGACACACCAAC-TCTGCTTGCATGTGGTACTCCCA 652  
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 TcerW2\_9 AATCAACAGACCTCTGAACGTATTAGACACACCGCC-TCTGCTTGCACGCGGTACTCCCA 661  
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 Tcer183\_5 AATCAACAGACCTCTGAACGTATTAGACACACCGCC-TCTGCTTGCACGCGGTACTCCCA 661  
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 ThDG\_13 AATCAACAGATCTCTGAACGTATTAGACACACCACC-TCTGCTTGCACGTGGTACTCCCA 451  
 ThDG\_12 AATCAACAGATTTCTGAACGTATTAGACACACCACC-TCTGCTTGCACGTGGTACTCCCA 452  
 ThDG\_14 AATCAACAGATTTCTGAACGTATTAGACACACCACC-TCTGCTTGCACGTGGTACTCCCA 456  
 ThDG\_11 AATCAACAGATTTCTGAACGTATTAGACACACCACC-TCTGCTTGCACGTGGTACTCCCA 451  
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 To9\_13 AATCAACAGACTTCTGAACGTATAAGACACACCACC-TCTCCTTGGAAAGTGGTTCTCCCA 897  
 To9\_10 AATCAACAGACTTCTGAACGTATAAGACACACCACC-TCTCCTTGGAAAGTGGTTCTCCCA 897  
 To11\_5 AATCAACAGACTTCTGAACGTATAAGACACACCACC-TCTCCTTGGAAAGTGGTCTCCCA 910  
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 Cfelis\_Tx AATCAACAGATTTCTGAACGTATTAGACACACCACC-TCTGCTTGCATGTGGTACTCCCA 603  
 Olonga ACTCACCGGGCGGTGGCGAGAAGTGACCTCGAACGGTCCGCCAAAGAGGGTGACAGCC 707

Tslk\_1 TTTCAGTGAACCTCAACTTC-TAAC--GCACA---ACCACTTT---GCAACAGAGGTTGC 1821  
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 TsCh\_1 TTTCAGTGAACCTCATCTTC-TAAC--AAACA---ACCGCTTC---GCGACTT--GTTGC 827  
 TbAr\_20 TTTCAGTGAACCTCATCTTC-TAAC--AAACA---ACCGCTTC---GCGACTT--GTTGC 836  
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 TbAr\_25 TTTCAGTGAACCTCATCTTC-TAAC--AAACA---ACCGCTTC---GCGACT--TGTTGC 835  
 TsCh\_5 TTTCAGTGAACCTCATCTTC-TAAC--AAACA---ACCGCTTC---GCGACTT--TGTTGC 824  
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 TbMi\_5 TTTCAGTGAACCTCATCTTC-TAAC--AAACA---ACCGCTTC---GCGACTT--GTTGC 837  
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 Tan7\_18 TTTCAGTGAACCTTTAATTC-TATCCAAAACA---ACCTAATG---GTGATCCCTAACGG 703  
 Tan1\_2 TTTCAGTGAACCTTTAATTC-TATCCAAAACA---ACCTAATG---GTGATCC----- 685  
 Tan5\_13 TTTCAGTGAACCTTTAATTC-TATCCAAAACA---ACCTAATG---GTGATCCCAACGG 705  
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 TmIn\_13 TTTCAGTGAACCTCAAATTCCTATCCCAACCT---AACTAATGGATGTGACTGATAACTT 801  
 TmIn\_3 TTTCAGTGAACCTCAAATTCCTATCCCAACCT---AACTAATGGATGTGACTGATAACTT 801

Tan1\_14 TTTCAGTGAACCTTCAATTC-TATCCAAAACA---ACCTAATG---GTGATCCCTAACGG 711  
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 Tan2\_5 TTTCAGTGAACCTTAAATTC-TATCCAAAACA---ACCTAATG---GTGATCCC-AACGG 703  
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 Tan2\_7 TTTCAGTGAACCTTAAATTC-TATCCAAAACA---ACCTAATG---GTGATCCC-AACGG 703  
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 TeerW2\_9 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTC-----TTTGAAAGT 705  
 TeerCanE\_10 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTC-----TTTGAAAGG 703  
 TeerCanE\_7 TTTCAGTGAGCCATAAACTT---CCTAAAATCGC-TTTCATTGAAAGTTTCTTTGAAAGG 718  
 TeerW1\_17 TTTCAGTGAGCCTCATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 704  
 TeerOkE\_13 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 705  
 TeerCanE\_1 TTTCAGTGAGCCATAAACTT---CCTAAAATCGC-TTTCATTGAAAGTTTCTTTGAAAGG 718  
 TeerCanE\_8 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTC-----TTTGAAAGG 703  
 TeerWisE TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTC-----TTTGAAAGG 703  
 Teer183\_8 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTC-----TTTGAAAGT 703  
 TeerOkE\_11 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTC-----TTTGAAAGT 701  
 TeerInE\_2 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTC-----TTTGAAAGT 705  
 Teer181\_1 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 704  
 TeerOkE\_10 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 701  
 TeerW2\_10 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 703  
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 TeerW1\_24 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 704  
 Teer183\_7 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 704  
 TeerW2\_3 TTTCAGTGAGCCTTATAAATT---CCTAAGATCAC-TTTCATTGAAAGT----- 705  
 Teer181\_10 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 704  
 TeerW1\_16 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 704  
 TeerW3\_8 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 704  
 TeerInE\_1 TTTCAGTGAGCCTCATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 705  
 TeerW3\_7 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 704  
 TeerInE\_3 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 705  
 TeerCanE\_11 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTCATTGAAAGG----- 702  
 Teer183\_5 TTTCAGTGAGCCTTATAAATT---CCTAAAATCAC-TTTCATTGAAAGT----- 705  
 ThDG\_10 TTTCAGTGAACCTCATCAT---CCTAAACCAGC-TCGCCTTGG----- 491  
 ThDG\_13 TTTCAGTGAACCTCATCAT---CCTAAACCAGC-TCGCCTTGG----- 490  
 ThDG\_12 TTTCAGTGAACCTCATCAT---CCTAAACCAGC-TCGCCTTGG----- 491  
 ThDG\_14 TTTCAGTGAACCTCATCAT---CCTAAACCAGC-TCGCCTTGG----- 495  
 ThDG\_11 TTTCAGTGAACCTCATCAT---CCTAAACCAGC-TCGCCTTGG----- 490  
 To8\_8 ATTTCAGTGAACCTCAATATT---TCTAA-CCCAT-TCGCTTGATGACCA--AGTTAGGGA 963  
 To9\_13 ATTTCAGTGAACCTCAAGATT---TCTAA-CCCAT-TCGCTTGATGACCA--AGTTAGGGA 950  
 To9\_10 ATTTCAGTGAACCTCAAGATT---TCTAA-CCCAT-TCGCTTGATGACCA--AGTTAGGGA 950  
 To11\_5 ATTTCAGTGAACCTCAAGATT---TCTAA-CCCAT-TCGCTTGATGACCA--AGTTAGGGA 963  
 To9\_11 ATTTCAGTGAACCTCAAGATT---TCTAA-CCCAT-TCGCTTGATGACCA--AGTTAGGGA 950  
 To9\_12 ATTTCAGTGAACCTCAAGATT---TCTAA-CCCAT-TCGCTTGATGACCA--AGTTAGGGA 959  
 To11\_1 ATTTCAGTGAACCTCAAGATT---TCTAACCATTTCGCTTGATGACCAAGTTAGGGATTGA 967  
 To8\_4 ATTTCAGTGAACCTCAAGATT---TCTAACCATTTCGCTTGATGACCAAGTTAGGGATTGA 967  
 To8\_9 ATTTCAGTGAACCTCAAGATT---TCTAACCATTTCGCTTGATGACCAAGTTAGGGATTGA 966  
 To9\_14 ATTTCAGTGAACCTCAAGATT---TCTAACCATTTCGCTTGATGACCAAGTTAGGGATTGA 967  
 To11\_2 ATTTCAGTGAACCTCAAGATT---TCTAACCATTTCGCTTGATGACCAAGTTAGGGATTGA 967  
 Cfelis\_Tx TTTCAGTGAAGTATAAAAATC---CTAAAAGTACAACCTTTTGTGTTCTTTGTGAGTAGA 660  
 Olonga CGTATGTGGTGCCGCTGCCTAACGAGTGGGTTGTGCAAGAGTCGGGTTGTTTTGTATTGC 767

TsIk\_1 GTAGTCCGGTGGCTG----- 1836  
 TbMi\_14 GT-----GCGGCTG----- 845  
 TsCh\_1 GT-----GCGACTG----- 836  
 TbAr\_20 GT-----GCGGCTG----- 845  
 TsIk\_2 GTAGTCCGGTGGCTG----- 1840  
 TbMi\_3 GT-----GCGGCTG----- 845  
 TsCh\_4 GT-----GCGGCTG----- 836  
 TsIk\_7 GTAGTCCGGTGGCTG----- 1838  
 TbTx\_6 GT-----GCGGCTG----- 846  
 TbAr\_15 GT-----GCGGCTG----- 845  
 TsIk\_6 GTAGTCCGGTGGCTG----- 1835  
 TbTx\_11 GT-----GCGGCTG----- 846  
 TbAr\_25 GT-----GCGGCTG----- 844  
 TsCh\_5 GT-----GCGACTG----- 833  
 TsCh\_2 GT-----GCGACTG----- 833

TbMi_5	GT----GCGGCTG----- 846
TbOk_10	GT----GCGGCTG----- 846
TbTx_5	GT----GCGGCTG----- 846
TsCh_3	GT----GCGACTG----- 833
TbOk_9	GT----GCGGCTG----- 846
TbMi_15	GT----GCGGCTG----- 845
TbOk_8	GT----GCGGCTG----- 846
Tan5_8	GATACCCTA---AGCCGTTGGAT-GTGAGTACTGCCTAATAACTCCG----- 750
Tan7_7	GTTAGCCTAGTGAACCCACCCGGGTAGCTGGTATCCCCAAAGGACCCTAGGTCTAGGA 749
Tan1_3	---ACCCTA---GCCGTTGGAT-GTGAGTACTACCG-----T----- 736
Tan2_12	GTTAGCCTAGTGAACCCATCTGGGTAGCTGGTATCCCCAAAGGACCCTAGGTACCTGGG 764
Tan3_9	GTTAGCCTA----- 713
Tan3_3	GTTAGCCTAGTGAACCCATCTGGGTAGCTGGTATCCCCAAAGGACCCTAGGTACCTGGG 770
Tan5_7	GTTACCCTA---AGCC----- 701
Tan3_8	GTTAGCCTAGTGAACCCATCTGGGTAGCTGGTATCCCCAAAGGACCCTAGGTACCTGGG 770
Tan6_11	GATAACC----- 701
Tan7_18	GTTAGCCTAGTGAACCCATCTGGGTAGCTGGTATCCCCAAAGGACCCTAGGTACCTGGG 763
Tan1_2	-----TAAAGGACACTAGGTCCTAGGA 707
Tan5_13	GTTAGCCTAATGAACCCACCCGGGTAGCTGGTATCCCTAAAGGACCCTAGGTACCTGGG 765
Tan2_3	GTTAGCC----- 688
Tan2_11	GTTAGCCTAGTGAACCCATCTGGGTAGCTGGTATCCCCAAAGGACCCTAGGTACCTGGG 764
Tan6_18	GTTACCC----- 692
Tan6_24	GTTACCC----- 704
Tan1_13	GGTTA--GCCAAAGCCGTTT----- 722
Tan7_13	GGTTA--GCCAAAGCCCTTT----- 713
Tpar_U	AGTTACCGTTAACTTTGTTATT----- 769
TmIn_10	AGTTACCGTTACCACTGTTA----- 822
Tpar_AF	AGTTACCAGTTAACACTGTTAGCAC----- 847
TmIn_13	AGTTACCGTTACCACTGTTA----- 822
TmIn_3	AGTTACCGTTACCACTGTTA----- 822
Tan1_14	GTTACCCAA----- 720
Tan5_12	GTTACCCTA----- 696
Tan2_5	GTTACCCAAAGCCC----- 716
Tan2_13	GTTAGCCAAAGTGCCATTG----- 726
Tan3_6	GTTACCCTAAGCC----- 705
Tan2_7	GTTACCCAAAGCCC----- 716
TcerOkE_12	GGGATTTTGTGAGTGTCTGCCCG----- 743
TcerW2_9	AGGATTTTGTGAGTGGCTGTCC----- 727
TcerCanE_10	AGGATTTTGTGAGTGGCTGTCC----- 725
TcerCanE_7	GGGATTTTGTGAGTGTCTGCCCG----- 741
TcerW1_17	AGGATTTTGTGAGTGGCTGTCC----- 726
TcerOkE_13	AGGATTTTGTGAGTGGCTGTCC----- 727
TcerCanE_1	GGGATTTTGTGAGTGTCTGCCCG----- 741
TcerCanE_8	AGGATTTTGTGAGTGGCTGTCC----- 725
TcerWisE	AGGATTTTGTGAGTGGCTGTCC----- 725
Tcer183_8	AGGATTTTGTGAGTGGCTGTCC----- 725
TcerOkE_11	AGGATTTTGTGAGTGGCTGTCC----- 723
TcerInE_2	AGGATTTTGTGAGTGGCTGTCC----- 727
Tcer181_1	AGGATTTTGTGAGTGGCTGTCC----- 726
TcerOkE_10	AGGATTTTGTGAGTGGCTGTCC----- 723
TcerW2_10	AGGATTTTGTGAGTGGCTGTCC----- 725
TcerCanE_6	GGGATTTTGTGAGTGTCTGCCCG----- 741
TcerW3_2	AGGATTTTGTGAGTGGCTGTCC----- 727
Tcer181_2	AGGATTTTGTGAGTGGCTGTCC----- 726
TcerW1_24	AGGATTTTGTGAGTGGCTGTCC----- 726
Tcer183_7	AGGATTTTGTGAGTGGCTGTCC----- 726
TcerW2-3	AGGATTTTGTGAGTGGCTGTCC----- 727
Tcer181_10	AGGATTTTGTGAGTGGCTGTCC----- 726
TcerW1_16	AGGATTTTGTGAGTGGCTGTCC----- 726
TcerW3_8	AGGATTTTGTGAGTGGCTGTCC----- 726
TcerInE_1	AGGATTTTGTGAGTGGCTGTCC----- 727
TcerW3_7	AGGATTTTGTGAGTGGCTGTCC----- 726
TcerInE_3	AGGATTTTGTGAGTGGCTGTCC----- 727
TcerCanE_11	AGGATTTTGTGAGTGGCTGTCC----- 724
Tcer183_5	AGGATTTTGTGAGTGGCTGTCC----- 727
ThDG_10	----TTTGTGAGTGGACGCC----- 508
ThDG_13	----TTTGTGAGTGGACGCC----- 507
ThDG_12	----TTTGTGAGTGGACGCC----- 508
ThDG_14	----TTTGTGAGTGGACGCC----- 512
ThDG_11	----TTTGTGAGTGGACACCC----- 507

To8\_8 TTGATTGTATTCGTTATAGTCT----- 985  
 To9\_13 TTGATTGTATTCGTTATAGTCT----- 972  
 To9\_10 TTGATTGTATTCGTTATAGTCT----- 972  
 To11\_5 TTGATTGTATTCGTTATAGTCT----- 985  
 To9\_11 TTGATTGTATTCGTTATAGTCT----- 972  
 To9\_12 TTGATTGTATTCGTTATAGTCT----- 981  
 To11\_1 TTGTATTCGTTATAGTC----- 984  
 To8\_4 TTGTATTCGTTATAGTC----- 984  
 To8\_9 TTGTATTCGTTATAGTC----- 983  
 To9\_14 TTGTATTCGTTATAGTC----- 984  
 To11\_2 TTGTATTCGTTATAGTC----- 984  
 Cfelis\_Tx GGTGATTACAATCCCTCTATA----- 682  
 Olonga AGCCCTAAGTGGGAG----- 782

TsIk\_1 -----T-GGTTGCGAGTAGTGGCCC-CTGAGGTCATTATTTTATAG-TTA 1877  
 TbMi\_14 -----TTAGTTGCGAGCAATGGCCCTCTGAGGCCGTTGTTTTATAG-TTA 888  
 TsCh\_1 -----TTGGTTGCGAGCAATGGCCCTTCGAGGCCGTTGGTTTTAT-TTA 879  
 TbAr\_20 -----TTAGTTGCGAGCAATGGCCCTCTGAGGCCGTTGTTTTATAG-TTA 888  
 TsIk\_2 -----T-GGTTGCGAGTAGTGGCCC-CTGAGGTCATTATTTTATAG-TTA 1881  
 TbMi\_3 -----TTAGTTGCGAGCAATGGCCCTCTGAGGCCGTTGTTTTATAG-TTA 888  
 TsCh\_4 -----TTAGTTGCGAGCAATGGCCCTTCGAGGCCGTTGGTTTTATAG-TTA 879  
 TsIk\_7 -----T-GGTTGCGAGTAGTGGCCC-CTGAGGTCATTATTTTATAG-TTA 1879  
 TbTx\_6 -----TTAGTTGCGAGCAATGGCCCTCTGAGGCCGTTGTTTTATAG-TTA 889  
 TbAr\_15 -----TTAGTTGCGAGCAATGGCCCTCTGAGGCCGTTGTTTTATAG-TTA 888  
 TsIk\_6 -----T-GGTTGCGAGTAGTGGCCC-CTGAGGTCATTATTTTATAG-TTA 1876  
 TbTx\_11 -----TTAGTTGCGAGCAATGGCCCTCTGAGGCCGTTGTTTTATAG-TTA 889  
 TbAr\_25 -----TTAGTTGCGAGCAATGGCCCTCTGAGGCCGTTGTTTTATAG-TTA 887  
 TsCh\_5 -----TTGGTTGCGAGCAATGGCCCTTCGAGGCCGTTGGTTTTATAG-TTA 876  
 TsCh\_2 -----TTGGTTGCGAGCAATGGCCCTTCGAGGCCGTTGGTTTTATAG-TTA 876  
 TbMi\_5 -----TTAGTTGCGAGCAATGGCCCTCTGAGGCCGTTGTTTTATAG-TTA 889  
 TbOk\_10 -----TTAGTTGCGAGCAATGGCCCTCTGAGGCCGTTGTTTTATAG-TTA 889  
 TbTx\_5 -----TTAGTTGCGAGCAATGGCCCTCTGAGGCCGTTGTTTTATAG-TTA 889  
 TsCh\_3 -----TTGGTTGCGAGCAATGGCCCTTCGAGGCCGTTGGTTTTATAG-TTA 876  
 TbOk\_9 -----TTAGTTGCGAGCAATGGCCCTCTGAGGCCGTTGTTTTATAG-TTA 889  
 TbMi\_15 -----TTAGTTGCGAGCAATGGCCCTCTGAGGCCGTTGTTTCTAG-TTA 888  
 TbOk\_8 -----TCAGTTGCGAGCAATGGCCCTCTGAGGCCGTTGTTTTATAG-TTA 889  
 Tan5\_8 -----TTTGGAGGTG----- 760  
 Tan7\_7 CCTTAAGGCCCTAGATTTGGATGTGAGTGACTGCCCC-----TAT-TTG 792  
 Tan1\_3 -----TTGG----- 740  
 Tan2\_12 ACTTAAAGCCCT-AGTTTGGATGTGAGTGACTACCAAATAACTCCGTTTGGGA-TGT-TTG 821  
 Tan3\_9 -----AGCC-----GTTTGGATGTGAGTGACTACC-----GT-TTG 743  
 Tan3\_3 GCCTAAGGCC--ATTTTGGATGTGAGTGACTGCC-----TGT-TTG 811  
 Tan5\_7 -----TTTGGATGTGAGTGACTGCC-----T-CTA 725  
 Tan3\_8 GCCTAAGGCC--ATTTTGGATGTGAGTGACTGCC-----TGT-TTG 811  
 Tan6\_11 -----AAGCC-----GTTTGGATGTGAGTGACTGCC-----GT-TTG 732  
 Tan7\_18 ACCTAAGGCCCTAGATTTGGATGTGAGTGACTACCATATAACTCCGTTTGGAGCGT-TTG 822  
 Tan1\_2 CCTTAAGGCCCT---TTGGATGTGAGTGACTGCC-----GTTG---- 743  
 Tan5\_13 ACTTAAAGCCCT-AGTTTGGATGTGAGTGACTGCC-----CCTGTTG---- 807  
 Tan2\_3 -----AAAGCC-----GTTTGGATGTGAGTGACTGCC-----TCTAGGTG---- 723  
 Tan2\_11 ACTTAAAGCCCT-AGTTTGGATGTGAGTGACTACCAAATAACTCCG-TTTGGATGT-TTG 821  
 Tan6\_18 ---AAGCA-----TTGGATGTGAGTGACTGCC-----CCTAGGTG---- 725  
 Tan6\_24 ---TAAGCC-----GTTTGGATGTGAGTGACTGCC-----CCTAGGTG---- 739  
 Tan1\_13 -----GGATGTGAGTGACTGCCCT--T-----G 744  
 Tan7\_13 -----GGATGTGAGTGACTGCCCTAGGT-----G 738  
 Tpar\_U -----AGGTTGGGAT-TGAGTGAAAACCTGTGTGT-----GTG-TAG 804  
 TmIn\_10 -----GAGTTGGGATGTGAGTGAAAACCCATGTTG-----G----G 854  
 Tpar\_AF ----TATGTTAGAGTTGGGATGTGAGTGAAAACCCATATTT-----ATATT-GTG 893  
 TmIn\_13 -----GAGTTGGGATGTGAGTGAAAACCCATGTTG-----GG 854  
 TmIn\_3 -----GAGTTGGGATGTGAGTGAAAACCCATGTTG-----GG 854  
 Tan1\_14 -----GGCC---TTTGGATGTGAGTGACTGCC-----T-TTG 750  
 Tan5\_12 -----AGCC---TTTGGATGTGAGTGACTGCC-----T-CTA 725  
 Tan2\_5 -----TTGGATGTGAGTGACTACCAT-----TTG 741  
 Tan2\_13 -----ATTTGGATGTGAGTGACTGCCATATAACTCCG-TTTGGATGT-TTG 770  
 Tan3\_6 -----GTTTGGATGTGAGTGACTGCC-----TAG-GTG 734  
 Tan2\_7 -----TTTGGATGTGAGTGACTACCAT-----TTG 741  
 TcerOkE\_12 -----ATTCTGGGTG-GGCGATTTAAGT-TGGTA--GTGGACTAGA--ATC 784  
 TcerW2\_9 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 766  
 TcerCanE\_10 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCTAGTGAGA--GTT 764  
 TcerCanE\_7 -----ATTCTGGGTG-GGCGATTTAAGT-TGGTA--GTGGACTAGA--ATC 782

TcerW1\_17 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 765  
 TcerOkE\_13 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCTAGTGAGA--GTT 766  
 TcerCanE\_1 -----ATTCTGGGTG-GGCGATTTAAGT-TGGTA--GTGGACTAGA--ATC 782  
 TcerCanE\_8 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCTAGTGAGA--GTT 764  
 TcerWisE -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCTAGTGAGA--GTT 764  
 Tcer183\_8 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 764  
 TcerOkE\_11 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 762  
 TcerInE\_2 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCTAGTGAGA--GTT 766  
 Tcer181\_1 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 765  
 TcerOkE\_10 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 762  
 TcerW2\_10 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 764  
 TcerCanE\_6 -----ATTCTGGGTG-GGCGATTTAAGT-TGGTA--GTGGACTAGA--ATC 782  
 TcerW3\_2 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 766  
 Tcer181\_2 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 765  
 TcerW1\_24 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 765  
 Tcer183\_7 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 765  
 TcerW2-3 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 766  
 Tcer181\_10 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 765  
 TcerW1\_16 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 765  
 TcerW3\_8 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 765  
 TcerInE\_1 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCTAGTGAGA--GTT 766  
 TcerW3\_7 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCGAGTGAGA--GTT 765  
 TcerInE\_3 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCTAGTGAGA--GTT 766  
 TcerCanE\_11 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCTAGTGAGA--GTT 763  
 Tcer183\_5 -----CTCCGGGCG-GCTTAATTTAGT-TGG-A--GCTAGTGAGA--GTT 766  
 ThDG\_10 -----GGTTGGGTG-TTTGAATTCTATCATTGCG--TTGTGCGATTTTGAT 551  
 ThDG\_13 -----GGTTGGGTG-TTCAATTCTATCATTGCA--TTGTGCGATTTTGAT 550  
 ThDG\_12 -----GGTTGGGTG-TTTCAATTCTATCATTGCA--TTGTGCGATTTCCGT 551  
 ThDG\_14 -----GGTTGGGTG-TTCAATTCTATCATTGCA--TTGTGCGATTT-GAT 554  
 ThDG\_11 -----GGTTGGGTG-TTTCAATTCTATCATTGCA--TTGTGCGATTTCCGT 550  
 To8\_8 -----CCCCTTG-GACTACTGTAGGTTTGGGATTGTGAGTGACGATTCT 1029  
 To9\_13 -----CCCCTTG-GACTACTGTAGGTTTGGGATTGTGAGTGACGATTCT 1016  
 To9\_10 -----CCCCTTG-GACTACTGTAGGTTTGGGATTGTGAGTGACGATTCT 1016  
 To11\_5 -----CCCCTTG-GACTACTGTAGGTTTGGGATTGTGAGTGACGATTCT 1029  
 To9\_11 -----CCCCTTG-GACTACTGTAGGTTTGGGATTGTGAGTGACGATTCT 1016  
 To9\_12 -----CCCCTTG-GACTACTGTAGGTTTGGGATTGTGAGTGACGATTCT 1025  
 To11\_1 -----TCCCGCTTGGACTACTGTAGGTTTGGGATTGTGAGTGACGATTCT 1029  
 To8\_4 -----TCCCGCTTGGACTACTGTAGGTTTGGGATTGTGAGTGACGATTCT 1029  
 To8\_9 -----TCCCGCTTGGACTACTGTAGGTTTGGGATTGTGAGTGACGATTCT 1028  
 To9\_14 -----TCCCGCTTGGACTACTGTAGGTTTGGGATTGTGAGTGACGATTCT 1029  
 To11\_2 -----TCCCGCTTGGACTACTGTAGGTTTGGGATTGTGAGTGACGATTCT 1029  
 Cfelis\_Tx -----TCTACATTCTAGAGATTAC-----TACCTCGCATCTC 715  
 Olonga -----

TsIk\_1 AACTTGTGTCTGTGTGCG-GGCCACTTT----TTA--GTGG-TGTGGAAC-TTAGAT 1927  
 TbMi\_14 AACTCGTGTCCGTGTGCAC-GGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 940  
 TsCh\_1 AACTCGTGTCTGTGTGCAC-AGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 931  
 TbAr\_20 AACTCGTGTCTGTGTGCAC-GGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 940  
 TsIk\_2 AACTTGTGTCTGTGTGCG-GGCCACTTT----TTA--GTGG-TGTGGAAC-TTAGAT 1931  
 TbMi\_3 AACTCGTGTCTGTGTGCAC-GGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 940  
 TsCh\_4 AACTCGTGTCTGTGTGCAC-GGCCACTGT----TTACAGTGG-TGTGGAAC-TTTGAT 931  
 TsIk\_7 AACCTGTGTCTGTGTGCG-GGCCACTTT----TTA--GTGG-TGTGGAAC-TTAGAT 1929  
 TbTx\_6 AACTCGTGTCTGTGTGCAC-GGCCGCTGT----TTACAGCGG-TGTGGAAC-TTTGAT 941  
 TbAr\_15 AACTCGTGTCTGTGTGCAC-GGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 940  
 TsIk\_6 AACTTGTGTCTGTGTGCG-GGCCACTTT----TTA--GTGG-TGTGGAAC-TTAGAT 1926  
 TbTx\_11 AACTCGTGTCTGTGTACAC-GGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 941  
 TbAr\_25 AACTCGTGTCTGTGTGCAC-GGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 939  
 TsCh\_5 AACTCGTGTCTGTGTGCAC-GGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 928  
 TsCh\_2 AACTCGTGTCTGTGTGCAC-AGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 928  
 TbMi\_5 AACTCGTGTCTGTGTGCAC-GGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 941  
 TbOk\_10 AACTCGTGTCTGTGTGCAC-GGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 941  
 TbTx\_5 AACTCGTGTCTGTGTGCAT-GGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 941  
 TsCh\_3 AACTCGTGTCTGTGTGCAC-GGCCACTGT----TTACAGTGG-TGTGGAAC-TTTGAT 928  
 TbOk\_9 AACTCGTGTCTGTGTGCAC-GGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 941  
 TbMi\_15 AACTCGTGTCTGTGTGCAC-GGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 940  
 TbOk\_8 AACTCGTGTCTGTGTGCAC-GGCCGCTGT----TTACAGTGG-TGTGGAAC-TTTGAT 941  
 Tan5\_8 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 817  
 Tan7\_7 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 849  
 Tan1\_3 -GTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 796

Tan2\_12 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 778  
 Tan3\_9 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 800  
 Tan3\_3 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 868  
 Tan5\_7 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 782  
 Tan3\_8 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 868  
 Tan6\_11 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 789  
 Tan7\_18 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 879  
 Tan1\_2 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 800  
 Tan5\_13 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 864  
 Tan2\_3 GGTAGTTGATTTTAGGCTCTGGTCACTAA-GTCATTGCTATGG-TATGAAACT-AT-GCT 779  
 Tan2\_11 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 878  
 Tan6\_18 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 782  
 Tan6\_24 GGTGGTTGATTTTAGGCTCTGGTCACTAA-GTCGTTGCTATGG-TATGAAACT-AT-GCT 795  
 Tan1\_13 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 801  
 Tan7\_13 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 795  
 Tpar\_U GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 856  
 TmIn\_10 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 906  
 Tpar\_AF GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 945  
 TmIn\_13 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 906  
 TmIn\_3 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 906  
 Tan1\_14 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 807  
 Tan5\_12 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 782  
 Tan2\_5 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 798  
 Tan2\_13 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 827  
 Tan3\_6 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 791  
 Tan2\_7 GGTGGTTGATTTTAGGCTCTGGTCACTAATGTCGTTGCTATGG-TATGAAACT-AT-GCT 798  
 TeerOkE\_12 GACTCGCAA-----CCTTCAACTCTTCGG---AGATGGAG-TTTGGAAC-TTTGCT 832  
 TeerW2\_9 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 808  
 TeerCanE\_10 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 806  
 TeerCanE\_7 GACTCGCAA-----CCTTCAGCTTTTCGG---AGATGGAG-TTTGGAAC-TTTGCT 829  
 TeerW1\_17 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 807  
 TeerOkE\_13 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 808  
 TeerCanE\_1 GACTCGCAA-----CCTTCAGCTTTTCGG---AGATGGAG-TTTGGAAC-TTTGCT 829  
 TeerCanE\_8 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 806  
 TeerWisE GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 806  
 Teer183\_8 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 806  
 TeerOkE\_11 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 804  
 TeerInE\_2 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCA 808  
 Teer181\_1 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 807  
 TeerOkE\_10 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 804  
 TeerW2\_10 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 806  
 TeerCanE\_6 GACTCGCAA-----CCTTCAGCTTTTCGG---AGATGGAG-TTTGGAAC-TTTGCT 829  
 TeerW3\_2 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 808  
 Teer181\_2 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 807  
 TeerW1\_24 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 807  
 Teer183\_7 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 807  
 TeerW2-3 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 808  
 Teer181\_10 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 807  
 TeerW1\_16 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 807  
 TeerW3\_8 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 807  
 TeerInE\_1 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 808  
 TeerW3\_7 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 807  
 TeerInE\_3 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 808  
 TeerCanE\_11 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 805  
 Teer183\_5 GACTCACGC-----CCTCCGCCTCGGCCG---AGTTA-----TGGAAC-TTTGCT 808  
 ThDG\_10 GATTGACGAA-----ACTGTGGATGTAAGC---AATTACT--CTCGTTTCT-GGTGTC 598  
 ThDG\_13 GATTGATGAA-----ACTGTGGATGTAANC---AATTACT--CTCGTTTCT-GGTGTC 597  
 ThDG\_12 GATTGATGAA-----ACTGTGGATGTAAGC---AATTGCT--CTCGTTTCT-GGTGTC 598  
 ThDG\_14 GATTGATGAA-----ACTGTGGATGTAAGC---AATTACT--CTCGTTTCT-GGTGTC 601  
 ThDG\_11 GATTGATGAA-----ACTGTGGATGTAAGC---AATTGCT--CTCGTTTCT-GGTGTC 597  
 To8\_8 ATTTAGCAGGTTGTACCCACTCTTTGATGACC-AAGTTAGGG-ATTGATTGTATTCGTT 1087  
 To9\_13 ATTTAGCAGGTTGTACCCACTCTTTGATGACC-AAGTTAGGG-ATTGATTGTATTCGTT 1074  
 To9\_10 ATTTAGCAGGTTGTACCCACTCTTTGATGACC-AAGTTAGGG-ATTGATTGTATTCGTT 1074  
 To11\_5 ATTTAGCAGGTTGTACCCACTCTTTGATGACC-AAGTTAGGG-ATTGATTGTATTCGTT 1087  
 To9\_11 ATTTAGCAGGTTGTACCCACTCTTTGATGACC-AAGTTAGGG-ATTGATTGTATTCGTT 1074  
 To9\_12 ATTTAGCAGGTTGTACCCACTCTTTGATGACC-AAGTTAGGG-ATTGATTGTATTCGTT 1083  
 To11\_1 ATTTAGCAGGTTGTACCCACTCTTTGATGACC-AAGTTAGGG-ATTGATTGTATTCGTT 1087  
 To8\_4 ATTTAGCAGGTTGTACCCACTCTTTGATGACC-AAGTTAGGG-ATTGATTGTATTCGTT 1087  
 To8\_9 ATTTAGCAGGTTGTACCCACTCTTTGATGACC-AAGTTAGGG-ATTGATTGTATTCGTT 1086  
 To9\_14 ATTTAGCAGGTTGTACCCACTCTTTGATGACC-AAGTTAGGG-ATTGATTGTATTCGTT 1087

To11\_2  
Cfelis\_Tx  
Olonga

ATTTAGCAGGTTGTACCCACTCTTTGATGACC-AAGTTAGGG-ATTGATTGTATTCGTT 1087  
GAAACTCTATTGATTTTATATACTCTACGTTTTGAGTGAGGGACATGAATTCATTATT 775  
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TsIk\_1 GTAAC---TCGTT---ACT-C-GCGTTCT---GCTT----TGC---GAGCACATTCACGT 1969  
TbMi\_14 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTAGGCTTTCACAT 982  
TsCh\_1 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTACGCCTTCACAT 973  
TbAr\_20 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTAGGCTGTCACGT 982  
TsIk\_2 GTAAC---TCGTT---ACT-C-GCGTTCT---GCTT----TGC---GAGCACATTCACGT 1973  
TbMi\_3 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTAGGCTTTCACAT 982  
TsCh\_4 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTACGCCTTCACAT 973  
TsIk\_7 GTAAC---TCGTT---ACT-C-GCGTTCT---GCTT----TGC---GAGCACATTCACGT 1971  
TbTx\_6 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTAGGCTTTCACAT 983  
TbAr\_15 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTAGGCTTTCACAT 982  
TsIk\_6 GTAAC---TCGTT---ACT-C-GCGTTCT---GCTT----TGC---GAGCACATTCACGT 1968  
TbTx\_11 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTAGGCTTTCACAT 983  
TbAr\_25 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTAGGCTTTCACGT 981  
TsCh\_5 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTACGCCTTCACAT 970  
TsCh\_2 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTACGCCTTCACAT 970  
TbMi\_5 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTAGGCTTTCACAT 983  
TbOk\_10 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTAGGCTTTCACAT 983  
TbTx\_5 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTAGGCTTTCACAT 983  
TsCh\_3 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTACGCCTTCACAT 970  
TbOk\_9 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTAGGCTTTCACAT 983  
TbMi\_15 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTAGGCTTTCACAT 982  
TbOk\_8 GTAAC---TCGTT---ACT-C-GTGTCT---GCTT----TGT---GTAGGCTTTCACAT 983  
Tan5\_8 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTTA-GAGT 866  
Tan7\_7 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTAA-GAGT 898  
Tan1\_3 GTATC---TAA-T---ACT-CTGTGTTTTTATACTTCA-ATGTCCAGTAGACTCA-GAGT 846  
Tan2\_12 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTCA-GAGT 927  
Tan3\_9 GTATC---AAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTTA-GAGT 849  
Tan3\_3 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTTA-GAGT 917  
Tan5\_7 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTCA-GAGT 831  
Tan3\_8 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTTA-GAGT 917  
Tan6\_11 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTCAAGATT 839  
Tan7\_18 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTCA-GAGT 928  
Tan1\_2 GTATC---AAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTTA-GAGT 849  
Tan5\_13 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTCAAGAGT 914  
Tan2\_3 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTCA-GAGT 828  
Tan2\_11 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTCA-GAGT 927  
Tan6\_18 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTCA-GAGT 831  
Tan6\_24 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTCA-GAGT 844  
Tan1\_13 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACT-CAGAGT 850  
Tan7\_13 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACT-CAAGAG 844  
Tpar\_U GTATG---CAAGT---ACT-CTATGTTTT-ACAATGCA-GTGGCTAGTGGACTATAGAGT 907  
TmIn\_10 GTATG---CAAGT---ACT-CTGTGTTTT-ACAATGCA-GTGGCTAGTGGACTATAGAGT 957  
Tpar\_AF GTATG---CAAGT---ACT-CTATGTTTT-ACAATGCA-GTGGCTAGTGGACTATAGAGT 996  
TmIn\_13 GTATG---CAAGT---ACT-CTGTGTTTT-ACAATGCA-GTGGCTAGTGGACTATAGAGT 957  
TmIn\_3 GTATG---CAAGT---ACT-CTGTGTTTT-ACAATGCA-GTGGTGAAGTGGACTATAGAGT 957  
Tan1\_14 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGACCAGTAGACTCA-AAGT 856  
Tan5\_12 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTCA-GAGT 831  
Tan2\_5 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTTA-GAGT 847  
Tan2\_13 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTCA-GAGT 876  
Tan3\_6 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTCA-GAGT 840  
Tan2\_7 GTATC---TAA-T---ACT-CTATGTTTT-ATACTTCA-ATGTCCAGTAGACTTA-GAGT 847  
TcerOkE\_12 GTAATGACTGATTT--GCT-CTACGTTCTTAGGAA-----ACGCGT---ATTGGTTCC 879  
TcerW2\_9 GTAAT--CTAATT---ACT-CGATGTTCTTAGAAA-----AAGTGT---TTTGGTTCT 852  
TcerCanE\_10 GTAAT--CTAATT---ACT-CGATGTTCTTAGAAA-----AAGTGT---TTCGGTTCT 850  
TcerCanE\_7 GTAATGACTGATTT--GCT-CTACGTTCTTAGGAA-----ACGCGT---ATTGGTTCC 876  
TcerW1\_17 GTAAT--TTAATT--ACT-CGATGTTCTTAGAAA-----AAGTGT---TTCGGTTCT 851  
TcerOkE\_13 GTAAT--CTAATT---ACT-CGATGTTCTTAGAAA-----AAGTGT---TTCGGTTCT 852  
TcerCanE\_1 GTAATGACTGATTT--GCT-CTACGTTCTTAGGAA-----ACGCGT---ATTGGTTCC 876  
TcerCanE\_8 GTAAT--CTAATT---ACT-CGATGTTCTTAGAAA-----AAGTGT---TTCGGTTCT 850  
TcerWisE GTAAT--CTAATT---ACT-CGATGTTCTTAGAAA-----AAGTGT---TTCGGTTCT 850  
Tcer183\_8 GTAAT--CTAATT---ACT-CGATGTTCTTAGAAA-----AAGTGT---TTCGGTTCT 850  
TcerOkE\_11 GTAAT--CTAATT---ACT-CGATGTTCTTAGAAA-----AAGTGT---TTCGGTTCT 848  
TcerInE\_2 GTAAT--CTAATT---ACT-CGATGTTCTTAGAAA-----AAGTGT---TTCGGTTCT 852  
Tcer181\_1 GTAAT--TTAATT--ACT-CGATGTTCTTAGAAA-----AAGTGT---TTCGGTTCT 851  
TcerOkE\_10 GTAAT--CTAATT---ACT-CGATGTTCTTAGAAA-----AAGTGT---TTCGGTTCT 848



TcerW2\_10 GTAAT--TCAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTCGGTTCT 850  
 TcerCanE\_6 GTAATGACTGATTT--GCT-CTACGTTCTTAGGAA-----ACGCGT--ATTGGTTCC 876  
 TcerW3\_2 GTAAT--CTAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTFGTTCT 852  
 Tcer181\_2 GTAAT--CTAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTCGGTTCT 851  
 TcerW1\_24 GTAAT--TCAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTCGGTTCT 851  
 Tcer183\_7 GTAAT--TCAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTCGGTTCT 851  
 TcerW2-3 GTAAT--CTAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTCGGTTCT 852  
 Tcer181\_10 GTAAT--TCAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTCGGTTCT 851  
 TcerW1\_16 GTAAT--TCAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTCGGTTCT 851  
 TcerW3\_8 GTAAT--CTAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTCGGTTCT 851  
 TcerInE\_1 GTAAT--CTAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTCGGTTCT 852  
 TcerW3\_7 GTAAT--CTAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTCGGTTCT 851  
 TcerInE\_3 GTAAT--CTAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTCGGTTCT 852  
 TcerCanE\_11 GTAAT--CTAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTCGGTTCT 849  
 Tcer183\_5 GTAAT--TCAATT--ACT-CGATGTTCTAGAAA-----AAGTGT--TTCGGTTCT 852  
 ThDG\_10 GTCGTGTCGTACAA--GTG-CG-TGAGTCTCTAG-----GAGTTGGTACCCGTGCC 647  
 ThDG\_13 GTCGTGTCGTACGG--GTG-CGGTGTAGCTCCTAG-----GAGTTT-----CGTACC 641  
 ThDG\_12 GTCGTGTCGTACAG--GTG-CGGTGTAGCTCCTAG-----GAGTTT-----TGTACC 642  
 ThDG\_14 GTCGTGTCGTGACAG--GTG-CGGTGTAGCTCCTAG-----GAGTTT-----CGTACC 645  
 ThDG\_11 GTCGTGTCGTACAG--GTG-CGGTGTAGCTCCTAG-----GAGTTT-----TGTACC 641  
 To8\_8 ATAGTCTCCCCTGGACTACTGTAGGTTTGGGAGTACTACGACCTGTTAAGCCGATCGA 1147  
 To9\_13 ATAGTCTCCCCTGGACTACTGTAGGTTTGGGAGTACTACGACCTGTTAAGCCGATCGA 1134  
 To9\_10 ATAGTCTCCCCTGGACTACTGTAGGTTTGGGAGTACTACGACCTGTTAAGCCGATCGA 1134  
 To11\_5 ATAGTCTCCCCTGGACTACTGTAGGTTTGGGAGTACTACGACCTGTTAAGCCGATCGA 1147  
 To9\_11 ATAGTCTCCCCTGGACTACTGTAGGTTTGGGAGTACTACGACCTGTTAAGCCGATCGA 1134  
 To9\_12 ATAGTCTCCCCTGGACTACTGTAGGTTTGGGAGTACTACGACCTGTTAAGCCGATCGA 1143  
 To11\_1 ATAGTCTCCCCTGGACTACTGTAGGTTTGGGAGTACTACGACCTGTTAAGCCGATCGA 1147  
 To8\_4 ATAGTCTCCCCTGGACTACTGTAGGTTTGGGAGTACTACGACCTGTTAAGCCGATCGA 1147  
 To8\_9 ATAGTCTCCCCTGGACTACTGTAGGTTTGGGAGTACTACGACCTGTTAAGCCGATCGA 1146  
 To9\_14 ATAGTCTCCCCTGGACTACTGTAGGTTTGGGAGTACTACGACCTGTTAAGCCGATCGA 1147  
 To11\_2 ATAGTCTCCCCTGGACTACTGTAGGTTTGGGAGTACTACGACCTGTTAAGCCGATCGA 1147  
 Cfelis\_Tx GAATGACGTGAGGAAGATCCGAACGGAGTGAGGAAG----TGTGGGATGTACCGACGTGT 831  
 Olonga -----

TsIk\_1 CGTTTAAACATCCCAT-TTTATTATATA-TTTTGGTAGC--ATCCAGAGCTTAAATAGGTT 2025  
 TbMi\_14 AGTTTAAACAACCTAT-TCTGTTACGT--TCTGGT----ATCTAGTGCTT-AATAGGTT 1032  
 TsCh\_1 AGTTTAAACAACCTAT-TCTGTTATGT--TCTGGTG----CTCCAGTGCTT-AATAGGTT 1024  
 TbAr\_20 AGTTTAAACAACCTAT-TCTGTTACGT--TCTGGT----ATCCAGTGCTT-AATAGGTT 1032  
 TsIk\_2 CGTTTAAACATCCCAT-TTTATTATATA-TTTTGGTAGC--ATCCAGAGCTTAAATAGGTT 2029  
 TbMi\_3 AGTTTAAACAACCTAT-TCTGTTACG--TTCTGGTA-----TCCAGTGCTT-AATAGGTT 1032  
 TsCh\_4 AGTTTAAACAACCTAT-TCTGTTATG--TTCTGGTG----CTCCAGTGCTT-AATAGGTT 1024  
 TsIk\_7 CGTTTAAACATCCCAT-TTTATTATATA-TTTTGGTAGC--ATCCAGAGCTTAAATAGGTT 2027  
 TbTx\_6 AGTTTAAACAACCTAT-TCTGTTACG--TTCTGGTA-----TCCAGTGCTT-AATAGGTT 1033  
 TbAr\_15 AGTTTAAACAACCTAT-TCTGTTACG--TTCTGGTA-----TCCAGTGCTT-AATAGGTT 1032  
 TsIk\_6 CGTTTAAACATCCCAT-TTTATTATATA-TTTTGGTAGC--ATCCAGTGCTTAAATAGGTT 2024  
 TbTx\_11 AGTTTAAACAACCTAT-TCTGTTACG--TTCTGGTA-----TCCAGTGCTT-AATAGGTT 1033  
 TbAr\_25 AGTTTAAACAACCTAT-TCTGTTACG--TTCTGGTA-----TCCAGTGCTT-AATAGGTT 1031  
 TsCh\_5 AGTTTAAACAACCTAT-TCTGTTATG--TTCTGGTG----CTCCAGTGCTT-AATAGGTT 1021  
 TsCh\_2 AGTTTAAACAACCTAT-TCTGTTATG--TTCTGGTG----CTCCAGTGCTT-AATAGGTT 1021  
 TbMi\_5 AGTTTAAACAACCTAT-TCTGTTACG--TTCTGGTA-----TCCAGTGCTT-AATAGGTT 1033  
 TbOk\_10 AGTTTAAACAACCTAT-TCTGTTACG--TTCTGGTA-----TCCAGTGCTT-AATAGGTT 1033  
 TbTx\_5 AGTTTAAACAACCTAT-TCTGTTACG--TTCTGGTA-----TCCAGTGCTT-AATAGGTT 1033  
 TsCh\_3 AGTTTAAACAACCTAT-TCTGTTATG--TTCTGGTG----TCCAGTGCTT-AATAGGTT 1021  
 TbOk\_9 AGTTTAAACAACCTAT-TCTGTTACG--TTCTGGTA-----TCCAGTGCTT-AATAGGTT 1033  
 TbMi\_15 AGTTTAAACAACCTAT-TCTGTTACG--TTCTGGTA-----TCCAGTGCTT-AATAGGTT 1032  
 TbOk\_8 AGTTTAAACAACCTAT-TCTGTTACG--TTCTGGTA-----TCCAGTGCTT-AATAGGTT 1033  
 Tan5\_8 CCCGG--GACTTCC--ATTCCCACAT-CACCTA-----TACTAGTCCATCTAGTATTC 915  
 Tan7\_7 CCGTT--AGCTTA--CCTCCCACAT-CACCTA-----TACTAGTCCATCTAGTATTC 947  
 Tan1\_3 CCGGT--TAGCTCAGACCTCCCACCCT-CACCTA-----TACTAGTCCATCTAGTATTC 897  
 Tan2\_12 CCCGG--GGACTTCC--ATTCCCACAT-CACCTA-----TACTAGTCCATCTAGTATTC 977  
 Tan3\_9 CCCGG--G-ACTTCC--ATTCCCACCTC-CATC-----ACT--CCCACGTGGAGT-- 891  
 Tan3\_3 CCCGG--G-ACTTCC--ATTCCCAC--T-CCTCT-----TACTCCCACGTGGAGTATC- 962  
 Tan5\_7 CCCGGG--G-ACTACC--ACTCCCACAT-CACCTA-----TACTAGTCCATCTAGTATTC 880  
 Tan3\_8 CCCGG--G-ACTTCC--ATTCCCAC--T-CCTCT-----TACTCCCACGTGGAGTATC- 962  
 Tan6\_11 CCGGG--GGACTTCC--ACTCCCACAT-CACCTA-----TACTAGTCCATCTAGTATTC 889  
 Tan7\_18 CCCTG--GGACTTCC--ATTCCCACCTC-CATC-----ACTCCCACGTGGAGTAT-- 973  
 Tan1\_2 C-----CTGGG-ACTTCCATTC-CACTCC-----TCTCACTCCCACGTGGA--- 889  
 Tan5\_13 CCGTT--AGCTCAA--CCTCCCACAT-CACCTA-----TACTAGTCCATCTAGTATTC 964  
 Tan2\_3 CC-GG--GGACTTCC--AGTCCCACAT-CACCTA-----TACTAGTCCATCTAGTATTC 877

Tan2\_11 CCCGG--GGACTTCC-ATTCCCACCAT-CACCTA-----TACTAGTCCATCTAGTATTC 977  
 Tan6\_18 C-----CCGGG-ACTTCCATTCC-CACCTA-----TACTAGACCATCTAGTATTC 874  
 Tan6\_24 CCGT--AGCTCAA-CCTCCCACAA-CACCTA-----TACTAGTCCATCTAGTATTC 894  
 Tan1\_13 CCGG--GGACTTC-CACTCCCAAC-----ACTCCCACGTGGAGTATC- 889  
 Tan7\_13 TCGG--TTAGTTC-TACCTCCCACCA-TCACCTA-----TACTAGTCCATCTAGTATTC 894  
 Tpar\_U CCCAAATGGATTTGGCAGTGTCAACAG-CAACGGATAGATTACCAGGTTGTGTAATAACT 966  
 TmIn\_10 CCCAAATGGATTTGGCAGTGTCAACAG-CAATGGATAAAATTACTAGGTTGTGTAATAACT 1016  
 Tpar\_AF TCCAAATGGATTTGGCAGTGTCAACAG-CAATAGATAGATTACCAGGTTGTGTAATAACT 1055  
 TmIn\_13 CCCAAATGGATTTGGCAGTGTCAACAG-CAATGGATAAAATTACTAGGTTGTGTAATAACT 1016  
 TmIn\_3 CCCAAATGGATTTGGCAGTGTCAACAG-CAATGGATAAAATTACTAGGTTGTGTAATAACT 1016  
 Tan1\_14 CCGT--AGCTTCA-CCTCCCACCAT-CACCTA-----TACTAGTCCATCTAGTATTC 905  
 Tan5\_12 CCGG--GACTTCC-ACTCCCACCAT-CACCTA-----TACTAGTCCATCTAGTATTC 880  
 Tan2\_5 TCTGG--GACTTCCAC-TCCCACCTT-CACCTA-----TACTAGTCCATCTAGTATTC 896  
 Tan2\_13 CCGT--AGCTCAAACCTCCCACCAT-CACCTA-----TACTAGATGGACTAGTATTC 926  
 Tan3\_6 CCGT--AGCTCT-ACCTCCCACCAT-CACCTA-----TACTAGTCCATCTAGTATTC 889  
 Tan2\_7 TCTGG--GACTTCCAC-TCCCACCTT-CACCTA-----TACTAGTCCATCTAGTATTC 896  
 TeerOkE\_12 CCACTATTGAACGCCCTCGGCTTCTA--AATTTAAATTTAGATTAAAAAG-----TTTTT 931  
 TeerW2\_9 CG----CGAACGACAACACCTCTC-----TGAGGACTTTTTTAACTC-----TGTTTC 895  
 TeerCanE\_10 CG----CGAACGACAACCCCTCTC-----TGAGGACTTTCCTAACTC-----TGTTTC 893  
 TeerCanE\_7 CC----ACTATTAACGCCCCTCGG-----CTTCTAAATTTAAATTTA-----GATTA 919  
 TeerW1\_17 CG----CGAACGACAACCTCTT-----TGAGGACTTTCCTAACTC-----TGTTTC 894  
 TeerOkE\_13 CG----CGAACGACAACCCCTCTC-----TGAGGACTTTCCTAACTC-----TGTTTC 895  
 TeerCanE\_1 CC----ACTATTAACGCCCCTCGG-----CTTCTAAATTTAAATTTA-----GATTA 919  
 TeerCanE\_8 CG----CGAACGACAACCCCTCTC-----TGAGGACTTTCCTAACTC-----TGTTTC 893  
 TeerWisE CG----CGAACGACAACCCCTCTC-----TGAGGACTTTCCTAACTC-----TGTTTC 893  
 Teer183\_8 CG----CGAACGACAACCCCTCTC-----TGAGGACTTTCCTAACTC-----TGTTTC 893  
 TeerOkE\_11 CG----CGAACGACAACCTCTT-----TGAGGACTTTCCTAACTC-----TGTTTC 891  
 TeerInE\_2 CG----CGAACGACAACACCTCTC-----TGAGGACTTTTTTAACTC-----TGTTTC 895  
 Teer181\_1 CG----CGAACGACAACCTCTC-----TTTGAGGACTTTCCTAACTC-----TGTTTC 894  
 TeerOkE\_10 CG----CGAACGACAACCTCTC-----TTTGAGGACTTTCCTAACTC-----TGTTTC 891  
 TeerW2\_10 CG----CGAACGACAACCTCTC-----TTTGAGGACTTTCCTAACTC-----TGTTTC 893  
 TeerCanE\_6 CC----ACTATTAACGCCCCTCGG--TTCTAAATTTAAATTTAGATTA---AAAGTTT 926  
 TeerW3\_2 CG----CGAACGACAACACCTC-----TCTGAGGACTTTTTTAACTC-----TGTTTC 895  
 Teer181\_2 CG----CGAACGACAACCTCTC-----TTTGAGGACTTTCCTAACTC-----TGTTTC 894  
 TeerW1\_24 CG----CGAACGACAACCTCTC-----TTTGAGGACTTTCCTAACTC-----TGTTTC 894  
 Teer183\_7 CG----CGAACGACAACCTCTC-----TTTGAGGACTTTCCTAACTC-----TGTTTC 894  
 TeerW2-3 CG----CGAACGACAACCCCTC-----TCTGAGGACTTTCCTAACTC-----TGATC 895  
 Teer181\_10 CG----CGAACGACAACCTCTC-----TTTGAGGACTTTCCTAACTC-----TGTTTC 894  
 TeerW1\_16 CG----CGAACGACAACCTCTC-----TTTGAGGACTTTCCTAACTC-----TGTTTC 894  
 TeerW3\_8 CG----CGAACGACAACCTCTT-----TGAGGACTTTCCTAACTC-----TGTTTC 894  
 TeerInE\_1 CG----CGAACGACAACACCTCTC-----TGAGGACTTTTTTAACTC-----TGTTTC 895  
 TeerW3\_7 CG----CGAACGACAACCTCTT-----TGAGGACTTTCCTAACTC-----TGTTTC 894  
 TeerInE\_3 CG----CGAACGACAACACCTCTC-----TGAGGACTTTTTTAACTC-----TGTTTC 895  
 TeerCanE\_11 CG----CGAACGACAACCCCTCTC-----TGAGGACTTTCCTAACTC-----TGTTTC 892  
 Teer183\_5 CG----CGAACGACAACCTCTT-----TGAGGACTTTCCTAACTC-----TGTTTC 895  
 ThDG\_10 AG-----GTACACCGGTACTTGGG--TACTGGGTACCTTTCTGTTCC----- 687  
 ThDG\_13 TG-----GTAC-----TGTG--TACTGGGTACCTTTCTGTTCC----- 672  
 ThDG\_12 TG-----GTAC-----TGTG--TGCTGGGTACCTTTCTGTTCC----- 673  
 ThDG\_14 TG-----GTAC-----TG-----GGTGCCTTTCTGTTCC----- 669  
 ThDG\_11 TG-----GTAC-----TGTG--TGCTGGGTACCATCTGTTCC----- 672  
 To8\_8 CTTGTTTTAGTCAACATCTTGTAGCAATGTCTACGTGCCCTTTGGAAACATTGGGTGATG 1207  
 To9\_13 CTTGTTTTAGTCAACATCTTGTAGCAATGTCTACGTGCCCTTTGGAAACATTGGGTGATG 1194  
 To9\_10 CTTGTTTTAGTCAACATCTTGTAGCAATGTCTACGTGCCCTTTGGAAACATTGGGTGATG 1194  
 To11\_5 CTTGTTTTAGTCAACATCTTGTAGCAATGTCTACGTGCCCTTTGGAAACATTGGGTGATG 1207  
 To9\_11 CTTGTTTTAGTCAACATCTTGTAGCAATGTCTACGTGCCCTTTGGAAACATTGGGTGATG 1194  
 To9\_12 CTTGTTTTAGTCAACATCTTGTAGCAATGTCTACGTGCCCTTTGGAAACATTGGGTGATG 1203  
 To11\_1 CTTGTTTTAGTCAACATCTTGTAGCAATGTCTACGTGCCCTTTGGAAACATTGGGTGATG 1207  
 To8\_4 CTTGTTTTAGTCAACATCTTGTAGCAATGTCTACGTGCCCTTTGGAAACATTGGGTGATG 1207  
 To8\_9 CTTGTTTTAGTCAACATCTTGTAGCAATGTCTACGTGCCCTTTGGAAACATTGGGTGATG 1206  
 To9\_14 CTTGTTTTAGTCAACATCTTGTAGCAATGTCTACGTGCCCTTTGGAAACATTGGGTGATG 1207  
 To11\_2 CTTGTTTTAGTCAACATCTTGTAGCAATGTCTACGTGCCCTTTGGAAACATTGGGTGATG 1207  
 Cfelis\_Tx GAGGATTATCACAGTATTCCTCAATACATCGATGTATCGATCTTCCTTC----- 880  
 Olonga -----

TsIk\_1 TGGGGA-ACC-----TTCCAGTTTA----- 2044  
 TbMi\_14 AGGGTTTATC-----ATTTAGTTCC----- 1052  
 TsCh\_1 AGGGTTTATA-----ATTTAGTTCC----- 1044  
 TbAr\_20 AGGGTTTATC-----ATTTAGTTCC----- 1052  
 TsIk\_2 TGGGGA-ACC-----TTCCAGTTTA----- 2048

TbMi_3	AGGGTTTATC-----ATTTAGTTCC-----	1052
TsCh_4	AGGGTTCATA-----ATTTAGTTCC-----	1044
TsIk_7	TGGGGA-ACC-----TTCCAGTTA-----	2046
TbTx_6	AGGGTTTATC-----ATTTAGTTCC-----	1053
TbAr_15	AGGGTTTATC-----ATTTAGTTCC-----	1052
TsIk_6	TGGGGA-ACC-----TTCCAGTATA-----	2043
TbTx_11	AGGG-----TTTA-----	1041
TbAr_25	AGGG-----TTTA-----	1039
TsCh_5	AGGGTTTATA-----ATTTAGTTCC-----	1041
TsCh_2	AGGGTTTATA-----ATTTAGTTCC-----	1041
TbMi_5	AGGGTTTATC-----ATTTAGTTCC-----	1053
TbOk_10	AGGGTTTATC-----ATTTAGTTCC-----	1053
TbTx_5	AGGATTTATC-----ATTTAGTTCC-----	1053
TsCh_3	AGGGTTTATA-----ATTTAGTTCC-----	1041
TbOk_9	AGGGTTTATC-----ATTTAGTTCC-----	1053
TbMi_15	AGGGTTTATC-----ATTTAGTTCC-----	1052
TbOk_8	AGGGTTTATC-----ATTTAGTTCC-----	1053
Tan5_8	GTGTTACA-----ATTTGTTCC-----	933
Tan7_7	GTGTTACA-----ATTTGTTCC-----	965
Tan1_3	GTGCTACA-----ATTTGTTCC-----	915
Tan2_12	GTGTTACA-----ATTTGTTCC-----	995
Tan3_9	----GAA-----ATTTGTTCC-----	904
Tan3_3	----A-----ATTTGTTCC-----	973
Tan5_7	GTGTTGAA-----ATTTGTTCC-----	898
Tan3_8	----A-----ATTTGTTCC-----	973
Tan6_11	GTGCTACA-----ATTTAGTTCC-----	907
Tan7_18	----CA-----ATTTGTTCC-----	985
Tan1_2	--GTGA-A-----ATTTGTTCC-----	904
Tan5_13	GTGTTA-C-----AATTTGTTCC-----	981
Tan2_3	GTGTTACA-----ATTTGTTCC-----	895
Tan2_11	GTGTTACA-----ATTTGTTCC-----	995
Tan6_18	GTGTTGAA-----ATTTGTTCC-----	892
Tan6_24	GTGTTATA-----AATTTGTTCC-----	912
Tan1_13	----A-----ATTTGTTCC-----	900
Tan7_13	GGGTTATA-----ATTTGTTCC-----	912
Tpar_U	AACTCAGTCAGTTGATATTACATACTATGGTTATTTGTTGCCGTGGACGATGTGCCGTAA	1026
TmIn_10	AACTCAGTAA---ATATTACATACTATGGTTATCAATTGCCGTGGACGATGCGCCGTAA	1072
Tpar_AF	AACTCAGT---TACTACATACT---GTTATCAGTTGCCGTGGACGATGTGCCGTAA	1105
TmIn_13	AACTCAGTAA---ATATTACATACTATGGTTATCAATTGCCGTGGACGATGCGCCGTAA	1072
TmIn_3	AACTCAGTAA---ATATTACATACTATGGTTATCAATTGCCGTGGACGATGCGCCGTAA	1072
Tan1_14	GTGTTACA-----ATTTGTTCC-----	923
Tan5_12	GTGTTGAA-----ATTTGTTCC-----	898
Tan2_5	GTGTTGAA-----ATTTGTTCC-----	914
Tan2_13	GTGTTGAA-----ATTTGTTCC-----	944
Tan3_6	GTGTTATA-----ATTTGTTCC-----	907
Tan2_7	GTGTTGAA-----ATTTGTTCC-----	914
TcerOkE_12	CGGGGA-----TACTTATT--CAGTCAACTAGGCTTACTTGGGGAGCTTCGACTC	979
TcerW2_9	TGAGTT-----GAGTTCC-----	908
TcerCanE_10	TGAGTT-----GAGTTCC-----	906
TcerCanE_7	AAAGTTTCCG---GGGATTCCTATTTCAGTCAACTAGGCTTACTTGGGGAGCTTCGACTC	976
TcerW1_17	TGAGTT-----GAGTTCC-----	907
TcerOkE_13	TGAGTT-----GAGTTCC-----	908
TcerCanE_1	AAAGTTTCCG---GGGATTCCTATTTCAGTCAACTAGGCTTACTTGGGGAGCTTCGACTC	976
TcerCanE_8	TGAGTT-----GAGTTCC-----	906
TcerWisE	TGAGTT-----GAGTTCC-----	906
Tcer183_8	TGAGTT-----GAGTTCC-----	906
TcerOkE_11	TGAGTT-----GAGTTCC-----	904
TcerInE_2	TGAGTT-----GAGTTCCTGAAATTGGGTGTGATGATCCAC-----	931
Tcer181_1	TGAGTT-----GAGTTCC-----	907
TcerOkE_10	TGAGTT-----GAGTTCC-----	904
TcerW2_10	TGAGTT-----GAGTTCC-----	906
TcerCanE_6	TCCGGG-----GATTCCTATTTCAGTCAACTAGGCTTACTTGGGGAGCTTCGACTCA	977
TcerW3_2	TGAGTT-----GAGTTCC-----	908
Tcer181_2	TGAGTT-----GAGTTCC-----	907
TcerW1_24	TGAGTT-----GAGTTCC-----	907
Tcer183_7	TGAGTT-----GAGTTCC-----	907
TcerW2-3	TGAGTT-----GAGTTCC-----	908
Tcer181_10	TGAGTT-----GAGTTCC-----	907
TcerW1_16	TGAGTT-----GAGTTCC-----	907
TcerW3_8	TGAGTT-----GAGTTCC-----	907

TcerInE\_1 TGAGTT-----GAGTTCCTGAAATTGGGTGTGATGATACCAC-932  
 TcerW3\_7 TGAGTT-----GAGTTC-----907  
 TcerInE\_3 TGAGTT-----GAGTTCCTGAAATTGGGTGTGATGATGCAC---931  
 TcerCanE\_11 TGAGTT-----GAGTTC-----905  
 Tcer183\_5 TGAGTT-----GAGTTC-----908  
 ThDG\_10 -----  
 ThDG\_13 -----  
 ThDG\_12 -----  
 ThDG\_14 -----  
 ThDG\_11 -----  
 To8\_8 GAACTTTGGAT--GTAATTTATTACTCTGTGTTCTTAAATAGTAGAGTGTGTTACAATGCA 1264  
 To9\_13 GAACTTTGGAT--GTAATTTATTACTCTGTGTTCTGAAATAGTAGAGTGTGTTACAATGCA 1251  
 To9\_10 GAACTTTGGAT--GTAATTTATTACTCTGTGTTCTGAAATAGTAGAGTGTGTTACAATGCA 1251  
 To11\_5 GAACTTTGGAT--GTAATTTATTACTCTGTGTTCTTAAATAGTAGAGTGTGTTACAATGCA 1264  
 To9\_11 GAACTTTGGAT--GTAATTTATTACTCTGTGTTCTTAAATAGTAGAGTGTGTTACAATGCA 1251  
 To9\_12 GAACTTTGGAT--GTAATTTATTACTCTGTGTTCTTAAATAGTAGAGTGTGTTACAATGCA 1260  
 To11\_1 GAACTTTGGAT--GTAATTTATTACTCTGTGTTCTTAAATAGTAGAGTGTGTTACAATGCA 1264  
 To8\_4 GAACTTTGGAT--GTAATTTATTACTCTGTGTTCTTAAATAGTAGAGTGTGTTACAATGCA 1264  
 To8\_9 GAACTTTGGAT--GTAATTTATTACTCTGTGTTCTGAAATAGTAGAGTGTGTTACAATGCA 1263  
 To9\_14 GAACTTTGGAT--GTAATTTATTACTCTGTGTTCTTAAATAGTAGAGTGTGTTACAATGCA 1264  
 To11\_2 GAACTTTGGAT--GTAATTTATTACTCTGTGTTCTTAAATAGTAGAGTGTGTTACAATGCA 1264  
 Cfelis\_Tx -----  
 Olonga -----  
  
 Tslk\_1 -----TGATTGGTTTTTTTTCAGTCT-AAATGATTGATAACCAGTTTATATTATTGA 2094  
 TbMi\_14 -----TGA--GATTGGGTGAGACT-ATCCAC-----1075  
 TsCh\_1 -----TGA--GATTGGGTGAGACT-ATCCAC-----1067  
 TbAr\_20 -----TGA--GATTGGGTGAGACT-ATCCAC-----1075  
 Tslk\_2 -----TGATTGGTTTTTTTTCAGTCT-AAATGATTGATAACCAGTTTATATGATTGA 2098  
 TbMi\_3 -----TGA--GATTGGGTGAGACT-ATCCAC-----1075  
 TsCh\_4 -----TGA--GATTGGGTGAGACT-ATCCAC-----1067  
 Tslk\_7 -----TGATTGGTTTTTTTTCAGTCT-AAATGATTGATAACCAGTTTATATGATTGA 2096  
 TbTx\_6 -----TGA--GATTGGGTGAGACT-ATCCAC-----1076  
 TbAr\_15 -----TGA--GATTGGGTGAGACT-ATCCAC-----1075  
 Tslk\_6 -----TGATT-GGTTTTTTTTCAGTCT-AAATGATTGATGACCAGTTTATATGATTGA 2092  
 TbTx\_11 -----TCATT-TAGTTCCTGAGATT-GGGTGA--GACTATCCAC-----1076  
 TbAr\_25 -----TCACT-TAGTTCCTGAGATT-GGGTGA--GACTATCCAC-----1074  
 TsCh\_5 -----TGA--GATTGGGTGAGACT-ATCCAC-----1064  
 TsCh\_2 -----TGA--GATTGGGTGAGACT-ATCCAC-----1064  
 TbMi\_5 -----TGA--GATTGGGTGAGACT-ATCCAC-----1076  
 TbOk\_10 -----TGA--GATTGGGTGAGACT-ATCCAC-----1076  
 TbTx\_5 -----TGA--GATTGGGTGAGACT-ATCCAC-----1076  
 TsCh\_3 -----TGA--GATTGGGTGAGACT-ATCCAC-----1064  
 TbOk\_9 -----TGA--GATTGGGTGAGACT-ATCCAC-----1076  
 TbMi\_15 -----TGA--GATTGGGTGAGACT-ATCCAC-----1075  
 TbOk\_8 -----TGA--GATTGGGTGAGACT-ATCCAC-----1076  
 Tan5\_8 -----TGA--GATTGGGTGAGATG-ATCCAC-----956  
 Tan7\_7 -----TGA--GATTGGGTGAGATG-ATCCAC-----988  
 Tan1\_3 -----TGA--GATTGGGTGAGATT-ATCCAC-----938  
 Tan2\_12 -----TGA--GATTGGGTGAGATG-ATCCAC-----1018  
 Tan3\_9 -----TGA--GATTGGGTGAGATGCATCCAC-----928  
 Tan3\_3 -----TGA--GATTGGGTGAGATG-ATCCAC-----996  
 Tan5\_7 -----TGA--GATTGGGTGAGATG-ATCCAC-----921  
 Tan3\_8 -----TGA--GATTGGGTGAGATG-ATCCAC-----996  
 Tan6\_11 -----TGA--GATTGGGTGAGATG-ATCCAC-----930  
 Tan7\_18 -----TGA--GATTGGGTGAGATG-AAACAC-----1008  
 Tan1\_2 -----TGA--TATTGGGTGAGATG-ATCCAC-----927  
 Tan5\_13 -----TGA--GATTGGGTGAGATG-ATCCAC-----1004  
 Tan2\_3 -----TGA--GATTGGGTGAGATG-ATCCAC-----918  
 Tan2\_11 -----TGA--GATTGGGTGAGATG-ATCCAC-----1018  
 Tan6\_18 -----TGA--GATTGGGTGAGATG-ATCCAC-----915  
 Tan6\_24 -----TGA--GATTGGGTGAGATG-ATCCAC-----935  
 Tan1\_13 -----TGA--GATTGGGTGAGATG-ATCCAC-----923  
 Tan7\_13 -----TGA--GATTGGGTGAGATG-ATCCAC-----935  
 Tpar\_U CGGAGTTCCTGA--GATTGGGTGAGGCT-ATCCA-----1057  
 TmIn\_10 CGGAGTTCCTGA--GATTGGGTGAGGCT-ATCCAC-----1104  
 Tpar\_AF CGGATTCCTGA--GATTGGGTGAGGCT-ATCCACTGAATTT-----1144  
 TmIn\_13 CGGAGTTCCTGA--GATTGGGTGAGGCT-ATCCAC-----1104  
 TmIn\_3 CGGAGTTCCTGA--GATTGGGTGAGGCT-ATCCAC-----1104

Tan1\_14 -----TGA--GATTGGGTGAGATG-ATCCAC-----946  
 Tan5\_12 -----TGA--GATTGGGTGAGATG-ATCCAC-----921  
 Tan2\_5 -----TGA--GATTGGGTGAGATG-ATCCAC-----937  
 Tan2\_13 -----TGA--GATTGGGTGAGATG-ATCCAC-----967  
 Tan3\_6 -----TGA--GATTGGGTGAGATGCATCCAC-----931  
 Tan2\_7 -----TGA--GATTGGGTGAGATG-ATCCAC-----937  
 TcerOkE\_12 ACTGAGATCCGAAGTTCC-----997  
 TcerW2\_9 -----  
 TcerCanE\_10 -----  
 TcerCanE\_7 ACTGAGATCCGAAGTTCTGAAGTTGGGTGCGATTATCCAC-----1017  
 TcerW1\_17 -----  
 TcerOkE\_13 -----  
 TcerCanE\_1 ACTGAGATCCGAAGTTCTGAAGTTGGGTGCGATTATCCAC-----1017  
 TcerCanE\_8 -----  
 TcerWisE -----  
 Tcer183\_8 -----  
 TcerOkE\_11 -----  
 TcerInE\_2 -----  
 Tcer181\_1 -----  
 TcerOkE\_10 -----  
 TcerW2\_10 -----  
 TcerCanE\_6 CTGAGATCCGAAGTTCTGAAGTTGGGTGCGATTATCCAC-----1017  
 TcerW3\_2 -----  
 Tcer181\_2 -----  
 TcerW1\_24 -----  
 Tcer183\_7 -----  
 TcerW2-3 -----  
 Tcer181\_10 -----  
 TcerW1\_16 -----  
 TcerW3\_8 -----  
 TcerInE\_1 -----  
 TcerW3\_7 -----  
 TcerInE\_3 -----  
 TcerCanE\_11 -----  
 Tcer183\_5 -----  
 ThDG\_10 -----  
 ThDG\_13 -----  
 ThDG\_12 -----  
 ThDG\_14 -----  
 ThDG\_11 -----  
 To8\_8 TGATTGACGCTTTATCTCGTGATAAGGTGTGTTTAGTTCCGTTTTTGTGGAACGTGTTAAA 1324  
 To9\_13 TGATTGACGCTTTATCTCGTGATAAGGTGTGTTTAGTTCCGTTTTTGTGGAACGTGTTAAA 1311  
 To9\_10 TGATTGACGCTTTATCTCGTGATAAGGTGTGTTTAGTTCCGTTTTTGTGGAACGTGTTAAA 1311  
 To11\_5 TGATTGACGCTTTATCTCTTGATAAGGTGTGTTTAGTTCCGTTTTTGTGGAACGTGTTAAA 1324  
 To9\_11 TGATTGACGCTTTATCTCGTGATAAGGTGTGTTTAGTTCCGTTTTTGTGGAACGTGTTAAA 1311  
 To9\_12 TGATTGACGCTTTATCTCGTGATAAGGTGTGTTTAGTTCCGTTTTTGTGGAACGTGTTAAA 1320  
 To11\_1 TGATTGACGCTTTATCTCTTGATAAGGTGTGTTTAGTTCCGTTTTTGTGGAACGTGTTAAA 1324  
 To8\_4 TGATTGACGCTTTATCTCTTGATAAGGTGTGTTTAGTTCCGTTTTTGTGGAACGTGTTAAA 1324  
 To8\_9 TGATTGACGCTTTATCTCGTGATAAGGTGTGTTTAGTTCCGTTTTTGTGGAACGTGTTAAA 1323  
 To9\_14 TGATTGACGCTTTATCTCGTGATAAGGTGTGTTTAGTTCCGTTTTTGTGGAACGTGTTAAA 1324  
 To11\_2 TGATTGACGCTTTATCTCTTGATAAGGTGTGTTTAGTTCCGTTTTTGTGGAACGTGTTAAA 1324  
 Cfelis\_Tx -----  
 Olonga -----  
  
 TsIk\_1 GAAGCATCCCATTCTATTGATAACAGCGATGGGTCTTGCTCACA CTGTTTGTA AAAAAAG 2154  
 TbMi\_14 -----  
 TsCh\_1 -----  
 TbAr\_20 -----  
 TsIk\_2 GAAGCATCCCATTCTATTGATAACAGCGATGGGTCTTGCTCACA CTGTTTGTA AAAAAAG 2158  
 TbMi\_3 -----  
 TsCh\_4 -----  
 TsIk\_7 GAAGCATCCCATTCTATTGATAACAGCGATGGGTCTTGCTCACA CTGTTTGTA AAAAAAG 2156  
 TbTx\_6 -----  
 TbAr\_15 -----  
 TsIk\_6 GAAGCATCCCATTCTATTGATAACAGCGATGGGTCTTGCTCACA CTGTTTGTA AAAAAAG 2152  
 TbTx\_11 -----  
 TbAr\_25 -----  
 TsCh\_5 -----  
 TsCh\_2 -----

TbMi_5	-----
TbOk_10	-----
TbTx_5	-----
TsCh_3	-----
TbOk_9	-----
TbMi_15	-----
TbOk_8	-----
Tan5_8	-----
Tan7_7	-----
Tan1_3	-----
Tan2_12	-----
Tan3_9	-----
Tan3_3	-----
Tan5_7	-----
Tan3_8	-----
Tan6_11	-----
Tan7_18	-----
Tan1_2	-----
Tan5_13	-----
Tan2_3	-----
Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
TmIn_3	-----
Tan1_14	-----
Tan5_12	-----
Tan2_5	-----
Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
TcerOkE_12	-----
TcerW2_9	-----
TcerCanE_10	-----
TcerCanE_7	-----
TcerW1_17	-----
TcerOkE_13	-----
TcerCanE_1	-----
TcerCanE_8	-----
TcerWisE	-----
Tcer183_8	-----
TcerOkE_11	-----
TcerInE_2	-----
Tcer181_1	-----
TcerOkE_10	-----
TcerW2_10	-----
TcerCanE_6	-----
TcerW3_2	-----
Tcer181_2	-----
TcerW1_24	-----
Tcer183_7	-----
TcerW2-3	-----
Tcer181_10	-----
TcerW1_16	-----
TcerW3_8	-----
TcerInE_1	-----
TcerW3_7	-----
TcerInE_3	-----
TcerCanE_11	-----
Tcer183_5	-----
ThDG_10	-----
ThDG_13	-----
ThDG_12	-----
ThDG_14	-----
ThDG_11	-----

To8_8	TTTATGTTCCCTGAAGTTGGGTGTGACTATCCAC-----	1357
To9_13	TTTATGTTCCCTGAAGTTGGGTGTGACTATCCAC-----	1344
To9_10	TTTATGTTCCCTGAAGTTGGGTGTGACTATCCAC-----	1344
To11_5	TTTATGTTCCCTGAAGTTGGGTGTGACTATCCAC-----	1357
To9_11	TTTATGTTCCCTGAAGTTGGGTGTGACTATCCAC-----	1344
To9_12	TTTATGTTCCCTGAAGTTGGGCGTGACTATCCAC-----	1353
To11_1	TTTATGTTCCCTGAAGTTGGGTGTGACTATCCAC-----	1357
To8_4	TTTATGTTCCCTGAAGTTGGGTGTGACTATCCAC-----	1357
To8_9	TTTATGTTCCCTGAAGTTGGGTGTGACTATCCAC-----	1356
To9_14	TTTATGTTCCCTGAAGTTGGGTGTGACTATCCAC-----	1357
To11_2	TTTATGTTCCCTGAAGTTGAGTGTGACTATCCAC-----	1357
Cfelis_Tx	-----	
Olonga	-----	

TsIk_1	TTCTGGATATGCGCCAGAGTTATAATATTGTCGATGGGCTTTTCTTTGCTCGTTATGGCA	2214
TbMi_14	-----	
TsCh_1	-----	
TbAr_20	-----	
TsIk_2	TTCTGGATATGCGCCAGAGTTATAATATTGTCGATGGGCTTTTCTTTGCTCGTTATGGCA	2218
TbMi_3	-----	
TsCh_4	-----	
TsIk_7	TTCTGGATATGCGCCAGAGTTATAATATTATCGATGGGCTTTTCTTTGCTCGTTATGGCA	2216
TbTx_6	-----	
TbAr_15	-----	
TsIk_6	TTCTGGATATGCGCCAGAGTTATAATATTGTCGATGGGCTTTTCTTTGCTCGTTATGGCA	2212
TbTx_11	-----	
TbAr_25	-----	
TsCh_5	-----	
TsCh_2	-----	
TbMi_5	-----	
TbOk_10	-----	
TbTx_5	-----	
TsCh_3	-----	
TbOk_9	-----	
TbMi_15	-----	
TbOk_8	-----	
Tan5_8	-----	
Tan7_7	-----	
Tan1_3	-----	
Tan2_12	-----	
Tan3_9	-----	
Tan3_3	-----	
Tan5_7	-----	
Tan3_8	-----	
Tan6_11	-----	
Tan7_18	-----	
Tan1_2	-----	
Tan5_13	-----	
Tan2_3	-----	
Tan2_11	-----	
Tan6_18	-----	
Tan6_24	-----	
Tan1_13	-----	
Tan7_13	-----	
Tpar_U	-----	
TmIn_10	-----	
Tpar_AF	-----	
TmIn_13	-----	
TmIn_3	-----	
Tan1_14	-----	
Tan5_12	-----	
Tan2_5	-----	
Tan2_13	-----	
Tan3_6	-----	
Tan2_7	-----	
TcerOkE_12	-----	
TcerW2_9	-----	
TcerCanE_10	-----	
TcerCanE_7	-----	

TcerW1\_17 -----  
 TcerOkE\_13 -----  
 TcerCanE\_1 -----  
 TcerCanE\_8 -----  
 TcerWisE -----  
 Tcer183\_8 -----  
 TcerOkE\_11 -----  
 TcerInE\_2 -----  
 Tcer181\_1 -----  
 TcerOkE\_10 -----  
 TcerW2\_10 -----  
 TcerCanE\_6 -----  
 TcerW3\_2 -----  
 Tcer181\_2 -----  
 TcerW1\_24 -----  
 Tcer183\_7 -----  
 TcerW2-3 -----  
 Tcer181\_10 -----  
 TcerW1\_16 -----  
 TcerW3\_8 -----  
 TcerInE\_1 -----  
 TcerW3\_7 -----  
 TcerInE\_3 -----  
 TcerCanE\_11 -----  
 Tcer183\_5 -----  
 ThDG\_10 -----  
 ThDG\_13 -----  
 ThDG\_12 -----  
 ThDG\_14 -----  
 ThDG\_11 -----  
 To8\_8 -----  
 To9\_13 -----  
 To9\_10 -----  
 To11\_5 -----  
 To9\_11 -----  
 To9\_12 -----  
 To11\_1 -----  
 To8\_4 -----  
 To8\_9 -----  
 To9\_14 -----  
 To11\_2 -----  
 Cfelis\_Tx -----  
 Olonga -----

TsIk\_1 TGTTCTGGTGTGACCTTAGCTGTGTCATACCTGGGCTGTCGTTACGGGTATAAGATGTTT 2274  
 TbMi\_14 -----  
 TsCh\_1 -----  
 TbAr\_20 -----  
 TsIk\_2 TGTTCTGGTGTGACCTTAGCTGTGTCATACCTGGGCTGTCGTTACGGGTATAAGATGTTT 2278  
 TbMi\_3 -----  
 TsCh\_4 -----  
 TsIk\_7 TGTTCTGGTGTGACCTTAGCTGTGTCATACCTGGGCTGTCGTTACGGGTATAAGATGTTT 2276  
 TbTx\_6 -----  
 TbAr\_15 -----  
 TsIk\_6 TGTTCTGGTGTGACCTTAGCTGTGTCATACCTGGGCTGTCGTTACGGGTATAAGATGTTT 2272  
 TbTx\_11 -----  
 TbAr\_25 -----  
 TsCh\_5 -----  
 TsCh\_2 -----  
 TbMi\_5 -----  
 TbOk\_10 -----  
 TbTx\_5 -----  
 TsCh\_3 -----  
 TbOk\_9 -----  
 TbMi\_15 -----  
 TbOk\_8 -----  
 Tan5\_8 -----  
 Tan7\_7 -----  
 Tan1\_3 -----



Tan2_12	-----
Tan3_9	-----
Tan3_3	-----
Tan5_7	-----
Tan3_8	-----
Tan6_11	-----
Tan7_18	-----
Tan1_2	-----
Tan5_13	-----
Tan2_3	-----
Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
TmIn_3	-----
Tan1_14	-----
Tan5_12	-----
Tan2_5	-----
Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
TcerOkE_12	-----
TcerW2_9	-----
TcerCanE_10	-----
TcerCanE_7	-----
TcerW1_17	-----
TcerOkE_13	-----
TcerCanE_1	-----
TcerCanE_8	-----
TcerWisE	-----
Tcer183_8	-----
TcerOkE_11	-----
TcerInE_2	-----
Tcer181_1	-----
TcerOkE_10	-----
TcerW2_10	-----
TcerCanE_6	-----
TcerW3_2	-----
Tcer181_2	-----
TcerW1_24	-----
Tcer183_7	-----
TcerW2-3	-----
Tcer181_10	-----
TcerW1_16	-----
TcerW3_8	-----
TcerInE_1	-----
TcerW3_7	-----
TcerInE_3	-----
TcerCanE_11	-----
Tcer183_5	-----
ThDG_10	-----
ThDG_13	-----
ThDG_12	-----
ThDG_14	-----
ThDG_11	-----
To8_8	-----
To9_13	-----
To9_10	-----
To11_5	-----
To9_11	-----
To9_12	-----
To11_1	-----
To8_4	-----
To8_9	-----
To9_14	-----

To11_2	-----
Cfelix_Tx	-----
Olonga	-----
TsIk_1	AGATTAGTTCCTGAGATTGGGTGAGACTATCCAC 2308
TbMi_14	-----
TsCh_1	-----
TbAr_20	-----
TsIk_2	AGATTAGTTCCTGAGATTGGGTGAGACTATCCAC 2312
TbMi_3	-----
TsCh_4	-----
TsIk_7	AGATTAGTTCCTGAGATTGGGTGAGACTATCCAC 2310
TbTx_6	-----
TbAr_15	-----
TsIk_6	AGATTAGTTCCTGAGATTGGGTGAGACTATCCAC 2306
TbTx_11	-----
TbAr_25	-----
TsCh_5	-----
TsCh_2	-----
TbMi_5	-----
TbOk_10	-----
TbTx_5	-----
TsCh_3	-----
TbOk_9	-----
TbMi_15	-----
TbOk_8	-----
Tan5_8	-----
Tan7_7	-----
Tan1_3	-----
Tan2_12	-----
Tan3_9	-----
Tan3_3	-----
Tan5_7	-----
Tan3_8	-----
Tan6_11	-----
Tan7_18	-----
Tan1_2	-----
Tan5_13	-----
Tan2_3	-----
Tan2_11	-----
Tan6_18	-----
Tan6_24	-----
Tan1_13	-----
Tan7_13	-----
Tpar_U	-----
TmIn_10	-----
Tpar_AF	-----
TmIn_13	-----
TmIn_3	-----
Tan1_14	-----
Tan5_12	-----
Tan2_5	-----
Tan2_13	-----
Tan3_6	-----
Tan2_7	-----
TcerOkE_12	-----
TcerW2_9	-----
TcerCanE_10	-----
TcerCanE_7	-----
TcerW1_17	-----
TcerOkE_13	-----
TcerCanE_1	-----
TcerCanE_8	-----
TcerWisE	-----
Tcer183_8	-----
TcerOkE_11	-----
TcerInE_2	-----
Tcer181_1	-----
TcerOkE_10	-----

TcerW2\_10 -----  
TcerCanE\_6 -----  
TcerW3\_2 -----  
Tcer181\_2 -----  
TcerW1\_24 -----  
Tcer183\_7 -----  
TcerW2-3 -----  
Tcer181\_10 -----  
TcerW1\_16 -----  
TcerW3\_8 -----  
TcerInE\_1 -----  
TcerW3\_7 -----  
TcerInE\_3 -----  
TcerCanE\_11 -----  
Tcer183\_5 -----  
ThDG\_10 -----  
ThDG\_13 -----  
ThDG\_12 -----  
ThDG\_14 -----  
ThDG\_11 -----  
To8\_8 -----  
To9\_13 -----  
To9\_10 -----  
To11\_5 -----  
To9\_11 -----  
To9\_12 -----  
To11\_1 -----  
To8\_4 -----  
To8\_9 -----  
To9\_14 -----  
To11\_2 -----  
Cfelis\_Tx -----  
Olonga -----

## APPENDIX 4

## 5.8S Gene Alignment

Ts\_Ch5 ---ACACTTTTAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAATTGC ---57  
 Ts\_Ch1 ---ACACTTTTAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGTGAATTGC ---57  
 Tb\_Ar20 ---ACACTTTTAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAATTGC ---57  
 Tb\_Tx ---ACACTTTTAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAATTGC ---57  
 Tb\_Mi ---ACACTTTTAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAATTGC ---57  
 Tb\_Ar ---ACACTTTTAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAATTGC ---57  
 Tb\_Ok ---ACACTTTTAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAATTGC ---57  
 Ts\_Ch2 ---ACACTTTTAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAATTGC ---57  
 Ts\_Ch4 ---ACACTTTTAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAATTGC ---57  
 Ts\_Ch3 ---ACACTTTTAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAATTGC ---57  
 Ts\_Ik ---ACACTTTTAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAATTGC ---57  
 Tan2\_13 ---AAACTTTCAGCGGTGGGTGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tan5\_12 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAAGACGCAGCGAAGTGC --57  
 Tan1\_13 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tan2\_5 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tan7 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tan6 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tan5 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tan3 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tan2 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tan1 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tan2\_12 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tan5\_8 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tan6\_18 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tmln\_3 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tan7\_7 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tp\_AF ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tmln ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 ThDG ---AAACTGTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 ThDG\_13 ---AAACTGTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Tan1\_2 ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 Cf\_Tx ---AAACTTTCAGCGGTGGATGTCTTGGCTCACACAACGATGAAGGACGCAGCGAAGTGC --57  
 TeOkE\_12 ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAATTGC ---57  
 TeCanE\_G ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAATTGC ---57  
 TeCanE\_6 ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAATTGC ---57  
 TeOkE\_13 ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAATTGC ---57  
 Te181 ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAAGTGC ---57  
 Te183 ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAAGTGC ---57  
 TeOkE ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAAGTGC ---57  
 TeWisE ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAAGTGC ---57  
 TeInE ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAAGTGC ---57  
 TeCanE\_10 ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAAGTGC ---57  
 TeW1 ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAAGTGC ---57  
 TeW2 ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAAGTGC ---57  
 TeW3 ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAAGTGC ---57  
 Te181\_2 ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAAGTGC ---57  
 TeCanE\_11 ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGTGAAGTGC ---57  
 TeCan\_8 ---AAACTTTCAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAAGTGC ---57  
 To8\_4 ---AAACTTATAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAATTGC ---57  
 To9\_11&12 ---AAACTTATAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAATTGC ---57  
 To11 ---AAACTTATAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAATTGC ---57  
 To8\_8 ---AAACTTATGGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAATTGC ---57  
 To8\_9 ---AAACTTATAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAATTGC ---57  
 To9 ---AAACTTATAGCGGTGGATGTCTCGGCTCATAACGATGAAGGACGCAGCGAATTGC ---57  
 OI ACCAAATTCTCAACGATGGATATCTTGGTCCCATACGATGAAGAACGCAGCGAAGTGC 60

Ts\_Ch5 GATAAGCATTGTGACTTGCAGTCTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Ts\_Ch1 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACGATTTCTGAACGTATTAGACAC 117  
 Tb\_Ar20 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tb\_Tx GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tb\_Mi GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tb\_Ar GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tb\_Ok GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Ts\_Ch2 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Ts\_Ch4 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Ts\_Ch3 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Ts\_lk GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan2\_13 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan5\_12 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan1\_13 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan2\_5 GATAAGCATTGTGACTTGAAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan7 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan6 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan5 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan3 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan2 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan1 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan2\_12 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan5\_8 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan6\_18 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tmln\_3 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan7\_7 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tp\_AF GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tmln GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 ThDG GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 ThDG\_13 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Tan1\_2 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 Cf\_Tx GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGATTTCTGAACGTATTAGACAC 117  
 TeOkE\_12 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAATGTATTAACGC 117  
 TeCanE\_G GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAATGTATTAACGC 117  
 TeCanE\_6 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAATGTATTAACGC 117  
 TeOkE\_13 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAACGTATTAGACAC 117  
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 Te183 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAACGTATTAGACAC 117  
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 TeWisE GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAACGTATTAGACAC 117  
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 Te181\_2 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAACGTATTAGACAC 117  
 TeCanE\_11 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAACGTATTAGACAC 117  
 TeCan\_8 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAACGTATTAGACAC 117  
 To8\_4 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAACGTATAAGACAC 117  
 To9\_11&12 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAACGTATAAGACAC 117  
 To11 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAACGTATAAGACAC 117  
 To8\_8 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAACGTATAAGACAC 117  
 To8\_9 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAACGTATAAGACAC 117  
 To9 GATAAGCATTGTGACTTGCAGACTTCTGCGAATCAACAGACTTCTGAACGTATAAGACAC 117  
 Ol GATAAGCAATGCGAATTGCAGAA---CCGTGAGTCATCAGATTTTGAACGCAACTG----GC 116

Ts\_Ch5 ACCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
 Ts\_Ch1 ACCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
 Tb\_Ar20 ACCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
 Tb\_Tx ACCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
 Tb\_Mi ACCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
 Tb\_Ar ACCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
 Tb\_Ok ACCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
 Ts\_Ch2 ACCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
 Ts\_Ch4 GCCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
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 Tan5\_12 ACCACCTCTGCTTGCATGTGGTACTCCCATTTCAGTGAACCT- -159  
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 Tan1 ACCACCTCTGCTTGCATGTGGTACTCCCATTTCAGTGAACCT- -159  
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 Tan5\_8 ACCAACTCTGCTTGCATGTGGTACTCCCATTTCAGTGAACCT- -159  
 Tan6\_18 ACCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
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 Tp\_AF ACCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
 Tmln ACCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
 ThDG ACCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
 ThDG\_13 ACCACCTCTGCTTGCACGTGGTACTCCCATTTCAGTGAACCT- -159  
 Tan1\_2 ACCACCTCTGCTTGCATGTGGTACTCCCATTTCAGTGAACCT- -159  
 Cf\_Tx ACCACCTCTGCTTGCATGTGGTACTCCCATTTCAGTGAACCT- -159  
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 TeCanE\_6 GCCGCCTCTGCTTGCAGTGGCACTCCCATTTCAGTGAACCT- -159  
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 Te183 ACCGCCTCTGCTTGCACGCGGTACTCCCATTTCAGTGAACCT- -159  
 TeOkE ACCGCCTCTGCTTGCACGCGGTACTCCCATTTCAGTGAACCT- -159  
 TeWisE ACCGCCTCTGCTTGCACGCGGTACTCCCATTTCAGTGAACCT- -159  
 TeInE ACCGCCTCTGCTTGCACGCGGTACTCCCATTTCAGTGAACCT- -159  
 TeCanE\_10 ACCGCCTCTGCTTGCACGCGGTACTCCCATTTCAGTGAACCT- -159  
 TeW1 ACCGCCTCTGCTTGCACGCGGTACTCCCATTTCAGTGAACCT- -159  
 TeW2 ACCGCCTCTGCTTGCACGCGGTACTCCCATTTCAGTGAACCT- -159  
 TeW3 ACCGCCTCTGCTTGCACGCGGTACTCCCATTTCAGTGAACCT- -159  
 Te181\_2 ACCGCCTCTGCTTGCACGCGGTACTCCCATTTCAGTGAACCT- -159  
 TeCanE\_11 ACCGCCTCTGCTTGCACGCGGTACTCCCATTTCAGTGAACCT- -159  
 TeCan\_8 ACCGCCTCTGCTTGCATGCGGTACTCCCATTTCAGTGAACCT- -159  
 To8\_4 ACCACCTCTCCTTGGAAGTGGTCTCCCAATTTCAGTGAACCT- -159  
 To9\_11&12 ACCACCTCTCCTTGGAAGTGGTCTCCCAATTTCAGTGAACCT- -159  
 To11 ACCACCTCTCCTTGGAAGTGGTCTCCCAATTTCAGTGAACCT- -159  
 To8\_8 ACCACCTCTCCTTGGAAGTGGTCTCCCAATTTCAGTGAACCT- -159  
 To8\_9 ACCACCTCTCCTTGGAAGTGGTCTCCCAATTTCAGTGAACCT- -159  
 To9 ACCACCTCTCCTTGGAAGTGGTCTCCCAATTTCAGTGAACCT- -159  
 Ol GCTGGTTGGTTATCCAGCCAGCATGCTTGTTCAGT----- -152

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Holman, P.J., Hsieh, M.M., Nix, J.L., Bendele, K.G., Wagner, G.G., Ball, J.M., 2002. A cathepsin L-like cysteine protease is conserved among *Babesia equi* isolates. *Molecular and Biochemical Parasitology*. 119,295-300.

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Holman, P.J., Bendele, K.G., Schoelkopf, L., Jones-Witthuhn, R.L., Jones, S.O., 2003. Ribosomal RNA analysis of *Babesia odocoilei* isolates from farmed reindeer (*Rangifer tarandus tarandus*) and elk (*Cervus elaphus canadensis*) in Wisconsin. *Parasitology Research*. 9,378-383.