

GENETIC DIVERSITY STUDIES OF BRUGIA SPECIES IN THAILAND

A THESIS

BY

SUNSANEE PHASOOK

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มีรายงานว่าพยาธิเท้าช้างชนิด *Brugia malayi* สามารถพบได้ทั้งในคน และสัตว์รังโรค เช่น สุนัข แมว เป็นต้น ในขณะที่ *B. pahangi* เป็นพยาธิเท้าช้างที่พบได้ในสัตว์รังโรคเป็นแมวเท่านั้น โดยยังไม่มีรายงานว่าพบพยาธิชนิดนี้ในคน การจำแนกทั้ง 2 ชนิดนี้ด้วยวิธีที่ใช้ในปัจจุบันยังไม่มีประสิทธิภาพเพียงพอและมักจะทำให้เกิดความผิดพลาดในการบ่งบอกชนิดของการติดเชื้อได้ ในการทดลองนี้ได้ทำการศึกษายีนบริเวณ 18S rDNA และ internal transcribed spacers (ITS) มาใช้หาความสัมพันธ์ทางวิวัฒนาการของ *Brugia* spp. สายพันธุ์ต่างๆ จากแมวที่อยู่ตามพื้นที่ต่างๆ ในประเทศไทย โดยนำเลือดที่ได้มาสกัด DNA และเพิ่มปริมาณโดยวิธี PCR ซึ่ง primer ที่ใช้มีความจำเพาะต่อยีน 18S rDNA, ITS1 และ ITS2 ทำให้ได้ PCR product ที่ได้มีขนาด 1,641 bp, 580 bp และ 660 bp ตามลำดับ ลำดับนิวคลีโอไทด์ของยีน 18S rDNA ก็จะถูกนำมาวิเคราะห์และเปรียบเทียบกับ *B. malayi* และ *W. bancrofti* ได้จากการวิเคราะห์ phylogenetic tree ของ ยีน 18S rDNA จะเป็นบริเวณที่มี conserve ที่สูง และเกิด single nucleotide polymorphisms (SNPs) ของลำดับนิวคลีโอไทด์ขึ้นภายใน *Brugia* spp. ในขณะที่ phylogenetic tree ของยีน ITS1 และ ITS2 แสดงให้เห็นถึงความหลากหลายทางพันธุกรรมภายใน *Brugia* spp. ผลที่ได้จากการวิเคราะห์ phylogenetic tree ของยีน ITS1 และ ITS2 โดยใช้ Neighbor Joining (NJ) และ DNA Parsimony (DNA PARS) จากข้อมูลแสดงให้เห็นการติดเชื้อเพียงอย่างเดียวของ *B. malayi* (แมวตัวที่ 1, 3 และ 4) หรือ *B. pahangi* (แมวตัวที่ 6 และ 7) และการติดเชื้อร่วมของ *B. malayi* และ *B. pahangi* (แมวตัวที่ 2 และ 5) แสดงให้เห็นว่ายีน ITS ใช้ศึกษาความหลากหลายทางพันธุกรรมของพยาธิเท้าช้างชนิดบรูเกียในแมวซึ่งเป็นสัตว์รังโรค เพื่อเป็นประโยชน์ในการศึกษาระบาดวิทยาของพยาธิเท้าช้างชนิดบรูเกียได้

GENETIC DIVERSITY STUDIES OF BRUGIA SPECIES IN THAILAND

AN ABSTRACT
BY
SUNSANEE PHASOOK

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Sunsanee Phasook. (2006). *Genetic diversity studies of Brugia species in Thailand*. Master thesis, M.Sc. (Molecular Biology). Bangkok: Graduated School, Srinakharinwirot University. Advisor Committee: Assoc. Prof. Dr. Kosum Chansiri, Assoc. Prof. Dr. Somchai Santiwatanakul, Asst. Prof. Dr. Roongtawan Supabphol and Asst. Prof. Dr. Wichet Leelamanit

It has been reported that *Brugia malayi* have infected not only human but also animals such as cats, monkeys, and dogs, whereas *B. pahangi* causes morbidity only in cat reservoirs. Due to their similarity in morphologies and others, the identification of both brugian species in such carriers based on traditional detection tools can be difficult and mostly lead to misdiagnosis. Hence, the data based on genes is the alternative useful information for not only parasite identification but also their genetic diversities. In this study, 18S rDNA and internal transcribed spacer (ITS) regions were used to determine the genetic diversity of *Brugia* spp. within domestic cat reservoirs from different geographical areas in Thailand. Microfilaria were separated and DNA was extracted prior to PCR amplification. The specific primers of 18S rDNA, ITS1 and ITS2 regions were used to yield the PCR products of 1,641 bp, 580 bp and 660 bp in size, respectively. The fragments were cloned, sequenced, and aligned in comparison to the reported data of *B. malayi* and *W. bancrofti*. It was found that the 18S rDNA phylogenetic tree was highly conserved and showed single nucleotide polymorphisms (SNPs) in some nucleotide positions. In contrast, the ITS1 and ITS2 phylogenetic trees demonstrated some genetic variation among *Brugia* spp. Phylogenetic tree construction based on ITS1 and ITS2 nucleotide sequences was analyzed by using the methods of Neighbor Joining (NJ) and DNA Parsimony (DNA PARS). The data revealed both single infection of either *B. malayi* (cat 1, 3 and 4) or *B. pahangi* (cat 6 and 7) and mix infection of both *Brugia* spp. (cat 2 and 5). It can be proposed that ITS regions could be used as genetic diversity for investigation of *Brugia* spp. in cat reservoirs which will be beneficial for epidemiological study.

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CHAPTER I

INTRODUCTION

Lymphatic filariasis or elephantiasis is the major public health problem that infected over billion people in over 80 countries. Among them, over 120 million have already been affected and over 40 million are seriously incapacitated and disfigured. The clinical manifestation of infection is elephantiasis, genital swelling and tropical eosinophilia. The lymphatic filariasis is abundant and widely spreads in the tropical and subtropical areas where the prevalence of infection is continuing to increase. It is mainly caused by three types of parasitic worms, *Wuchereria bancrofti*, *Brugia malayi*, and *B. timori*. Referring to previous reports, *W. bancrofti* is widely distributed in endemic regions i.e. Africa, India, the Pacific Islands, South America and Southeast Asia whereas *B. malayi* is mainly distributed in Asia countries such as China, South Korea, Japan, India, Myanma, Indonesia, Malaysia, Borneo island, the Philippines, and Thailand. At present, *B. timori* is found only in Indonesia especially at the island of Alor, Flores, Timor.⁽¹⁻⁵⁾ In Thailand, only two types of parasitic worms, *W. bancrofti* and *B. malayi* are found to spread from person to person via vector mosquitoes.^(6,7) It has been reported that *B. malayi* has infected not only human but also animal such as cats, monkeys, and dogs.⁽⁸⁻¹⁰⁾ The successful experimental transmission of the parasite between men and animals have strengthened the belief that zoonotic infection can occur in nature because of their close relationship so that the transmission of the infection from domestic cat to human is possible.^(11,12) These animal reservoirs play an important role as the disease carriers which can lead to the problem of eradication in endemic area.

Among animal reservoirs of filariasis, cats have been found to be the host of various filarial parasites. Generally, *B. pahangi* and *Dirofilaria repens* are the two important feline filaria. However *D. immitis* has also been found to infect cats but shows no obvious symptom.⁽¹³⁾

In Malaysia, *B. pahangi* coexists in many of the same hosts as the zoonotically transmitted subperiodic *B. malayi*^(9-11,13,14) and develops in some similar mosquito vectors such as *Mansonia* spp.⁽¹⁵⁾ *B. pahangi* does not infect man naturally, although its

experimental transmission to man was documented by Edeson and colleagues.⁽⁸⁾ However, Mak and coworkers indicated that natural infection in man could exist but previously might confused with *B. malayi* when routine diagnosis with standard Giemsa and Haematoxylin preparations.

Differentiation of *B. malayi* and *B. pahangi* microfilaria among the diverse species and strains of filarial has been investigated. The traditional Giemsa staining is cheap and convenient but cannot morphologically distinguish between those two species. In contrast, the acid phosphatase staining is effective but it is not reproducible and the procedure is complicated. The molecular methods based on PCR has been introduced to use as tools for differentiation of *B. malayi* and *B. pahangi*. However, due to the high homology over 95% in many nucleotides sequences of various genes of those two species, this makes it difficult to reach high validity and fidelity of the differentiation.

To achieve these criteria, the reliable molecular phylogenetic analysis for the specific identification of microfilaria of *Brugia* species based on small subunit ribosomal (18S rDNA) and internal transcribed spacers genes (ITSs) were investigated. The spacer regions, ITS1 and ITS2, of the rDNA gene are routinely used for studies on phylogenetic reconstruction, genetic variability and divergence of closely related species for a wide range of organisms, including particularly within groups with controversial taxonomy. The phylogenetic trees obtained in this study are useful for determination of the relationship between the closely related *B. malayi* and *B. pahangi* in cat reservoirs. The information is beneficial for epidemiological studies and for the control and eradication of the filarial disease in endemic area.

CHAPTER II

LITERATURE REVIEW

1. Human lymphatic filariasis

Lymphatic Filariasis, known as Elephantiasis, remains a major public health problem in tropical countries around the world. The World Health Organization launched a global program to eliminate lymphatic filariasis as a public health problem by the year 2020.⁽¹⁶⁾ Lymphatic filariasis is mainly caused by three types of parasitic worms, including *W. bancrofti*, *B. malayi*, and *B. timori* which are transmitted by mosquitoes. Ninety percent of lymphatic filariasis infections are caused by *W. bancrofti* which is widely distributed in endemic regions such as Africa, India, the Pacific islands, South America, and Southeast Asia. *B. malayi* is widely distributed in Asia countries such as China, Korea, India, Indonesia, Malaysia, Philippines, and Sri Lanka. *B. timori* infection occurs in Indonesia (islands of Alor, Flores, Timor).^(4,5) (Figure 1) The adult worms actually live in the lymphatic vessels near the lymph nodes where they distort the vessels and cause local inflammation. In advanced stages, the worms can actually obstruct the vessels, causing the surrounding tissue to become enlarged. Bancroftian filariasis caused by *W. bancrofti* affects the legs and genitals; where as, the Malayan filariasis caused by *B. malayi* affects the legs below the knees. Repeated episodes of inflammation lead to blockage of the lymphatic system, especially in the genitals and legs. This causes the affected area to become grossly enlarged, with thickened and coarse skin which is called elephantiasis.^(2,17)

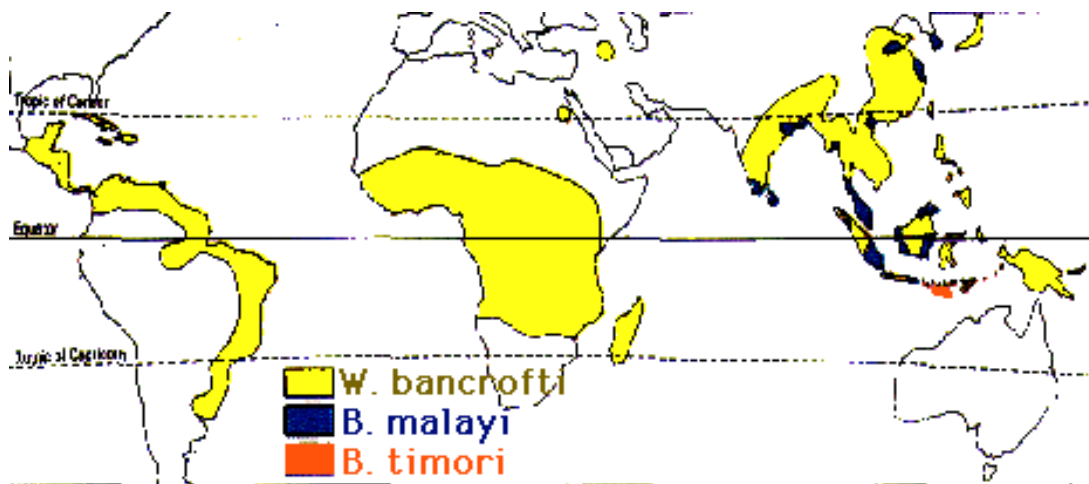


Figure 1 Geographical distribution of lymphatic filariasis.⁽¹⁸⁾

The endemic range of *B. malayi* is confined to South and South-East Asia from India in the west to Korea in the east. Similar to *W. bancrofti*, its distribution is depended on its mosquito vectors. The nocturnally periodic form is found in areas with rice fields and the nocturnally subperiodic form is found in rural villages and plantations along the lower reaches of major rivers in swamp forests. In 1983, Partono has proposed the subdivision of *B. malayi* into zoophilic and anthropophilic strains.⁽¹⁸⁾ The former is transmissible to cats, monkeys, and laboratory gerbils.

1.1 Taxonomy

Human filariasis is classified as shown below.⁽⁵⁾

Phylum	Nematoda
Class	Secernentea
Subclass	Spiruria
Order	Spirurida
Suborder	Spirurina
Superfamily	Filarioidea
Family	Filariidae
Genus	<i>Brugia</i> sp.
Species	<i>Brugia malayi</i>

1.2 Morphology

The adult worms of *B. malayi* are smaller than those of *W. bancrofti*. The microfilariae of *B. malayi* are 170 – 230 µm in length and have 2 terminal nuclei that are distinctly separated from the other nuclei in the tail.^(19,20) (Figure 3) The last terminal nucleus is quite small and located at the tip of the tail. The sheath stains deep purple with haematoxylin stain.



Figure 2 Microfilaria of *B. malayi*. These sheathed microfilariae are measured approximately 170 – 230 μm in length and have 2 terminal nuclei that are distinctly separated from the other nuclei in the tail. The microfilariae of *Brugia* species are tightly coiled, and the nuclear column is more tightly packed, preventing the visualization of individual cells. (Haematoxylin stain, x400)⁽²⁰⁾

1.3 Life cycle

The life cycle of *B. malayi* and *W. bancrofti* are essentially similar. Adult worms normally live in the lymphatic system and produce blood circulating microfilariae. The microfilaremic host serves as the source of infection to vector mosquitoes which, depending on the locality, belong to the genera *Mansonia*, *Anopheles*, *Culex* and *Aedes*. Microfilariae taken up by vector mosquitoes ex-sheath and have penetrated the mid-gut to migrate within an hour and to the thoracic muscles to undergo further development. In the thoracic muscles, the parasite becomes thicker and shorter when compared to the microfilariae.

The first stage (L1) larva of *B. malayi* at 2.5 days has a mean length of $143.7 \pm 3.8 \mu\text{m}$. and a maximum width of $16.5 \pm 0.7 \mu\text{m}$. At about 5 days the L1 moults to become the second stage (L2) larva. The 12 at 5.5 days has a mean length of $441 \pm 27 \mu\text{m}$. and maximum width of $29.4 \pm 1.8 \mu\text{m}$. It is slightly more active than

the L1 which is seen to twitch only occasionally. By the 9th-10th day, the L2 moults again to become the third or infective stage (L3) which at 10.5 days has a mean length of $1503 \pm 40.6 \mu\text{m}$ and maximum width $30.5 \pm 0.7 \text{ mm}$. The L3 which is a very active stage at maturity, migrates mainly to the proboscis but can be seen in other parts of the insect body. When the infective mosquito bites a susceptibility host, the L3 larvae are deposited on the skin surface during the process of probing by mosquito prior to puncture with the proboscis. After withdrawal of the proboscis, the L3 actively migrate into the wound and travel to afferent lymphatic and subcapsular sinus. Approximately 9-10 days after entry into the definitive host, the L3 moults to the fourth stage (L4). In two-week old experimental infections in the leaf monkey *Presbytis melalophos*, *B. malayi* female L4 larvae have a mean length of $4710 \pm 214.3 \mu\text{m}$ and a maximum width of $38.6 \pm 2.7 \mu\text{m}$. The male L4 larvae measure $4236 \pm 120.8 \mu\text{m}$ and $37.9 \pm 1.9 \mu\text{m}$, respectively.

The final moult occurs approximately 35-40 days after initial infection by the 5th week juvenile adults in *P. melalophos* have mean lengths of $13.7 \pm 0.3 \mu\text{m}$ and $12.6 \pm 0.5 \text{ mm}$ in female and male, respectively.⁽²¹⁾ The maximum width are $76.4 \pm 2.8 \mu\text{m}$ and $64.7 \pm 2.2 \mu\text{m}$, respectively. Sexual maturity occurs two to three months post infection in *B. malayi* with mean pre-patent periods of 67 days in *P. melalophos* and 80 days in cats and jirds.⁽²²⁾ The pre-patent period for *W. bancrofti* in monkeys is about 8-18 months. In man, the per patant period for *B. malayi* infection is about 3.5 months, while for *W. bancrofti* is about 11 months.⁽²³⁾

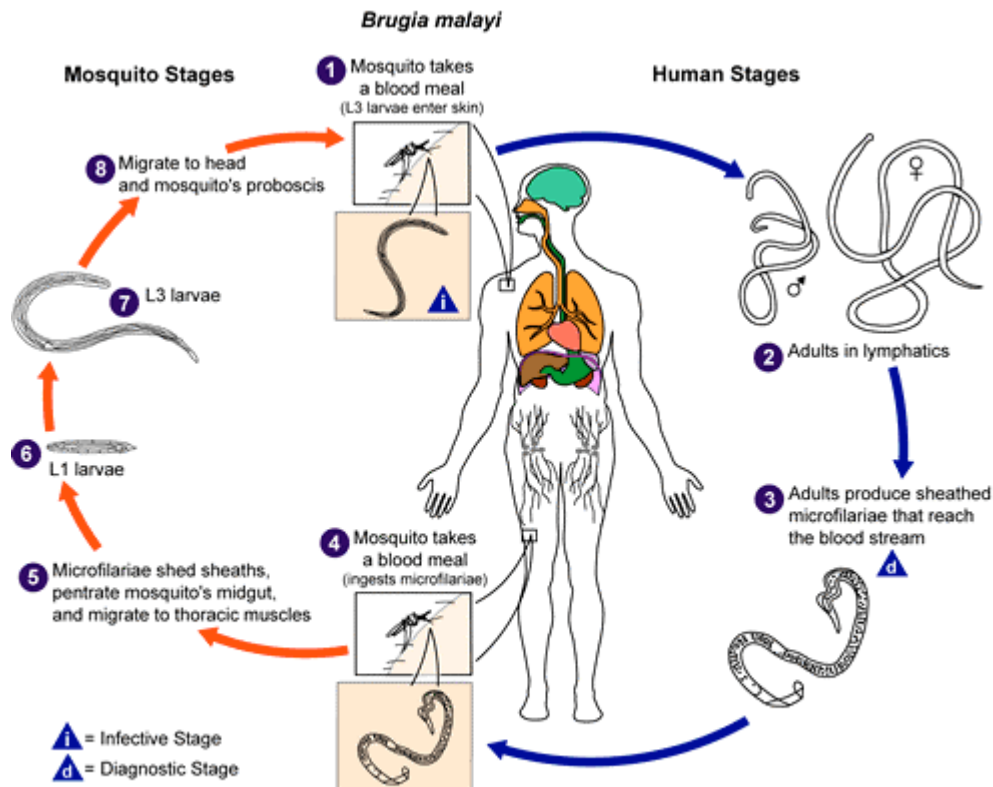


Figure 3 Life cycle of *B. malayi*.⁽²⁴⁾

1.4 Pathology

The clinical picture of *B. malayi* infection is somewhat different from that of *W. bancrofti*. The symptoms of Brugian filariasis begin earlier than those of Bancroftian filariasis, often within a month or less. Quickly immune responses to the worms lead to lymphoedema and swelling of the legs is a prominent early symptom. Bouts of fever and lymphangitis are common and often more frequent than those found in patents infected with *W. bancrofti*. Unlike bancroftian infection, the lymphoedema in the legs is below the knees and in the arms below the elbows. Gross elephantiasis is very uncommon. However, when it does occur it generally develops more quickly in Brugian (1 to 2 years) than the Bancroftian filariasis. (3 or more years) (Figure 4)



Figure 4 Early (left) and late (right) stages of Brugian elephantiasis.

1.5 Parasitological diagnosis

The clinical features of filariasis may be so clear-cut. For example, lymphoedema and elephantiasis are found in patients living in endemic areas of filariasis that diagnosis is usually not a problem. However, very few infected people shows evidence of gross chronic disease manifestation. The mean elephantiasis rate in most endemic areas of Malaysia is only about 1%. Most microfilarial carriers are asymptomatic although in certain endemic areas as many people may have clinical sign suggestion of filariasis. Diagnosis is normally based on clinical, parasitological, immunological and occasionally histopathological features.

Parasitological techniques involve the demonstration and identification of the presence of circulating microfilariae in various body fluids e.g. hydrocele fluid and chylous urine. Normally, 60 μ l thick blood smear films are prepared from peripheral blood taken at night, and then are allowed to dry preferably overnight and stained with diluted Giemsa or Field's stain.

The detection of *W. bancrofti* and *B. malayi* infection is essentially importance for monitoring the effectiveness control of the traditional programs relying on antimosquito measure and on single oral administration of diethylcarbamazine (DEC) therapy. Parasitological diagnosis by detection of microfilariae in blood or in hydrocele fluid (in chyluria) can be done. The conventional thick blood film is still the best method in the field work, but it is limited which depended on the presence of microfilariae in blood at the night time. Despite it is simplicity and low cost, the sensitivity is depended

on the volume of blood sample (typically 20-60 µl), the time of blood collection, skill and dedication of the microscopist .

The DEC provocation test can detect the presence of microfilariae in day time after provoking the microfilaria in the lung capillaries to invade the peripheral blood. This is suitable for areas where night blood collection of nocturnal periodic *W. bancrofti* is impossible. However, it is insensitive, labor-intensive, and has some side effect “Mazzoti reaction” in patient with coinfection of *W. bancrofti* and *O. volvulus*.

The membrane filtration is one of the diagnostic tool for identification of filaria parasites but it is more sensitive than thick smear, labor-intensive and time-consuming. Capillary tube technique is rather rapid assessment to work efficiently in the field when immediate result is required, but is labor-intensive, insensitive and cumbersome in the field condition, as same as membrane filtration. Antibody test seems to be an alternative method for detection of the infected people, but does not distinguish between active and past-infections. Antibody titers are not correlated with infection intensity (or worm load) in the patient. To date, the microfilaria DNA detection by PCR is very sensitive with species specific but imperfectly performs with contamination in the field condition, expensive, and impractical for routine use in endemic area.

1.6 Epidemiology

Thailand has an area of approximately 514,000 km² and a population of 35 millions, 62 millions in 1970, and 1999, subsequently. The land may be divided roughly into five geographic regions: 1) the hilly region in the northwest, with the rainy season from May to October, and dry season from November to April; 2) the central, alluvial region which is low and flat, with extensive flooding during the rainy season; 3) the dry plateau regions in the northeast, traversed by tributaries of the Mekong River; 4) the densely forested area in the southeast at the head of the Gulf of Thailand; and 5) the southern peninsular regions consisting of a narrow strip of land situated between the Indian Ocean and the South of China sea.

Malayan filariasis is reported in Thailand where its endemic is in swampy area along the eastern coast of peninsular region, and is a serious health problem for the people in several. The parasite is mostly the nocturnally periodic form, but the occurrence of a superiodic form of *B. malayi* has also been recorded recently from this region.

1.7 Malayan filariasis in Thailand

In 1998, the Public Health Department of Thailand notes the frequent occurrence of elephantiasis in the peninsular part and called for reporting of the disease by the headman of the village in this region. As a result, elephantiasis cases were reported from 10 of 15 provinces of the peninsular regions which were Pattani, Narathiwat, Phattalung, Nakhon-Srithamrat, Suratthani, Chumphon, Yala, Krabi, Trang and Ranong. (Figure 4)⁽²⁵⁾ The province of Nakhon-Srithamrat headed the list with 1,246 cases, followed by Pattani with 603 cases. As for the four provinces of Yala, Trang, Krabi, and Ranong, which were not in the eastern coastal area only small number of cases were reported and seemed that they were mostly imported from endemic foci outside these provinces.

At present, Narathiwat province is still endemic area of Brugian filariasis. Thus, the populations living in this region confront the high risk to infection which is an important problem of public health and must be intensive surveillance. Although there are the spontaneous epidemic and appearance in some group of local people, the foci group is present in many infective larvae. On the other hand, there are many times of bite by filarial infective mosquitoes around the living hood and their workplace. For the special feature groups of the local people are difference that re-infection. Although the government officers belonging to these area whose responsibility to investigate and treatment for longtime but they cannot success in eradication of the Brugian filariasis from these area. One of the factors that influences the epedimiology of Brugian filaria is that it can infect the domestic animals such as cats, monkeys and dogs. It has been reported that cats are the important reservoir of the disease.⁽²⁶⁾

1. Bangkok
2. Chiang Mai
3. Chiang Rai
4. Chon Buri
5. Chumphon
6. Hat Yai
7. Kamphaeng
8. Krabi
9. Mae Hong Son
10. Nakhon Phanom
11. Nakhon Si Thammarat
12. Nakhon Phanom
13. Nakhon Phanom
14. Nakhon Phanom
15. Nakhon Phanom

Surat Thani

Nakorn Si Thammarat

Naratiwat

Brugia malayi



Figure 6 *Mansonia* species: Brugia filariasis vectors.

1.9 Animal reservoirs and zoonotic lymphatic filariasis

Several wild and domestic animals have been nocturnally infected with subperiodic *B. malayi*.⁽⁸⁻¹⁰⁾ The successful experimental transmission of the parasite between man and animals.^(11,12) have strengthened the belief that zoonotic infection can occur in nature because of their closely relationship. The transmission of the infection from domestic cat to human is possible. The study of *B. pahangi*, which is a common filarial parasite of wild and domestic animals in Southeast Asia, have been used as an experimental model for studying filariasis.^(9,12-14,27,28)

Differentiation of *B. malayi* and *B. pahangi* microfilaria among the diverse species and strains of filarial parasites has been studied. In Malaysia, *B. pahangi* coexists in many of the same hosts as the zoonotically transmitted subperiodic *B. malayi*^(9-11,13,14) and develops in some similar mosquito vectors.⁽¹⁵⁾ *B. pahangi* dose not infect man naturally, although its experimental transmission to man was documented by Edeson and coworkers.⁽¹⁵⁾ The clinical manifestation of the same tropical pulmonary eosinophilia syndrome were reported in a human volunteer experimentally exposed to *B. pahangi* . Mak and colleagues assumed that natural infection in man could exist but previously might confused with *B. malayi* when using routinely diagnosis because of the similarity of the microfilariae in standard Giemsa and Haematoxylin preparations.⁽⁸⁾ In case of the possible zoonostic implications of filariae, a reliable method for the specific identificaton would be advantage in any epidemiological and zoonotic studies.

1.10 Differentiation of *B. malayi* and *B. pahangi*

Various methods identifying the species of *Brugia* spp. have been described such as standard measuring techniques,⁽²⁹⁾ differences in the length of the Innenkorper,⁽³⁰⁾ and in sheath casting frequency,⁽³¹⁾ and morphological differences in rectal protrusions.⁽³²⁾ In 1995, Cheong and coworkers⁽³³⁾ attempted to separate these two species using vector susceptibility and more recently a histochemical method described by several groups of workers.⁽³⁴⁻³⁸⁾ All these techniques have their limitations and drawbacks.

Although examination of certain morphological characters of adult filariae is the most reliable method in differentiating the closely related species like *B. malayi* and *B. pahangi*, obtaining the adults for the study poses some difficulties. The susceptible mosquitoes have to be allowed to feed on an infected animal or human which has the microfilariae to be identified circulating in the blood. The third stage (infective) larvae obtained from the mosquitos 10-12 days after the infection have to be injected intraperitoneally into a gerbil (*Meriones unguiculatus*). It takes approximately 60 days for the larvae to grow the adult stage which can be removed from the peritoneal cavity of the animal for identification.⁽³⁹⁾ Moreover, the adult worms need to be fixed in hot 70% alcohol and cleared in glycerine before mounting in glycerine as a permanent hanging-drop preparation on a cavity separately slide for examination under a microscope. It is clearly seen that microfilariae are generally easier to obtain from man and animals than the adults.

The inner body, central body or Innenkorper⁽⁴⁰⁾ is well known in light microscope preparations of certain genera of microfilariae. Feng⁽⁴¹⁾ showed that the inner body of *Brugia* spp. occupied the position of the developing filarial larva and this observation has been confirmed by later studies on filarial development.⁽⁴²⁻⁴⁴⁾

The ability to distinguish between microfilariae of *B. malayi* and *B. pahangi* has a great epidemiological significance since it has been reported many studies that *B. pahangi* which is an animal parasite can be experimentally transmitted to man. It is shown in the present study that measurements of various parts of microfilariae cannot be used in differentiating the two species except the relative length of the Innenkorper to the overall length of the microfilaria and the absolute length of the Innenkorper. However, there is an overlap between the longest measurement of the Innenkorper of *B. malayi* microfilariae and the shortest measurement of that *B. pahangi* microfilariae which cannot confirm the result reported by Sivanandam and Fredericks.⁽³⁰⁾ Therefore,

measurement of the Innenkorper should not be used as a criterion in differentiating the two species. Moreover, it is not practical for their use in blood surveys which involve examination of hundreds of slides at a time.

In another attempt to differentiate the two species of *Brugia* spp. by staining for the acid phosphatase activity distribution in the microfilariae, the result fails to show the uniqueness of the characteristic pattern of the enzyme activity distribution in microfilariae of each species although the microfilariae are obtained from the same experimental cats with known infections. This method is chosen for trial because the difference can be observed directly under the microscope without involving any measurement but the result is rather disappointing. However, results reported by many workers did not mention whether the characteristic pattern of enzyme activity distribution was the same in all microfilariae of one species.^(34-38,45) If this method has to be used for species identification of *Brugia* spp. using the above characteristic, it is suggested that all microfilariae present in the slide preparation must be examined for the majority of worms which have the same characters. However, it is not quite suitable for epidemiological surveys as the blood films might contain microfilariae of more than one species. The method has the disadvantage of involving the steps of refrigeration (4 °C) and incubation (37 °C) as described earlier which makes it inconvenient for use in routine examination of blood samples. Besides, the blood films have to be processed soon after drying for 30 minutes. If the slides have to be transported for staining in the laboratory, best results could be obtained only if they are stored in plastic box at -20 °C.

Giemsa staining is standard method which does not include the dehaemoglobulinization of the blood films followed by fixation with absolute methanol before staining. This method is very difficult to outline the Innenkorper for measurement and to observe the density of nuclei in the structure. It is suggested that for more accurate identification of the species, staining the blood films with the method involving the use of Haematoxylin and Eosin or Giemsa (special method for staining Innenkorper) should be selected. However, although staining with Haematoxylin and Eosin give a clearer view of the whole structure of the microfilariae with a clean background, the method is more time- consuming and therefore is less practical for use in the field than staining with Giemsa (method for staining Innenkorper). When Giemsa stain is used, it is necessary to do a trial stain for each new batch of stain to find out the optimum dilution which gives good staining results.⁽⁸⁸⁾

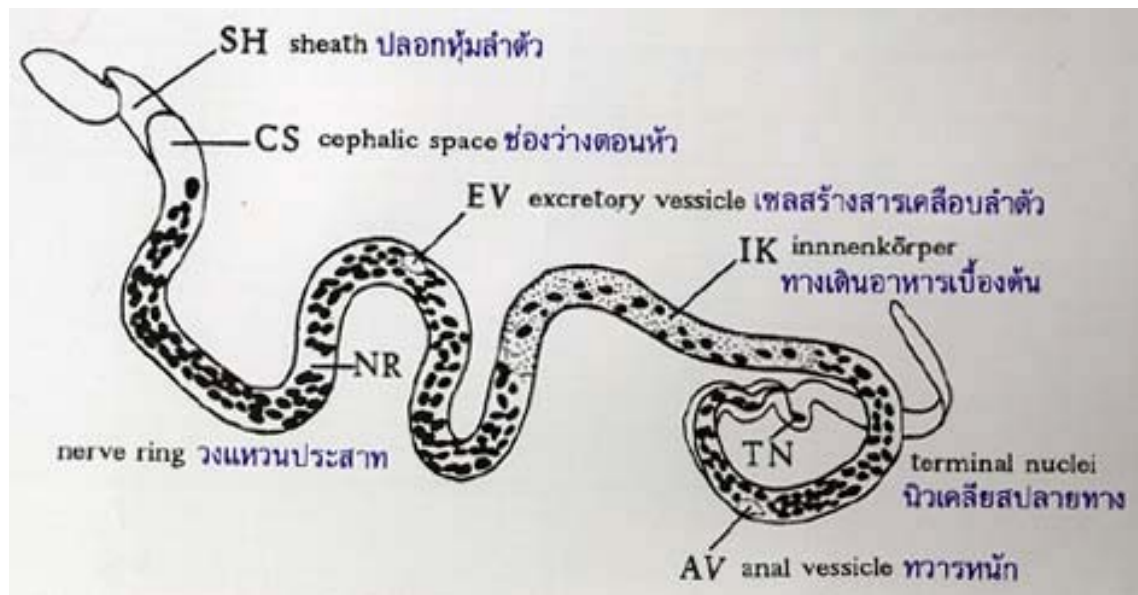


Figure 7 Microfilaria of *B. malayi*



Figure 8 Geimsa stain of blood smear, A *Microfilaria* of *B. malayi* in human (left) and of *B. pahangi* in cat (right).⁽⁴⁷⁾

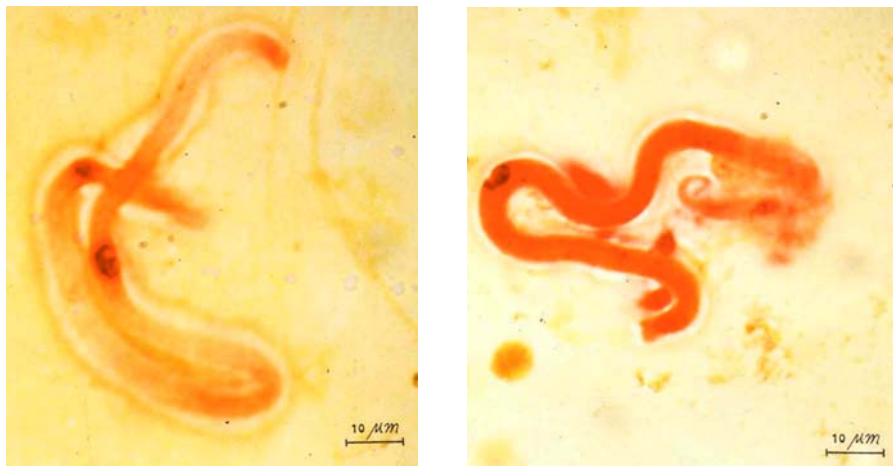


Figure 9 Acid phosphatase stain of blood smear, A Microfilaria of *B. malayi* in human (left) and of *B. pahangi* in cat (right).⁽⁴⁷⁾

Table 1 Comparison of the size and the dimension (in μm) of surface structures of microfilaria of *B. malayi* and *B. pahangi*.⁽⁴⁸⁻⁵⁰⁾

	<i>B. malayi</i>	<i>B. pahangi</i>
1) Body length (mm)	210 $\pm$ 15	218 $\pm$ 32
2) Body width (μm)	3.88 $\pm$ 0.68	3.59 $\pm$ 0.46
3) Mouth diameter (μm)	0.26	0.26
4) Hook length (μm)	0.76	0.46
5) Annulation width (at the middle region) (μm)	0.34 $\pm$ 0.04	0.36 $\pm$ 0.02
6) Tail length (μm)	5.41 $\pm$ 1.34	3.06 $\pm$ 0.51
7) Morphology of sheath (μm)	translucent and rather smooth	granular sheath

The microfilarial stage of *B. malayi* and *B. pahangi* are engulfed with sheath. The sheath could be used to differentiate species since the sheath of *B. pahangi* was granular; whereas, that of *B. malayi* is translucent and rather smooth. The unsheathed microfilaria of both species shared common pattern of the cuticular surface structure. The anterior end carries the cephalic cap with the hook, mouth, amphidial openings, and spines. The cuticle shows annulations.

At the third-stage larve, the anterior end of *B. malayi*, *B. pahangi* and *W. bancrofti* shows two circles of four cephalic papillae around the mouth and two amphidial opening lined at the inner circle. The anal opening is situated at posterior region. The cuticle is transverse annulations. The posterior end has two ventrolateral papillae and one dorsoterminal papillae. The ventrolateral papillae in *Brugia* has an indentation around its base while this indentation is absent in *Wuchereria*, and that it is wider in *B. malayi* than in *B. pahangi*. Futhermore, the ventrolateral papillae of *Brugia* is round-shape and those of *B. malayi* are more protruded and bigger than that of *B. pahangi*, while the shape of these papillae in *W. bancrofti* are bubble-like. Ribbons of longitudinal folds at the surface annulations are found at the entire body surface of *W. bancrofti*, while they are present at some part of the surface of *Brugia*. Besides, a small papilliform process at the left side of posterior region is only found in third stage larva of *Brugia* and is absent in *W. bancrofti*.

In the adult of *B. malayi* and *B. pahangi*, the mouth, amphidial openings and cephalic papillae are still present. The vulva and the anus are found at the anterior and posterior parts of female worm, respectively. The small round tubercles are found in both sexes but they are prominent at the posterior region of the female worm. Ribbons of short longitudinal ridges of each annulation on ventral aspect of the posterior region are observed only in male worm. Indentification of different species of adult male worm is based on the appearance of long copulatory spicules, in which *B. malayi* spicule has spatulated tip; whereas, that of *B. pahangi* had tapered cylindrical tip. In female adult worms, the tubercles at the posterior region can be used for differentiation of *Brugia* species. The size of the tubercles in the vicinity of the anus of *B. malayi* are larger than that of *B. pahangi* .

The scanning electron microscopic study gives more valuable informations about the structural differentiation among the three stages: microfilaria, third-stage larva and adult of *B. malayi* and *B. pahangi*. Therefore, this method might be utilized for precisely characterization of species. The life cycles of human filariae and animal filariae are

known to be potentially zoonotic, especially in the sympatric area that is more than one species occur in many of the same hosts.

In addition, Difference of surface features in microfilaria, third stage larva and adult filarial worms can also be used as diagnostic characteristics.

1.11 Molecular phylogenetic studies

Recently, molecular techniques such as DNA (deoxyribonucleic acid) and protein sequencing have been successfully for construction of phylogenetic tree of life that allows assessment of phylogenetic used relationships among animal taxa. Most common, DNA sequence data of highly conserved genes, for example genes coding for ribosomal RNA (rRNA), are used in the studies.

During the passed three decades, the field of systematic biology has undergone several simultaneous revolutions. The three most significant changes have been in the development and refinement of data analysis bring on by the development of computers, and the introduction of molecular analysis. Although molecular biology is not a panacea for systematic, molecular systematists can approach many problems previously considered intractable by morphologists.⁽⁵¹⁻⁵³⁾ For instance, there are very few homologous morphological characters that can be compared among all living organisms. In contrast, a number of genes with fundamental biochemical functions are found in all species and they can be sequenced, aligned and analysed to study phlogenetic relationships among morphologically indistinguishable but otherwise distinct species.⁽⁵⁴⁾ This entire of applications, from the origin of life to relatively recent evolutionary events, has been addressed by studying the ribosomal RNA (rRNA) genes and their associated spacer regions, collectively called ribosomal DNA.^(55,56) Some properties of rRNA are so sufficiently distinct from other molecular sequences that a number of special considerations are necessary or desirable when considering the use of rRNA in systematic studies.

Several distinct rRNAs combine with ribosomal proteins to form ribosomes, the organelles that direct protein synthesis from messenger RNA. Ribosomes are composed of two major subunits, each with distinct rRNAs and ribosomal proteins. The small ribosomal subunit contains a single type of rRNA and about 20 proteins in prokaryotes and 30 proteins in eukaryotes. The large ribosomal subunit contains two (prokaryotes) or three (eukaryotes) rRNAs and about 30 (prokaryotes) to 40 (eukaryotes) ribosomal proteins. A single copy of each of the proteins is present per ribosome. Because protein

synthesis is a prerequisite for life, ribosomes (and hence rRNAs) are universally present in living systems.

The rDNA array of a eukaryotes nuclear genome typically consists of several hundred tendemly repeated copies of the transcription unit and nontranscribed spacer shown in Figure 10.⁽⁵⁷⁾ The number of copies of the this transcription unit; however, may be as few as one,⁽⁵⁸⁾ or as many as several thousands.⁽⁵⁹⁾ In prokaryotes, there are one to several copies of the rRNA genes and they may be either organized in a single operon (in which they are usually separated by tRNA genes) or dispersed throughout the genome.⁽⁶⁰⁻⁶²⁾ There are usually three or four distinct nonorganelar rRNAs in a species^(57,63) which are often characterized in sedimentation velocity units "S" (Svedburg). Firstly, a large subunit rRNA, which ranges in size from 16S [approximately 1,500 nucleotides in most prokaryote genomes, and up to 28S (over 4,000 nt) in eukaryote nuclear genomes.^(64,65) Secondly, a 5.8S rRNA (~ 160 nt) in eukaryotes, which is derives from a part of the 23S rRNA of prokaryotes⁽⁶⁶⁻⁶⁹⁾ and is still structurally, functionally and closely related to the large rRNA. Thirdly, a small subunit rRNA, which range from 12S (~900 nt) in vertebrate mitochondria to 6S (~1500 nt) in prokaryotes and up to 18S (~1800 nt) in eukaryotes.⁽⁷⁰⁻⁷²⁾ Lastly, a 5S rRNA (~120 nt), the gene of which is closely associated with the other rRNA genes in many prokaryotes but is found elsewhere in the nuclear genome of most eukaryotes.⁽⁷³⁾ Although these are the most common themes, numerous variations have been discovered.^(74,75) The large and small subunit rRNA genes of chloroplasts and mitochondria are more similar to those of their eukaryotes hosts.⁽⁷⁶⁻⁸²⁾

In eukaryote, two internal transcribed spacers(ITS-1 and ITS-2) separate the 18S, 5.8S and 28S gene (or their homologs) and an external transcribed spacer (ETS) is located upstream of the 18S gene (Figure). The transcribed spacers contain signals for processing the rRNA transcript. Adjacent copies of the rDNA repeat unit are separated by a nontranscribed spacers (NTS), also called an intergenic spacers by some workers. This region contains subrepeating elements that serve as enhancers of trancription.⁽⁸³⁻⁸⁷⁾

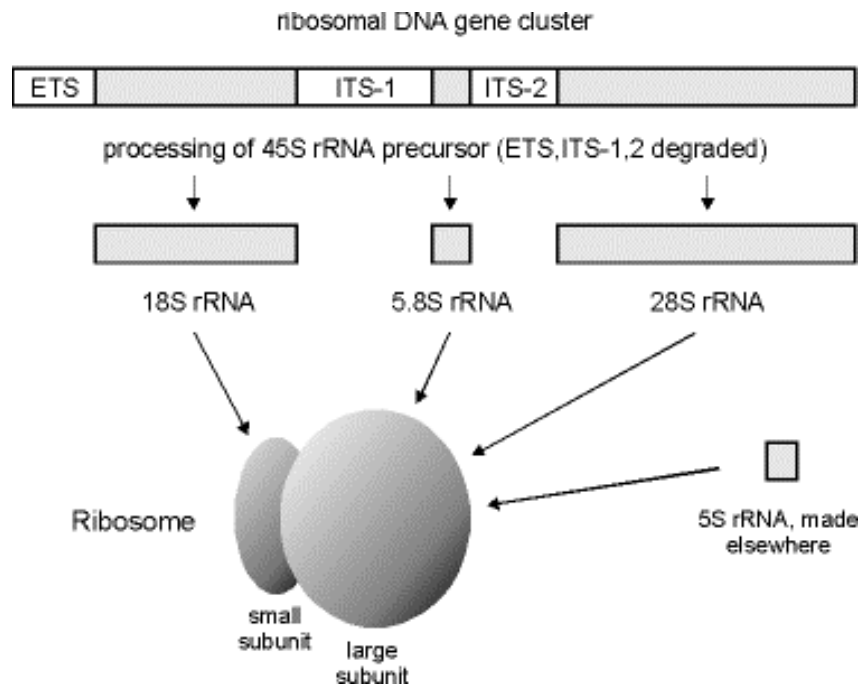


Figure 10 Structure of nuclear ribosomal DNA in eukaryotes.

1.12 Structure and evolution of rRNA: Implication for phylogenetic analysis

One of the reasons why rDNA is useful for phylogenetic analysis is that different regions of the rDNA repeat unit evolve at very different rates. Thus, regions of rDNA arrays that are particularly likely to yield informative data for almost any systematic question can be selected for analysis. In addition, the islands of highly conserved sequences within most rRNA genes are very useful for constructing 'universal' primers that can be used for sequencing either rRNA or rDNA from many species, for amplifying regions of interest by use of the PCR, or for use as probes in restriction enzyme analyses.^(54,88,89) Although intraindividual length heterogeneity causes problems for direct sequencing of amplified DNA in some regions of the repeat, the amplified DNA can be cloned and sequenced relatively easily.

The process of choosing a region that is likely to be appropriate for a particular systematic question is perhaps the most critical step in any phylogenetic analysis. If the region chosen is evolutionarily too conserved (i.e., the sequences are nearly the same in all study taxa), then considerable time will be wasted collection invariant data. On the

other hand, regions that differ among taxa to the extent that alignments are difficult or questionable also are unlikely to yield robust phylogenies.⁽⁹⁰⁾ There are two reasons that highly divergent sequences yield less robust results: (1) the level of homoplasy (parallelisms, convergences and reversals) increases as the probability for change at each position increases and, (2) the number of possible alignment that are nearly equally good becomes prohibitively large. Since alignment (positional homologs is an assumption of the phylogenetic analysis, it is best to delete from analyses any regions where the alignment is questionable.⁽⁹⁰⁾

The most studied rRNA is the small subunit nuclear gene, 16S-18S rRNA. This gene has been studied most extensively because it is among the slowest evolving sequence found throughout living organisms, and has therefore been very useful for examining ancient evolutionary events. In addition, the slow rate of change permits the construction of many nearly universal primers, which facilitates sequencing efforts from groups that have not been studied previously. Much of the gene is useful for comparisons among phyla of eukaryotes, however, and some comparisons between eukaryotes and prokaryotes are possible. It has been most successfully for reconstruction phylogenetic events from the Precambrian.

The large subunit (23S-28S) nuclear rRNA gene is large and shows more variation in rates of evolution of its different domains than does the small subunit. Although ancient comparisons are also possible with this gene,⁽⁹¹⁻⁹³⁾ it has primarily been used to examine evolutionary events through the Paleozoic and Mesozoic.⁽⁹⁴⁻⁹⁹⁾ The large subunit rRNA gene has many divergent domains or expansion segments.⁽¹⁰⁰⁾ Therefore, the size of the gene varies considerably among phyla.⁽⁶⁴⁾ These divergent domains are useful for relative reconstruction. The recent for study must be chosen carefully if the taxa have recently diverged.

The 5.8S rRNA gene of eukaryotes (and the corresponding region of the large subunit gene of prokaryotes) is similar to the small subunit gene in its useful phylogenetic range, although the shortness of the sequence limits its effectiveness in inferring phylogeny across great time scales. It shows very little variation in comparisons of taxa that is diverged after the Paleozoic.⁽¹⁰¹⁾ The 5S gene shows similar levels of variation, but it is even shorter than the 5.8S sequence.⁽¹⁰²⁾ The shortness of the sequence greatly restricts its phylogenetic usefulness.^(103,104)

The mitochondrial rRNA gene evolves much more rapidly than the nuclear rRNA genes, and they can be used for most Cenozoic comparisons. They are easily amplified through use of the PCR.^(88,105)

The spacer regions of rDNA arrays have been used less frequently for phylogenetic studies,⁽¹⁰⁶⁻¹¹⁰⁾ except in restriction analyses of entire rDNA arrays.^(70,111-119) These studies have shown that the spacer regions can be used to infer phylogeny among closely related taxa (taxa that have diverged within the last 50 million years). In addition, variation in the spacer regions has been used to identify species or strains, to study hybridization, and as makers in population genetic studies.^(29,116,120-125) Among the spacers, the NTS evolves most rapidly,⁽¹²⁶⁾ and the transcribed spacers are somewhat more conserved.⁽¹²⁷⁻¹²⁹⁾ Amplification of the two internal transcribed spacers via the PCR is facilitated by conserved flanking regions of the 18S, 5.8S and 28S genes. Hence the use of these spacers in studies involving closely related species is increasing.

This study has focused on the genetic diversity of *Brugian filaria* in cat reservoirs using phylogenetic tree analysis based on 18S rDNA and ITS genes. The data are useful for differentiation and identification of within the *Brugia* spp. as well as epidemiological studies, the control and eradication of the parasite.

CHAPTER III

MATERIALS AND METHODS

1. Blood Samples

Blood samples of infected cats containing microfilaria of *Brugia* spp. were collected from endemic areas of Thailand, Lad Krabang district of Bangkok and Narathiwat. The samples were previously screened for *Brugia* spp. by using the traditional blood smear technique before undergoing the parasite isolation.

2. Isolation of parasites

Five milliliters of microfilaria infected blood were taken from host and transferred to a test tube containing 7 mg/ml of EDTA as an anticoagulant agent. The blood was diluted with equal volume of phosphate buffered saline, pH 7.0 (PBS; 0.137 M NaCl, 10 mM Na₂HPO₄, 3.2 mM KH₂PO₄) and filtered through a 5- μ m polycarbonate membrane (Minipore). Microfilariae were then resuspended in PBS and centrifuged at 5,000 rpm for 10 mins at 4 °C. The pellet of microfilariae was washed with PBS for three times prior to storage at -70 °C until use.

3. Isolation of genomic DNA

The genomic DNA was extracted from filarial parasites by using genomic DNA Purification Kit (Gentra). The procedure of isolation was performed according to the instruction manual provided by the company. The microfilaria pellet was digested in 300 μ l of Cell Lysis Solution (0.01 M Tris-2%, SDS-0.01 M, EDTA pH 8) and 1.5 μ l of Proteinase K Solution (200 mg/ml) at 55 °C for 4-6 hrs. After that, the lysate was further digested by the addition of 0.12 units of RNase A Solution (1 mg/ml in 5 mM Tris-HCl, pH 8.0) and incubated at 37 °C for 15-60 mins. A 100 μ l of Protein Precipitation Solution (3 M ammonium acetate pH 7.4) was added to the cell lysate, quickly spun at high speed for 20 secs and centrifuged at 13,000 rpm for 3 mins. Supernatant containing DNA was transferred to a new tube, precipitated by the addition of 300 μ l of 100% isopropanol, and centrifuged at 13,000 rpm for 3 mins. The supernatant was removed and DNA pellet was washed once with 300 μ l of 70% ethanol. The

sample was mixed and centrifuged at 13,000 rpm for 3 mins. DNA pellet was dried (air-dry) for 10 mins, dissolved in 20 µl of DNA Hydration Solution (TE; 0.01 M Tris-0.001 M, EDTA pH 7.4) and incubated at 65 °C for 60 mins. The genomic DNA of parasites were stored at 4 °C until use. DNA concentration was determined by using UV spectrophotometer and the absorbance was measured at 260 nm. Molar extinction of DNA was calculated as; 1 O.D. at 260 nm = DNA concentration of 50 ng/ml.

4. Primers

The sets of primer were used for amplification of the gene encoding for 18S, ITS1 and ITS2 from *Brugia* spp. The primers were designed based on the nucleotide sequence comparison among 18S, ITS1 and ITS2 genes of *Brugia* spp.

5. PCR amplification of 18S rDNA, ITS1, and ITS2 genes

5.1 PCR amplifications of partial 18S rDNA gene of purified parasites DNA were performed using specific primers namely Bmsr /F and Bmsr/R. (Table 2)

Table 2. Nucleotide sequences of specific primers, Bmsr/F and Bmsr/R.

Primers	Nucleotide sequences	Tm
Forward primer(Bmsr/F)	5'...AAT ACA TGC ACC AAA GCT CCG A ... 3'	69 °C
Reverse primer(Bmsr/R)	5'...CCT TCC GCA GGT TCA CCT ACG ... 3'	71 °C

$$T_m = 59.9 + 41[\%GC] - [675/\text{Primer Length}]$$

$$\%GC = \frac{[\#G+\#C+\#S+E+O+0.5(\#N+\#X+\#M+\#Y+\#K+\#R)+0.6(\#B+\#V)+0.33(\#H+\#D)]}{\text{Total number of all bases}}$$

All reactions were manipulated in 25 µl volume containing 50 ng of genomic DNA in 10x PCR buffer (200 mM Tris-HCl (pH 8.4), 500 mM KCl), 1 µM each of primers, 100 µM each of dATP, dTTP, dCTP and dGTP, 1.5 mM MgCl₂ and 1.5 units of *Taq* DNA polymerase (GIBCOBRL[®]). Sterile distilled water was added to adjust volume to 25 µl. PCR was performed using DNA thermal cycler (MJ Research PTC-200 Peltier thermal cycler) for 30 cycles. Each cycle consisted of denaturation at 94 °C for 1 min, annealing at 65 °C for 1 min and extension at 72 °C for 1 min. The PCR products were analyzed by electrophoresis on 1.5 % agarose gel at 110 Volts for approximately 30 mins prior to ethidium bromide staining and observation under ultraviolet light.

5.2 PCR amplification of ITS1 gene from purified parasite DNA was performed by using specific primers, ITS1F and ITS1R. (Table 3)

Table 3. Nucleotide sequences of specific primers, ITS1F and ITS1R.

Primers	Nucleotide sequences	T _m
Forward primer (ITS1F)	5'...GGT GAA CCT GCG GAA GGA TC... 3'	75°C
Reverse primer (ITS1R)	5'...AAC CCA ATG GTG CAA TGT GC... 3'	73°C

$$T_m = 59.9 + 41[\%GC] - [675/\text{Primer Length}]$$

$$\%GC = \frac{[\#G+\#C+\#S+\#E+\#O+0.5(\#N+\#X+\#M+\#Y+\#K+\#R)+0.6(\#B+\#V)+0.33(\#H+\#D)]}{\text{Total number of all bases}}$$

All reactions were manipulated in 25 µl volume containing 50 ng of genomic DNA in 10x PCR buffer (200 mM Tris-HCl (pH 8.4), 500 mM KCl), 1 µM each of primers, 100 µM each of dATP, dTTP, dCTP and dGTP, 1.5 mM MgCl₂ and 1.5 units of *Taq* DNA polymerase

(GIBCOBRL[®]). Sterile distilled water was added to adjust volume to 25 μ l. PCR was performed by using DNA thermal cycler (MJ Research PTC-200 Peltier thermal cycler) for 30 cycles. Each cycle consisted of denaturation at 94 $^{\circ}$ C for 1 min, annealing at 65 $^{\circ}$ C for 1 min and extension at 72 $^{\circ}$ C for 1 min. The PCR products were analyzed by electrophoresis on 1.5 % agarose gel at 110 Volts for approximately 30 mins prior to ethidium bromide staining and observation under ultraviolet light.

5.3 PCR amplifications of ITS2 gene of purified parasites DNA were performed using specific primers namely ITS2F and ITS2R. (Table 4)

Table 4. Nucleotide sequences of specific primers, ITS2F and ITS2R.

Primers	Nucleotide sequences	Tm
Forward primer (ITS2F)	5'...GGT TGA TTC CCG ATG GTA ... 3'	43 $^{\circ}$ C
Reverse primer (ITS2R)	5'...AGC GGG TAA TCA CGA CTG ... 3'	45 $^{\circ}$ C

$$T_m = 59.9 + 41[\%GC] - [675/\text{Primer Length}]$$

$$\%GC = \frac{[\#G + \#C + \#S + \#E + \#O + 0.5(\#N + \#X + \#M + \#Y + \#K + \#R) + 0.6(\#B + \#V) + 0.33(\#H + \#D)]}{\text{Total number of all bases}}$$

All reactions were manipulated in 25 μ l volume containing 50 ng of genomic DNA in 10x PCR buffer (200 mM Tris-HCl (pH 8.4), 500 mM KCl), 1 μ M each of primers, 100 μ M each of dATP, dTTP, dCTP and dGTP, 1.5 mM MgCl₂ and 1.5 units of *Taq* DNA polymerase (GIBCOBRL[®]). Sterile distilled water was added to adjust volume to 25 μ l. PCR was performed by using DNA thermal cycler (MJ Research PTC-200 Peltier thermal cycler) for 30 cycles. Each cycle consisted of denaturation at 94 $^{\circ}$ C for 1 min, annealing at 41 $^{\circ}$ C for 1 min and extension at 72 $^{\circ}$ C for 1 min. The PCR products were analyzed by electrophoresis on 1.5

% agarose gel at 110 Volts for approximately 30 mins prior to ethidium bromide staining and observation under ultraviolet light.

6. Cloning of the PCR fragment

6.1 Purification of PCR fragment

The PCR fragment was eluted from the gel and purified using QIAGEN[®] Purification system prior to cloning. The procedure of purification was performed according to the instruction manual provided by the company. The DNA fragment was excised from the agarose gel with a clean, sharp scalpel. The gel slice was weighed in a colorless tube and added 3 volumes of Buffer QG (4 M guanidine thiocyanate pH 7.5) to 1 volume of gel. Then, the gel slice was incubated at 50 °C for 10 mins until the gel slice was completely dissolved. After that, the color of the mixture was checked and it should be yellow. After that, 100-200 µl of isopropanol was added to the reaction and mixed. The mixture was placed into a QIAquick spin column, centrifuged at 10,000 rpm for 1 min, discarded flow-through and placed QIAquick column back in the same collection tube. Then, the DNA bound QIAquick column was washed with 0.5 ml of Buffer QG and centrifuged at 10,000 rpm for 1 min followed by washing with 0.75 ml of Buffer PE (3 M sodium acetate in 80% ethanol) to QIAquick column and centrifuged at 10,000 rpm for 1 min. The DNA bound QIAquick column was centrifuged again at 10,000 rpm for 1 min and placed QIAquick column into a clean 1.5 ml microcentrifuge tube. The DNA was eluted with 50 µl of Buffer EB (10 mM Tris-Cl, pH 8.5). The column was centrifuged at 10,000 rpm for 2 mins.

6.2 Ligation of PCR fragment and vector

The purified 200 ng of PCR fragment was further ligated to the pGEM[®]-T Easy vector using protocol of pGEM[®]-T Easy Vector Systems (Invitrogen, Promega). The reaction was consisted of 4 µl of PCR product, 1 µl of 2X Rapid Ligation Buffer (60 mM Tris-HCl, pH 7.8, 20 mM MgCl₂, 20 mM DTT, 2 mM ATP 10% PEG), 1 µl of the pGEM[®]-T Easy vector and 1 µl of T4 DNA Ligase (3 Unit final concentration). The reaction was mixed, and incubated for 12-14 hrs at 4 °C.

6.3 Preparation of ultra-competent *E. coli* cells for transformation

The competent *E. coli* cells were prepared for transformation. Single colony of selected *E. coli* strain (DH5 α) was cultured in 5 ml of LB-broth and incubated for 12-14 hrs at 37 °C with moderate agitation (~250 rpm). Then, 1 ml of the overnight culture was added to 150 ml of LB-broth and grown at 37°C with moderate agitation until lag phase. (the OD₆₀₀ nm $\approx$ 0.5) Subsequently, the culture was placed on ice for 10 mins and centrifuged at 5,000 rpm for 10 mins at 4°C. The bacteria pellet was washed twice in 10 ml and 5 ml of sterile 10% glycerol and, centrifuged 5,000 rpm at 4°C for 10 mins. Finally, the pellet was resuspended in 0.02-0.2 ml of cold 10% glycerol, and aliquots of 40 μ l was transferred to a new eppendorf tubes for further transformation or kept at -70°C until use.

6.4 Transformation by electroporation

Electroporation transformation was performed using BioRad MicroPulser (BIO-RAD MicroPulserTM) according to the protocols provided by the company. BioRad MicroPulser was set to "Ec 2" for 2 mm cuvettes (2.50kV). Four microliters of the ligation product were added to the competent cells. Transformation reaction was transferred to a chilled electroporation cuvette, and immediately pulsed in the electroporator. Then, 250 μ l of LB broth was added to the reaction. The mixture was transferred into 1.5 ml eppendorf tubes and incubated at 37 °C for 45 mins.

After that, 100 to 150 μ l of the mixture was spread on the LB-ampicillin agar plates containing X-gal and IPTG (40 μ l of 20 mg/ml X-gal and 10 μ l of 200 mg/ml IPTG were spread on the LB-ampicillin agar plates 30 minutes prior to plating the transformations). The plates were incubated for 17 hrs at 37 °C. Colonies containing plasmids without inserts were blue color. Colonies containing plasmids with inserts remained white and were selected for further examination by transferring to a new LB–ampicillin agar plate containing X-gal and IPTG for verification of the phenotype.

7. Recombinant DNA purification

White colonies containing the recombinant DNAs were selected and cultured in 5 ml of LB media in the presence of 100 μ g/ml of ampicillin for 24 hrs. The recombinant DNAs were purified using QIAGEN[®] QIAprep Spin Miniprep Kit Protocol. The procedure of extraction was

performed according to the instruction manual provided by the company. The *E. coli* cells containing recombinant DNA were grown in 5 ml of LB broth for 12-14 hrs at 37 °C. Each cultures was transferred to a microcentrifuge tube and centrifuged for 1 min at 5,000 rpm to harvest the cells using an eppendorf microcentrifuge. The supernatant was removed and each cell pellet was resuspended by spinning in 250 µl of "Buffer P1" (2 mg/ml lysozyme, 50 mM glucose, 10 mM CDTA (cyclohexane diamine tetraacetate), 25 mM Tris-HCl, pH 8.0). After resuspension of the pellet, 250 µl of Buffer P2 (0.2 N NaOH, 1% SDS (sodium dodecyl sulfate)) was added to the mixture and the tube was gently inverted for 4-6 times. Then, 350 µl of Buffer N3 (3 M NaOAc (sodium acetate), pH 4.8) was added and the solution was mixed gently but thoroughly, immediately after addition of Buffer N3. All reaction were centrifuged at 13,000 rpm for 10 mins. Then, the supernatant was applied from top step into the QIAprep Spin Column, centrifuged at 10,000 rpm for 1 min. After that, QIAprep Spin Column was washed by 0.5 ml of Buffer PB (contains guanidine hydrochloride and isopropanol) and followed by centrifugation at 10,000 rpm for 1 min. Subsequently, QIAprep Spin Column was washed with 0.75 ml of Buffer PE (3 M sodium acetate in 80% ethanol and centrifuged at 10,000 rpm for 1 min. The flow-through was discarded and the column was placed for centrifugation at 10,000 rpm for 1 min. The QIAprep column was transferred to a clean 1.5 ml microcentrifuge tube and DNA was eluted with 20 µl of Buffer EB (10 mM Tris-Cl, pH 8.5) prior to centrifugation at 10,000 rpm for 2 mins.

8. Analysis of inserted 18S rDNA, ITS1, and ITS2 genes

The purified recombinant DNAs were tested by PCR amplification and restriction enzyme digestion. The PCR reaction was performed according to the methods described above. Each of restriction enzyme digestions was manipulated in 20 µl volume containing 100-200 ng of the purified recombinant DNA, 10x buffer *EcoRI* (50 mM Tris-HCl (pH 7.5), 10 mM MgCl₂, 100 mM NaCl, 0.02% Triton X-100, 0.1 mg/ml BSA.) and 10 unit of *EcoRI* (GIBCOBRL[®]). The reaction was subsequently incubated at 37 °C for 4 hrs and followed by heating at 68 °C for 10 mins. The PCR product or the digested product was analyzed by electrophoresis on 1.2% agarose gel at 110 Volts prior to ethidium bromide staining and observation under ultraviolet light.

9. DNA sequencing of 18S rDNA, ITS1, and ITS2 genes

The DNA sequence analysis was performed by BSU (Bioservice Unit), National Science and Technology Development Agency (NSTDA), by using Big Dye Terminator Cycle Sequencing procedure and analyzed by using ABI PRISM 3100 (Perkin Elmer). The PCR condition for DNA sequencing was accomplished by using 25 cycles of denaturation at 95 °C for 5 secs, annealing at 50 °C for 4 secs and extension at 60 °C for 4 mins. The nucleotide sequencing data was analyzed by using software of ABI PRISM Model 3100 version 3.7 and analysis procedure were accomplished according to the manual instruction provided from company.

10. Analysis of the nucleotide sequences of 18S rDNA, ITS1, and ITS2 genes

The partial and complete nucleotide sequences of 18S rDNA, ITS1 and ITS2 were analyzed using BLAST program from <http://www.ncbi.nlm.gov/BLAST>. The nucleotide sequences of interested gene fragments were compared to those of various organisms that have been previously submitted in GenBank. The percentage of nucleotide and amino acid sequence homology in comparison to various organisms were reported. All sequence data were analyzed using Clustal W sequence alignment program for The European Molecular Biology Laboratory (EMBL, U.K.) at <http://www.ebi.ac.uk/>. All alignment data were inspected with sequence data in GenBank by using PAUP program version 4.0 for construction of evolutionary trees of 18S rDNA, ITS1, and ITS2.

Table 5. Nucleotide sequences of primers for PCR amplification of 18S rDNA, ITS1, and ITS2 gene.

Primers	Names	Nucleotide sequences (5' → 3')	Tm (°C)
Forward primers	Bmsr/F	...AAT ACA TGC ACC AAA GCT CCG A ...	69 °C
	ITS1F	...GGT GAA CCT GCG GAA GGA TC...	75 °C
	ITS2F	...GGT TGA TTC CCG ATG GTA ...	43 °C
Reverse primers	Bmsr/R	...CCT TCC GCA GGT TCA CCT ACG ...	71 °C
	ITS1R	...AAC CCA ATG GTG CAA TGT GC...	73 °C
	ITS2R	...AGC GGG TAA TCA CGA CTG ...	45 °C

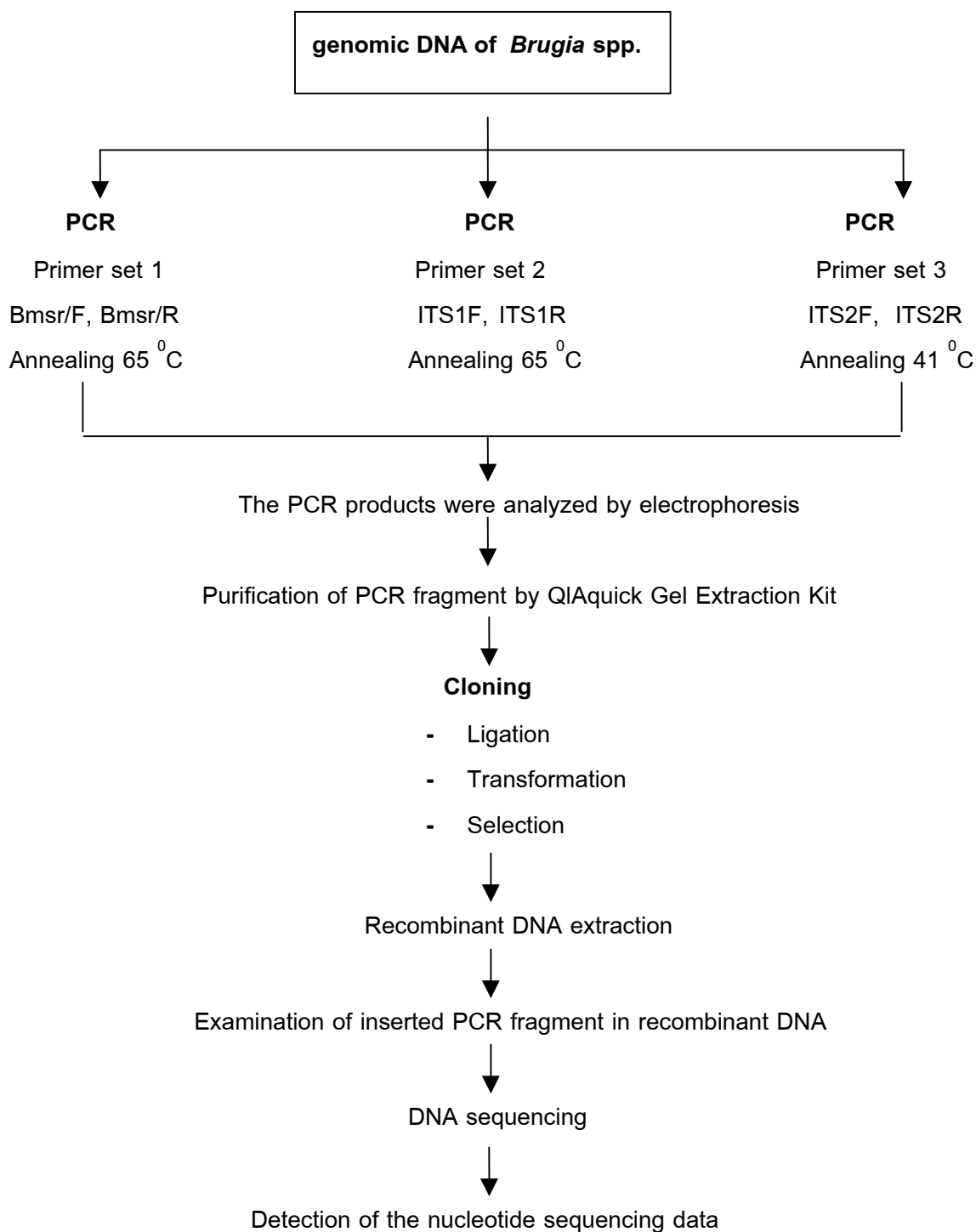


Figure 11. Steps for achievement of complete 18S rDNA, ITS1 and ITS2 genes.

CHAPTER IV

RESULTS

1. *B. malayi* genomic DNA extraction

The genomic DNA of *B. malayi* was extracted from one sample as described in Materials and Methods 3. Agarose gel electrophoresis was used to determine genomic DNA before PCR amplification. A single band of high molecular weight DNA size more than 23 kb was observed after ethidium bromide staining as shown in Figure 12. The quantity and purity of the DNA were investigated by measurement of the absorbance at 260 nm and 280 nm and shown that they were 0.001 and 0.002 with the ratio of $A_{260}/A_{280} = 0.5$.

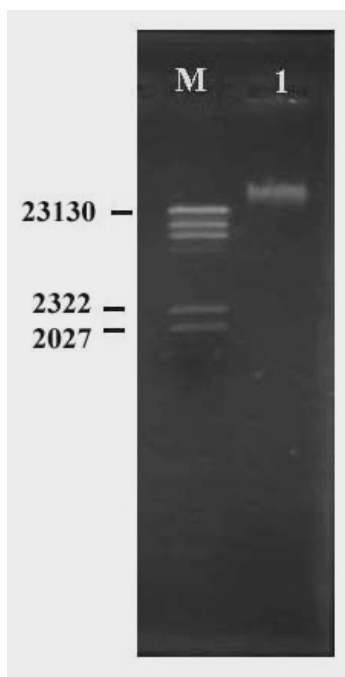


Figure 12 Electrophoresis profile of 50 ng *B. malayi* genomic DNA in 0.8% agarose gel.

Lane M: Lamda *Hind* III marker

Lane 1: 50 ng of *B. malayi* genomic DNA

2. PCR amplification and DNA sequencing of 18S rDNA

2.1 PCR amplification of 18S ribosomal DNA gene

The PCR amplification was performed and analyzed according to the Materials and Methods 5. Figure 13 showed that the PCR product of approximately 1,640 bp in size was observed when Bmsr/F and Bmsr/R were used as primers.

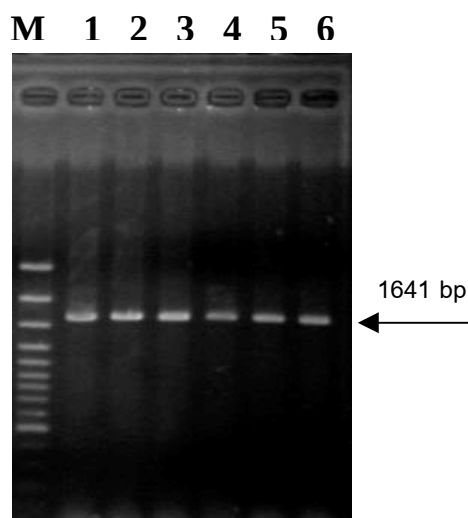


Figure 13 The PCR amplification profile of 18S rDNA from purified *Brugia* spp. DNA from cats in Narathiwat and Lad krabang. The PCR product of 1,641 bp in size was observed on 1.2% agarose gel electrophoresis by using Bmsr/F and Bmsr/R were used as primers.

Lane M = 100 bp DNA ladder marker

Lane 1 = PCR product of *Brugia* spp. from cat1

Lane 2 = PCR product of *Brugia* spp. from cat2

Lane 3 = PCR product of *Brugia* spp. from cat3

Lane 4 = PCR product of *Brugia* spp. from cat5

Lane 5 = PCR product of *Brugia* spp. from cat6

Lane 6 = PCR product of *Brugia* spp. from cat7

2.2 DNA sequencing of 18S rDNA

PCR products of 18S rDNA from PCR amplification were proceeded to cloning and DNA sequencing. Among 18S rDNA clones, 25 clones of them were randomly selected and recombinant DNA were extracted and purified prior to DNA sequencing (Table 6). The nucleotide sequence data of 18S rDNA were shown in Table 7 and 8, respectively.

Table 6 Summary of 25 clones selected from 18S rDNA library of feline *Brugia* spp.

Region1

Cat	clone
Cat 2	C6, C9
Cat 3	C15, C16, C18, C21
Cat 6	C25, C33, C35
Cat 7	C7

Region 2

Cat	clone
Cat 1	C1, C2, C3, C4, C20
Cat 2	C11, C13
Cat 3	C14
Cat 5	C22, C23
Cat 6	C24, C26, C32
Cat 7	C27, C29

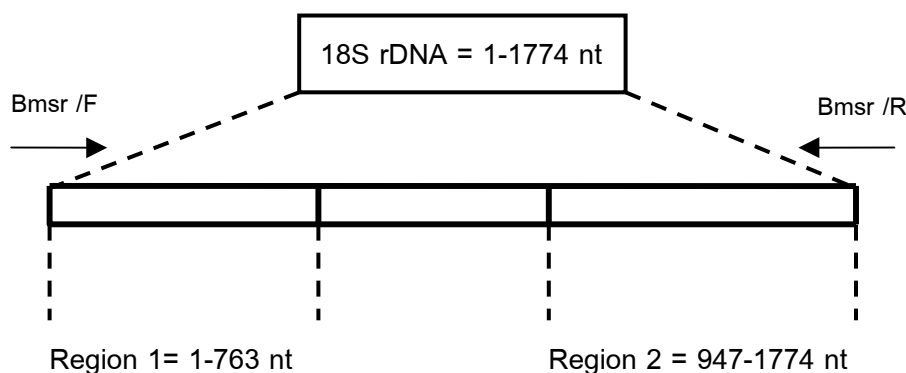


Table 7 Nucleotide sequence data of 18S rDNA of *Brugia* spp. from cat reservoirs. (Region 1)

C6 Cat2	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTAACCAATC GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGGTTATCGGAATGGG TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGATGGAATAATGAAAT GGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC GGGGGCATTTCGTATCGCTGCGTGAGAGGTGAAATTCTTGACC
C9 Cat2	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTAACCAATC GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGGTTATCGGAATGGG TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGATGGAATAATGAAAT AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC GGGGGCATTTCGTATCGCTGCGTGAGAGGTGAAATTCTTGACC

Table 7 (continued)

C15 Cat3	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTAACCAATC GGATTATTAATTTTAAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGGTTATCGGAATGGG TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT AGGATCTCGGTTCTATTTTGTGGTTCTCTGATCTGAGATAATGGTTAAGAGGGACGGAC GGGGGCATTTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC
C16 Cat3	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTAACCAATC GGATTATTAATTTTAAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCACAAATTACCCACTCTCAGAAT GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGGTTATCGGAATGGG TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGG AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC GGGGGCATTTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC
C18 Cat3	TATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTAACCAATCG GATTATTAATTTTAAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGTC TTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATGT GCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCTG AGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAATG AGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGGTTATCGGAATGGGT ACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCGG TAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGAT CTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTGC CAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGAA AAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAATA GGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTCAAGAGGGACGGACG GGGGCATTTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC

Table 7 (continued)

C21 Cat3	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTAACCAATC GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCACAATTACCCACTCTCAGAAT GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGGTTATCGGAATGGG TACAATTTAAACCTGTAAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGG AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC GGGGGCATTTCGTATCGCTGCGTGAGAGGTGAAATTCTTGACC
C25 Cat6	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTAACCAATC GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTCCGATGGTAGTTTATG TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGGTTATCGGAATGGG TACAATTTAAACCTGTAAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC GGGGGCATTTCGTATCGCTGCGTGAGAGGTGAAATTCTTGACC
C33 Cat6	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTAACCAATC GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGAT CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGGTTATCGGAATGGG TACAATTTAAACCTGTAAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC GGGGGCATTTCGTATCGCTGCGTGAGAGGTGAAATTCTTGACC

Table 7 (continued)

C35 Cat6	TAATACATGCACCAAAGCTCCGAATTTTTACGAGCGCATCTATTAGATTAACCAATCG GATTATTAATTTTAAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGTC TTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATGT GCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTCGACTCCGGAGAGGGAGCCTG AGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAATG AGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGGTTATCGGAATGGGT ACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCGG TAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGAT CTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTGC CAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGAA AAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAATA GGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGACG GGGGCATTTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC
C7 Cat7	TATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTAACCAATCG GATTATTAATTTTAAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGTC TTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATGT GCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTCGACTCCGGAGAGGGAGCCTG AGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAATG AGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGGTTATCGGAATGGGT ACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCGG TAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGAT CTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTGC CAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGAA AAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAATA GGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGACG GGGGCATTTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC

Table 8 Nucleotide sequence data of 18S rDNA of *Brugia* spp. from cat reservoirs. (Region 2)

C1 Cat1	GAACGAAAGTCAGAGGTTTCAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCGCTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCGGGGGAAGTATGGTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACCTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCCGGTGGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGGCT CTAGCCTACTAAATAGTTACTGGATAATTTTTATCGTCCAGACAACCTCTTAGAGGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTACCGAAAGGTATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCA ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAAACTGCTTTAATCGCAGTGCTTGAACC GGGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA
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Table 8 (continued)

C2 Cat1	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCGGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCGGGGGAAGTATGGTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGGTATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCA ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAACTGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA
C3 Cat1	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCGGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCGGGGGAAGTATGGTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGATATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCA ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAACTGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA
C4 Cat1	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCGGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCGGGGGAAGTATGGTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGATATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCA ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAACTGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA

Table 8 (continued)

C20 Cat1	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCGGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCGGGGGAAGTATGGTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGATATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCA ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAACTGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA
C11 Cat2	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCGGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCGGGGGAAGTATGGTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGATATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCCTAGTAAGTGTGAGTCATCGGCTCACGTTGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCA ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAGACTGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA
C13 Cat2	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCGGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCGGGGGAAGTATGGTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGATATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCA ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAAACCGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA

Table 8 (continued)

C14 Cat3	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCGGGGGAAGTATGGTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGGTATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCA ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAACTGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA
C22 Cat5	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCGGGGGAAGTATGGTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGGTATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCCTAGTAAGTGTGAGTCATCAGCTCACGTCGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCA ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAACTGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTTGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA
C23 Cat5	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCGGGGGAAGTATGGTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGGTATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCCTAGTAAGTGTGAGTCATCAGCTCACGTCGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCA ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAACTGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTTGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA

Table 8 (continued)

C24 Cat6	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCGGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCGGGGGAAGTATGGTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGAGAAATCAGCGTGCTGTAACCATTACCGAAAGGTATTGG TAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGA GGAATTCCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACA CACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAA TACCTTTCAAGGGTAGAGATTCTTTGGTGGAACTGCTTTAATCGCAGTGGCTTGAACCG GGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA
C26 Cat6	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCGGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCGGGGGAAGTATGGTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTACCGAAAGGTATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCA ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAACTGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA
C32 Cat6	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCGGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCGGGGGAAGTATGGTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGGCT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTACCGAAAGGTATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCA ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAACTGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA

Table 8 (continued)

C27 Cat7	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCCGTGCGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTACCGAAAGGTATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCA ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAACTGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA
C29 Cat7	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCCGTGCGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTATCGTCCAGACAACCTTCTTAGAGGGACAAG CGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGG GCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTACCGAAAGGTATTGG TAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGA GGAATTCCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACA CACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAA TACCTTTCAAGGGTAGAGATTCTTTGGTGGAACTGCTTTAATCGCAGTGGCTTGAACCG GGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA

2.3 Identification and analysis of nucleotide sequence data

BLAST program was used for the identification of *Brugia* spp. isolated from cat reservoirs in comparison to the previously reported data in GenBank. The nucleotide sequences revealed that the *Brugia* spp. from cats in Thailand were similar to *B. malayi*.

Clustal W was used for the nucleotide sequence alignment of 18S rDNA and compared to those of others filaria in GenBank (Table 9). Upon alignment, some nucleotide regions were deleted to generate the appropriate alignment and the sequences were manually corrected. The alignment of each region was shown in Table 10 and 11.

Table 9 GenBank accession numbers of 18S rDNA regions of *B. malayi* and *W. Bancrofti*.

AF036588Bm (<i>B. malayi</i>)	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCCGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCCGGGGGAAGTATGTTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTACCGAAAGGTATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTAC CACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTTCA TACCTTTTCAAGGGTAGAGATTCTTTGGTGGAACCTGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA
AY843438Wu (<i>W. Bancrofti</i>)	GAACGAAAGTCAGAGGTTCTGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGAT ACCAACTAGCGTTCCGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAA GTTTTTCGGTTCCGGGGGAAGTATGTTTGCAAAGCTGAACTTAAAGAAATTGACGGAAG GGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGG CCCGGACACCGTGAGGATTGACAGATTGAGAGCTCTTTCATGATTCGGTGTTGGTGGTG CATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTTATTCCGATAACGAGCGAGACT CTAGCCTACTAAATAGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAA GCGGTGTTTAGCCGCATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAG GGCTGCACGCGCGCTACACTGGAGGAATCAGCGTGCTGTAACCATTACCGAAAGGTATTG GTAACCCCTTGAAAATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACG AGGAATTCTAGTAAGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTAC ACACCGCCCGTCGCTGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTTG ATACCTTTCAAGGGTAGAGATTCTTTGGTGGAACCTGCTTTAATCGCAGTGGCTTGAACC GGGCAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCAGCAGGA

Table 10 Nucleotide sequence alignment of the 18S rDNA of *Brugia* spp. compared to *B. malayi* and *W. bancrofti*. (Region 1=1-763 nt)

C18 Cat3	TA-TACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTA AAAACCAATC	59
C7 Cat7	TA-TACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTA AAAACCAATC	59
C15 Cat3	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTA AAAACCAATC	60
C33 Cat6	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTA AAAACCAATC	60
AF036588Bm	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTA AAAACCAATC	60
C21 Cat3	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTA AAAACCAATC	60
C16 Cat3	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTA AAAACCAATC	60
C6 Cat2	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTA AAAACCAATC	60
C25 Cat6	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTA AAAACCAATC	60
C9 Cat2	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTA AAAACCAATC	60
C35 Cat6	TAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTA AAAACCAATC	59
AY843438Wu	TAATACATGCACCAAAGCTCCGATTTTAAACGAGCGCATCTATTAGATTA AAAACCAATC	60
** *****		
C18 Cat3	GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT	119
C7 Cat7	GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT	119
C15 Cat3	GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT	120
C33 Cat6	GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT	120
AF036588Bm	GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT	120
C21 Cat3	GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT	120
C16 Cat3	GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT	120
C6 Cat2	GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT	120
C25 Cat6	GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT	120
C9 Cat2	GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT	120
C35 Cat6	GGATTATTAATTTTAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT	119
AY843438Wu	GGATTATTAATT--AACCCGTTAATTGGTGACTCTGAATAGCTATGGCTGATCGCATGGT	118
***** ** *****		
C18 Cat3	CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG	179
C7 Cat7	CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG	179
C15 Cat3	CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG	180
C33 Cat6	CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG	180
AF036588Bm	CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG	180
C21 Cat3	CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG	180
C16 Cat3	CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG	180
C6 Cat2	CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG	180
C25 Cat6	CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG	180
C9 Cat2	CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG	180
C35 Cat6	CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG	179
AY843438Wu	CTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTTCGATGGTAGTTTATG	178
***** *****		
C18 Cat3	TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT	239
C7 Cat7	TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT	239
C15 Cat3	TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT	240
C33 Cat6	TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT	240
AF036588Bm	TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT	240
C21 Cat3	TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT	240
C16 Cat3	TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT	240
C6 Cat2	TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT	240
C25 Cat6	TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT	240
C9 Cat2	TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT	240
C35 Cat6	TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT	239
AY843438Wu	TGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTTCGACTCCGGAGAGGGAGCCT	238

Table 10 (continued)

C18 Cat3	GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT	299
C7 Cat7	GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT	299
C15 Cat3	GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT	300
C33 Cat6	GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT	300
AF036588Bm	GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT	300
C21 Cat3	GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT	300
C16 Cat3	GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT	300
C6 Cat2	GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT	300
C25 Cat6	GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT	300
C9 Cat2	GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT	300
C35 Cat6	GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT	299
AY843438Wu	GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCTCAGAAT	298

C18 Cat3	GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGTTATCGGAATGGG	359
C7 Cat7	GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGTTATCGGAATGGG	359
C15 Cat3	GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGTTATCGGAATGGG	360
C33 Cat6	GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGTTATCGGAATGGG	360
AF036588Bm	GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGTTATCGGAATGGG	360
C21 Cat3	GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGTTATCGGAATGGG	360
C16 Cat3	GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGTTATCGGAATGGG	360
C6 Cat2	GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGTTATCGGAATGGG	360
C25 Cat6	GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGTTATCGGAATGGG	360
C9 Cat2	GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGTTATCGGAATGGG	360
C35 Cat6	GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGTTATCGGAATGGG	359
AY843438Wu	GAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGTTATCGGAATGGG	358

C18 Cat3	TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG	419
C7 Cat7	TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG	419
C15 Cat3	TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG	420
C33 Cat6	TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG	420
AF036588Bm	TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG	420
C21 Cat3	TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG	420
C16 Cat3	TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG	420
C6 Cat2	TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG	420
C25 Cat6	TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG	420
C9 Cat2	TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG	420
C35 Cat6	TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG	419
AY843438Wu	TACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCAGCAGCCGCG	418

C18 Cat3	GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA	479
C7 Cat7	GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA	479
C15 Cat3	GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA	480
C33 Cat6	GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA	480
AF036588Bm	GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA	480
C21 Cat3	GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA	480
C16 Cat3	GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA	480
C6 Cat2	GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA	480
C25 Cat6	GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA	480
C9 Cat2	GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA	480
C35 Cat6	GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA	479
AY843438Wu	GTAATTCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTCGTAGTTGGA	477

Table 10 (continued)

C18 Cat3	TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG	539
C7 Cat7	TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG	539
C15 Cat3	TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG	540
C33 Cat6	TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG	540
AF036588Bm	TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG	540
C21 Cat3	TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG	540
C16 Cat3	TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG	540
C6 Cat2	TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG	540
C25 Cat6	TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG	540
C9 Cat2	TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG	540
C35 Cat6	TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGGCTAATATTG	539
AY843438Wu	TCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAG-CTAATATTG	536

C18 Cat3	CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA	599
C7 Cat7	CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA	599
C15 Cat3	CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA	600
C33 Cat6	CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA	600
AF036588Bm	CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA	600
C21 Cat3	CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA	600
C16 Cat3	CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA	600
C6 Cat2	CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA	600
C25 Cat6	CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA	600
C9 Cat2	CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA	600
C35 Cat6	CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA	599
AY843438Wu	CCAGTTTTCCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGTTTACCTTGA	596

C18 Cat3	AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT	659
C7 Cat7	AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT	659
C15 Cat3	AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT	660
C33 Cat6	AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT	660
AF036588Bm	AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT	660
C21 Cat3	AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT	660
C16 Cat3	AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT	660
C6 Cat2	AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT	660
C25 Cat6	AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT	660
C9 Cat2	AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT	660
C35 Cat6	AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT	659
AY843438Wu	AAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAATAATGAAAT	656

C18 Cat3	AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTCAAGAGGGACGGAC	719
C7 Cat7	AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC	719
C15 Cat3	AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC	720
C33 Cat6	AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC	720
AF036588Bm	AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC	720
C21 Cat3	AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC	720
C16 Cat3	AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC	720
C6 Cat2	GGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC	720
C25 Cat6	AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC	720
C9 Cat2	AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC	720
C35 Cat6	AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC	719
AY843438Wu	AGGATCTCGGTTCTATTTTGTGGTTTTCTGATCTGAGATAATGGTTAAGAGGGACGGAC	715

Table 10 (continued)

C18 Cat3	GGGGGCATTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC	762
C7 Cat7	GGGGGCATTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC	762
C15 Cat3	GGGGGCATTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC	763
C33 Cat6	GGGGGCATTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC	763
AF036588Bm	GGGGGCATTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC	763
C21 Cat3	GGGGGCATTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC	763
C16 Cat3	GGGGGCATTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC	763
C6 Cat2	GGGGGCATTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC	763
C25 Cat6	GGGGGCATTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC	763
C9 Cat2	GGGGGCATTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC	763
C35 Cat6	GGGGGCATTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC	762
AY843438Wu	GGGGGCATTCGTATCGCTGCGTGAGAGGTGAAATTCTTGGACC	758

Table 11 Nucleotide sequence alignment of the 18S rDNA of *Brugia* spp. compared to *B. malayi* and *W. bancrofti*. (Region 2 = 947-1774 nt)

AF036588Bm	AAAGATTAAGCCATGCATGTCTAAGTTCAAATAAACCTATAATGGTGAAACCGCGAACGG	60
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	-----AGCCATGCATGTCTAAGTTCAAATAAACCTATAATGGTGAAACCGCGAACGG	52
AF036588Bm	CTCATTATAACAGCTATAATGTACTTGATGTTGATTATCTAACGTGGATAACTGTGGCAA	120
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	CTCATTATAACAGCTATAATGTACTTGATGTTGATTATCCAACGTGGATAACTGTGGCAA	112

Table 11 (continued)

AF036588Bm	TTCTAGAGCTAATACATGCACCAAAGCTCCGAATTTTAAACGAGCGCATCTATTAGATTA	180
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	TTCTAGAGCTAATACATGCACCAAAGCTCCGATTTTATAGACGAGCGCATCTATTAGATTA	172
AF036588Bm	AAACCAATCGGATTATTAATTTTAAATCCGTTAATTGGTGACTCTGAATAGCTATGGCTGA	240
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	AAACCAATCGGATTATTAATT - AACCCGTTAATTGGTGACTCTGAATAGCTATGGCTGA	230
AF036588Bm	TCGCATGGTCTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTCGATGG	300
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	TCGCATGGTCTTGTACCGGCGACGTATCTATCAAGTGTCTGCCTTATCAACTTTCGATGG	290

Table 11 (continued)

AF036588Bm	TAGTTTATGTGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTCGACTCCGGAG	360
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	TAGTTTATGTGCCTACCATGGTTGTAACGGGTAACGGAGAATAAGGGTTCGACTCCGGAG	350
AF036588Bm	AGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAC	420
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	AGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAC	410
AF036588Bm	TCTCAGAATGAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGRGGCCGGTTAT	480
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	TCTCAGAATGAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTTTGAGGCCGGTTAT	470

Table 11 (continued)

AF036588Bm	CGGAATGGGTACAATTTAAACCTGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCA	540
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	CGGAATGGGTACAATTTAAACCCGTTAACGAGGATCTATGAGAGGGCAAGTCTGGTGCCA	530
AF036588Bm	GCAGCCGCGGTAATTCCAGCTCTCAAAGTGTATATCGTCATTGCTGCGGTTAAAAAGCTC	600
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	GCAGCCGCGGTAATTCCAGCTCTCAAAGTGTATATCGTCATTGC-GCGGTTAAAAAGCTC	589
AF036588Bm	GTAGTTGGATCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAGG	660
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	GTAGTTGGATCTGCGTCTCAGGACCTGGTCCATCCATTGGATGAGAACTAGGCTCCTAG-	648

Table 11 (continued)

AF036588Bm	CTAATATTGCCAGTTTTTCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGT	720
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	CTAATATTGCCAGTTTTCCATACGTTACCTTAATTGGTTGCATATGGTGGCTAGCAAGT	708
AF036588Bm	TTACCTTGAAAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAA	780
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	TTACCTTGAAAAAATTAGAGTGCTCAATGCGGGCTAATGCCTGAATACTCGTGCATGGAA	768
AF036588Bm	TAATGAAATAGGATCTCGGTTCTATTTTGTTGGTTTTCTGATCTGAGATAATGGTTAAGA	840
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	TAATGAAATAGGATCTCGGTTCTATTT - GTTGGTTTTCTGATCTGAGATAATGGTTAAGA	827

Table 11 (continued)

AF036588Bm	GGGACGGACGGGGGCATTTCGTATCGCTGCGTGAGAGGTGAAATTCCTTGGACCGTAGCGAG	900
C29 Cat7	-----	
C26 Cat6	-----	
C1 Cat1	-----	
C11 Cat2	-----	
C13 Cat2	-----	
C3 Cat1	-----	
C4 Cat1	-----	
C20 Cat1	-----	
C22 Cat5	-----	
C23 Cat5	-----	
C2 Cat1	-----	
C14 Cat3	-----	
C32 Cat6	-----	
C27 Cat7	-----	
C24 Cat6	-----	
AY843438Wu	GGGACGGACGGGGGCATTTCGTATCGCTGCGTGAGAGGTGAAATTCCTTGGACCGTAGCGAG	887
AF036588Bm	ACGTACGACTGCGAAAGCATTTGCCAAGAATGTCTTCATTAATCAAGAACGAAAGTCAGA	960
C29 Cat7	-----GAACGAAAGTCAGA	14
C26 Cat6	-----GAACGAAAGTCAGA	14
C1 Cat1	-----GAACGAAAGTCAGA	14
C11 Cat2	-----GAACGAAAGTCAGA	14
C13 Cat2	-----GAACGAAAGTCAGA	14
C3 Cat1	-----GAACGAAAGTCAGA	14
C4 Cat1	-----GAACGAAAGTCAGA	14
C20 Cat1	-----GAACGAAAGTCAGA	14
C22 Cat5	-----GAACGAAAGTCAGA	14
C23 Cat5	-----GAACGAAAGTCAGA	14
C2 Cat1	-----GAACGAAAGTCAGA	14
C14 Cat3	-----GAACGAAAGTCAGA	14
C32 Cat6	-----GAACGAAAGTCAGA	14
C27 Cat7	-----GAACGAAAGTCAGA	14
C24 Cat6	-----GAACGAAAGTCAGA	14
AY843438Wu	ACGTACGACTGCGAAAGCATTTGCCAAGAATGTCTTCATTAATCAAGAACGAAAGTCAGA	947

AF036588Bm	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	1020
C29 Cat7	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C26 Cat6	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C1 Cat1	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C11 Cat2	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C13 Cat2	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C3 Cat1	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C4 Cat1	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C20 Cat1	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C22 Cat5	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C23 Cat5	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C2 Cat1	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C14 Cat3	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C32 Cat6	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C27 Cat7	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
C24 Cat6	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	74
AY843438Wu	GGTTCGAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTC	1007

Table 11 (continued)

AF036588Bm	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	1080
C29 Cat7	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C26 Cat6	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C1 Cat1	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C11 Cat2	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C13 Cat2	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C3 Cat1	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C4 Cat1	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C20 Cat1	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C22 Cat5	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C23 Cat5	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C2 Cat1	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C14 Cat3	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C32 Cat6	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C27 Cat7	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
C24 Cat6	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	134
AY843438Wu	CGTCGGCGGTAAATACGCCTTGACGGGCAGCTTCCCGGAAACGAAAGTTTTTCGGTTCCG	1067

AF036588Bm	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	1140
C29 Cat7	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C26 Cat6	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C1 Cat1	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C11 Cat2	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C13 Cat2	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C3 Cat1	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C4 Cat1	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C20 Cat1	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C22 Cat5	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C23 Cat5	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C2 Cat1	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C14 Cat3	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C32 Cat6	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C27 Cat7	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
C24 Cat6	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	194
AY843438Wu	GGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAG	1127

AF036588Bm	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	1200
C29 Cat7	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C26 Cat6	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C1 Cat1	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C11 Cat2	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C13 Cat2	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C3 Cat1	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C4 Cat1	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C20 Cat1	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C22 Cat5	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C23 Cat5	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C2 Cat1	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C14 Cat3	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C32 Cat6	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C27 Cat7	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
C24 Cat6	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	254
AY843438Wu	TGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCTGGCCCGGACACCGTGA	1187

Table 11 (continued)

AF036588Bm	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	1260
C29 Cat7	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C26 Cat6	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C1 Cat1	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C11 Cat2	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C13 Cat2	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C3 Cat1	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C4 Cat1	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C20 Cat1	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C22 Cat5	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C23 Cat5	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C2 Cat1	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C14 Cat3	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C32 Cat6	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C27 Cat7	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
C24 Cat6	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	314
AY843438Wu	GGATTGACAGATTGAGAGCTCTTTTCATGATTCCGGTGGTTGGTGGTGCATGGCCGTTCTTA	1247

AF036588Bm	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	1320
C29 Cat7	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C26 Cat6	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C1 Cat1	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C11 Cat2	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C13 Cat2	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C3 Cat1	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C4 Cat1	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C20 Cat1	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C22 Cat5	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C23 Cat5	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C2 Cat1	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C14 Cat3	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C32 Cat6	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C27 Cat7	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
C24 Cat6	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	374
AY843438Wu	GTTGGTGGAGTGATTGTCTGGTTTATTCGATAACGAGCGAGACTCTAGCCTACTAAAT	1307

AF036588Bm	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	1380
C29 Cat7	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	433
C26 Cat6	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
C1 Cat1	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
C11 Cat2	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
C13 Cat2	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
C3 Cat1	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
C4 Cat1	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
C20 Cat1	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
C22 Cat5	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
C23 Cat5	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
C2 Cat1	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
C14 Cat3	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
C32 Cat6	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
C27 Cat7	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
C24 Cat6	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	434
AY843438Wu	AGTTACTGGATAATTTTATCGTCCAGACAACCTTCTTAGAGGGACAAGCGGTGTTTAGCCG	1367

Table 11 (continued)

AF036588Bm	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	1440
C29 Cat7	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	493
C26 Cat6	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
C1 Cat1	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
C11 Cat2	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
C13 Cat2	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
C3 Cat1	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
C4 Cat1	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
C20 Cat1	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
C22 Cat5	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
C23 Cat5	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
C2 Cat1	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
C14 Cat3	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
C32 Cat6	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
C27 Cat7	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
C24 Cat6	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	494
AY843438Wu	CATGAAGTTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCAGGGCTGCACGCGCGC	1427

AF036588Bm	TACACTGGAGGAATCAGCGTGCTGTAACCATTACCGAAAGGTATTGGTAACCCCTTGAAA	1500
C29 Cat7	TACACTGGAGGAATCAGCGTGCTGTAACCATTACCGAAAGGTATTGGTAACCCCTTGAAA	553
C26 Cat6	TACACTGGAGGAATCAGCGTGCTGTAACCATTACCGAAAGGTATTGGTAACCCCTTGAAA	554
C1 Cat1	TACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGATATTGGTAACCCCTTGAAA	554
C11 Cat2	TACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGATATTGGTAACCCCTTGAAA	554
C13 Cat2	TACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGATATTGGTAACCCCTTGAAA	554
C3 Cat1	TACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGATATTGGTAACCCCTTGAAA	554
C4 Cat1	TACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGATATTGGTAACCCCTTGAAA	554
C20 Cat1	TACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGATATTGGTAACCCCTTGAAA	554
C22 Cat5	TACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGGTATTGGTAACCCCTTGAAA	554
C23 Cat5	TACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGGTATTGGTAACCCCTTGAAA	554
C2 Cat1	TACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGGTATTGGTAACCCCTTGAAA	554
C14 Cat3	TACACTGGAGGAATCAGCGTGCTGTAACCATTATCGAAAGGTATTGGTAACCCCTTGAAA	554
C32 Cat6	TACACTGGAGGAATCAGCGTGCTGTAACCATTACCGAAAGGTATTGGTAACCCCTTGAAA	554
C27 Cat7	TACACTGGAGGAATCAGCGTGCTGTAACCATTACCGAAAGGTATTGGTAACCCCTTGAAA	554
C24 Cat6	TACACTG - AGAAATCAGCGTGCTGTAACCATTACCGAAAGGTATTGGTAACCCCTTGAAA	553
AY843438Wu	TACACTGGAGGAATCAGCGTGCTGTAACCATTACCGAAAGGTATTGGTAACCCCTTGAAA	1487
***** ** *****		
AF036588Bm	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	1560
C29 Cat7	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	613
C26 Cat6	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	614
C1 Cat1	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	614
C11 Cat2	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	614
C13 Cat2	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	614
C3 Cat1	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	614
C4 Cat1	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	614
C20 Cat1	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	614
C22 Cat5	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	614
C23 Cat5	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	614
C2 Cat1	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	614
C14 Cat3	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	614
C32 Cat6	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	614
C27 Cat7	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	614
C24 Cat6	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	613
AY843438Wu	ATCCTCCGTGATCGGGATCGGGAATTGCAATTATTTCCCTTGAACGAGGAATTCCTAGTA	1547

Table 11 (continued)

AF036588Bm	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	1620
C29 Cat7	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	673
C26 Cat6	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	674
C1 Cat1	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	674
C11 Cat2	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	674
C13 Cat2	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	674
C3 Cat1	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	674
C4 Cat1	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	674
C20 Cat1	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	674
C22 Cat5	AGTGTGAGTCATCAGCTCACGTCGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	674
C23 Cat5	AGTGTGAGTCATCAGCTCACGTCGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	674
C2 Cat1	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	674
C14 Cat3	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	674
C32 Cat6	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	674
C27 Cat7	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	674
C24 Cat6	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	673
AY843438Wu	AGTGTGAGTCATCAGCTCACGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGC	1607

AF036588Bm	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTTCAAGG	1680
C29 Cat7	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	732
C26 Cat6	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	733
C1 Cat1	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	733
C11 Cat2	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	733
C13 Cat2	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	733
C3 Cat1	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	733
C4 Cat1	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	733
C20 Cat1	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	733
C22 Cat5	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	733
C23 Cat5	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	733
C2 Cat1	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	733
C14 Cat3	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	733
C32 Cat6	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	733
C27 Cat7	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	733
C24 Cat6	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTCAATACCTTTT-CAAGG	732
AY843438Wu	TGCCCGGGACTGAGCCGTTTCGAGAAAAGCGGAGACTGCTGTTTGTATACCTTTT-CAAGG	1666

AF036588Bm	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	1740
C29 Cat7	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	792
C26 Cat6	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	793
C1 Cat1	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	793
C11 Cat2	GTAGAGATTCTTTGGTGAGACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	793
C13 Cat2	GTAGAGATTCTTTGGTGAAACCCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	793
C3 Cat1	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	793
C4 Cat1	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	793
C20 Cat1	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	793
C22 Cat5	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTTGT	793
C23 Cat5	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTTGT	793
C2 Cat1	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	793
C14 Cat3	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	793
C32 Cat6	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	793
C27 Cat7	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	793
C24 Cat6	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	792
AY843438Wu	GTAGAGATTCTTTGGTGAAACTGCTTTAATCGCAGTGGCTTGAACCGGGCAAAAAGTCGT	1726

Table 11 (continued)

AF036588Bm	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCA	1776
C29 Cat7	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	825
C26 Cat6	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	826
C1 Cat1	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	826
C11 Cat2	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	826
C13 Cat2	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	826
C3 Cat1	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	826
C4 Cat1	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	826
C20 Cat1	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	826
C22 Cat5	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	826
C23 Cat5	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	826
C2 Cat1	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	826
C14 Cat3	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	826
C32 Cat6	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	826
C27 Cat7	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	826
C24 Cat6	AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA---	825
AY843438Wu	AACAAGGTTTCCGTAGGTGAACCTGCAGCAGG----	1758
	***** * **	

Nucleotide sequence alignment of the 18S rDNA of *Brugia* spp. compared to *B. malayi* and *W. bancrofti*. (Region1 and Region2) revealed some positions that had nucleotide insertion, deletion and Single Nucleotide Polymorphism (SNPs) as shown in Table 12 and 13. Since, the nucleotide sequences of feline *Brugia* spp., *B. malayi*, and *B. pahangi* were highly conserved, the phylogenetic trees based on these data were collapsed and failed to demonstrate parasite classification.

Table 12. Positions of nucleotide insertion, deletion and SNPs of 10 clones from region 1 of 18S DNA from feline *Brugia* spp. in comparison to *B. malayi* (AF036588). (Region1)

Clone	Positions of nucleotide insertion, deletion and SNPs											
	3	29	31	119	165	279	341	549	600	661	687	707
C6 Cat2	A	A	A	G	T	G	A	C	A	G	T	T
C9 Cat2	A	A	A	G	T	G	A	C	A	A	T	T
C15 Cat3	A	A	A	G	T	G	A	C	A	A	C	T
C16 Cat3	A	A	A	G	T	A	A	C	G	A	T	T
C18 Cat3	-	A	A	G	T	G	A	C	A	A	T	C
C21 Cat3	A	A	A	G	T	A	A	C	G	A	T	T
C25 Cat6	A	A	A	G	C	G	A	C	A	A	T	T
C33 Cat6	A	A	A	A	T	G	A	C	A	A	T	T
C35 Cat6	A	T	-	G	T	G	A	C	A	A	T	T
C7 Cat7	-	A	A	G	T	G	A	C	A	A	C	T
AF036588Bm (<i>B. malayi</i>)	A	A	A	G	T	G	C	T	A	A	T	T

Table 13. Positions of nucleotide insertion, deletion and SNPs of 15 clones from region 2 of 18S rDNA from feline *Brugia* spp. in comparison to *B. malayi* (AF036588). (Region2)

Clone	Positions of nucleotide insertion, deletion and SNPs												
	1304	1337	1448	1451	1474	1481	1574	1583	1675	1700	1703	1704	1738
C1 Cat1	A	T	G	G	T	A	A	T	-	A	T	A	C
C2 Cat1	A	T	G	G	T	G	A	T	-	A	T	G	C
C3 Cat1	A	T	G	G	T	A	A	T	-	A	T	G	C
C4 Cat1	A	T	G	G	T	A	A	T	-	A	T	G	C
C20 Cat1	A	T	G	G	T	A	A	T	-	A	T	G	C
C11 Cat2	A	T	G	G	T	A	G	T	-	G	T	G	C
C13 Cat2	A	T	G	G	T	A	A	T	-	A	C	G	C
C14 Cat3	A	T	G	G	T	G	A	T	-	A	T	G	C
C22 Cat5	A	T	G	G	T	G	A	C	-	A	T	G	T
C23 Cat5	A	T	G	G	T	G	A	C	-	A	T	G	T
C24 Cat6	A	T	-	A	C	G	A	T	-	A	T	G	C
C26 Cat6	A	T	G	G	C	G	A	T	-	A	T	G	C
C32 Cat6	G	T	G	G	C	G	A	T	-	A	T	G	C
C27 Cat7	A	T	G	G	C	G	A	T	-	A	T	G	C
C29 Cat7	A	-	G	G	C	G	A	T	-	A	T	G	C
AF036588Bm (<i>B. malayi</i>)	A	T	G	G	C	G	A	T	T	A	T	G	C

3. PCR amplification and DNA sequencing of ITS1 region

3.1 PCR amplification of ITS1 region

The PCR amplification was performed and analyzed according to the Materials and Methods 5. Figure 14 showed that the PCR product of approximately 600 bp in size was observed when ITS1F and ITS1R were used as primers.

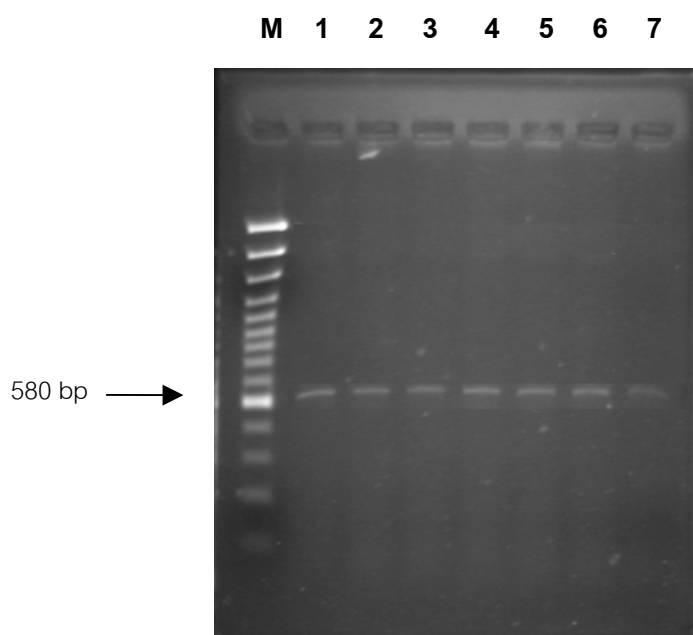


Figure 14 The PCR amplification profile of ITS1 from purified *Brugia* spp. DNA of cats in Narathiwat and Lad krabang. The PCR product of 600 bp in size was observed on 1.2% agarose gel electrophoresis using ITS1F and ITS1R as primers.

Lane M = 100 bp DNA ladder marker

Lane 1 = PCR product of *Brugia* spp. from cat1

Lane 2 = PCR product of *Brugia* spp. from cat2

Lane 3 = PCR product of *Brugia* spp. from cat3

Lane 4 = PCR product of *Brugia* spp. from cat4

Lane 5 = PCR product of *Brugia* spp. from cat5

Lane 6 = PCR product of *Brugia* spp. from cat6

Lane 7 = PCR product of *Brugia* spp. from cat7

3.2 DNA sequencing of ITS1 region

PCR products of ITS1 gene from PCR amplification using ITS1F and ITS1R were used for cloning and DNA sequencing. Among ITS1 clones, 45 clones of them were randomly selected for proceeding to DNA sequencing (Table 14). The nucleotide sequence data of ITS1 were shown in Table 15.

Table 14 Summary of 45 clones of *Brugia* spp. ITS1 region from 7 cat reservoirs.

Cats	Clones
Cat 1	C1, C2, C3, C4, C5, C6, C7, C8
Cat 2	C15, C19, C22, C30, C36, C46, C48
Cat 3	C12, C23, C30, C31, C54, C58, C62
Cat 4	C3, C4, C28, C33, C38
Cat 5	C7, C8, C9, C13, C17, C36, C41
Cat 6	C2, C5, C6, C8, C10, C45
Cat 7	C3, C9, C18, C22, C41

Table 15 Nucleotide sequence data of 45 clones of *Brugia* spp. ITS1 region from cat reservoirs.

C1 Cat1	TTATCGTGTTTCAAAAAAAAAATAACCCAACAATGATTGATTGATTTATTA CTATTACTATAGCTACCATATTATATTATGATACTATATTAACAACATATT GTGGTATGTGTGTTACCCTAATAGATTGATTTTAATATGGTAGTAGCTTAA ATAATAATAGTAATAATAGGAATAAACGGTGATATTCGTGGGTGTCTATAC TTTATCCAAGTTATCGCCTAACCGTCGATAACAATGAAGATAAAGCGATAG CTTAATTAATTTTATCATTTAATTAAGTAGACTTAATAAGCATTTATGCTA GATATGCTCCACCAAAAAAAAAAAAAAAAAAAAAAAAAACATACACAAA TTATATATATTATAGTAATAAATTTTAACTCTTAGCGGTGGATCACTTGG CTCATGGATCGATGAAGAACGCAGCTAGCTGCGATAAATAGTGCGAATTGC AGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATTGGGTTATC ACGA
C2 Cat1	TCTGTGCTTCAAAAAAAAAATAACACAACAATGATTGATTGATTTATTACT ATTACTATAGCTACCATATTATATTATGATACTATATTAACAACATATTGT TGTATGTGTGTTACCCTAATAGATTGATTTTAATATGGTAGTAGCTTAAAT AATAATAGTAATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTT TATCCAAGTTATCGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCT TAATTAATTTTATCATTTAATTAAGTAGACTTAATAAGCATTTATGCTAGA TATGCTACCAACAAAAAAAAAAAAAAAAAAAAAAAAACATACCCAAATTA TATATATTATAGTAATAAATTTTAACTCTTAGCGGTGGATCACTTGGCTC ATGGATCGATGAAAAACGCAGCTAGCTGCGATAAATAGTGCGAATTGCAAA CGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATTGGGTTAATCTG AATTCGTCTG
C3 Cat1	TTATCGTGCTTCAAAAAAAAAATAACACACCAATGATTGATTGATTTATT ACTATTACTATAGCTCCCATATTATATTATGATACTATATTAACAACATAT TGTTGTATGTGTGTTACCCTAATAGATTGATTTTAATATGGTAGTAGCTTA AATAATAATAGTAATAATATGAATAAACGGTGATATTCGTTGGTGTCTATA CTTTATCCAAGTTATCGCCTAACCGTCGATAACAATGAAGATAAAGCGATA GCTTAATTAATTTTATCATTTAATTAAGTAGACTTAATAAGCATTTATGCT AGATATGCTCCACCAAAAAAAAAAAAAAAAAAAAAAAAAACATACACAA ATTATATATATTATAGTAATAAATTTTAACTCTTAGCGGTGGATCACTTG GCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATAAATAGTGCGAATTG CAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATTGGGTTAA TCACGA

Table 15 (continued)

C4 Cat1	TCTTTGCGTTCAAAAAAAAAAATAACACCGGCAATGATTGTATTGATTTAATACTATT ACCTCCTCGAACATAGGGTAATAATGACAACCCTCTTCCCGATCAGTTTGGCTGTAT GGGTTTTTACCCCTAATAGATTGATTTGGAATCTGGGAGGAGCTTTAATTATTTTAG TTATAATATGCAAAACCCGGGATTATCGTTGGTGGCTAAACTTTATCCAAGGTTTTA CCCTATCGCCCATATAAATGGAGAAAAAGCCAAGCTTAAATCACTTTTAACCATGG AATTAGTAAACCACAAAAAGGCTTTTTGCTGCACATTGGTCCCAACCTGAGGGCAAT TATCTTTAAAAAGAAGTCGTGCCCCCCTTTCAAGTCATATTTGCGCTAAAAATTTT TTTGACCTTACCGGGGGGATCCCCTGGGGCCTGGGGCCTTTTAAAAAAGTATCAAT ATCTGTTTATTAATAAATTTGCAATTGCCCTCCCCTTTTGTACGAAGATTACTCA TAGACTCTTGCGCCTTGAGGGGTGAAATAATCA
C5 Cat1	TTTTGGTGTTCAAAAAAAAAATACCCACCAGGGGTGGATTGATTTTTTATTATTC CTATAGCTCCCATATTATTTTAGGATCCTATATTACCACCATATTGTGGTAGGTGTG TTCCCTAAAAGATGGATTTTAATAGGGTAGTGGCTTAAATAATAATGGTATTAATA GGATTAACCGGGGATTTTGGTGGGTGTTTATTTTTATCCAAGTTATCGCTTACCCG TGGATAACAATGAAGATAAAGCGAGAGCTTAATTAATTTTATCATTTAATTAGGTAG ACTTAATAAGCTTTTATGCTAGATATGCTCCACCAAAAAAAAAAAAAAAAAAAAAA AGCCTGCCCAAATTATATATATTATAGTAATAAATTTTTAACTCTTAGCGGTGGATC ACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATAAATAGTGCGAATTGC AGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATTGGGTTAATCACGA
C6 Cat1	TCTGTGCTTCAAAAAAAAAAATAACACAACAATGATTGATTGATTTATTACTATTACT ATAGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTGT ACCCTAATAGATTGATTTTAATATGGTAGTAGCTTAAATAATAATAGTAATAATATG AATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTAACCGTC GATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTATCATTTAATTAAGTAGAC TTAATAAGCATTTTATGCTAGATATGCTACCCACAAAAAAAAAAAAAAAAAAAAA ACCCTACCCAAATTATATATATTATAGTAATAAATTTTTAACTCTTAGCGGTGGATC ACTTGGCTCATGGATCGATGAAAAACGCAGCTAGCTGCGATAAATAGTGCGAATTGC AAACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATTGGGTTAATCTGAAT TCGTCG
C7 Cat1	ATCGTGCTTCAAAAAAAAAAATAACACAACAATGATTGATTGATTTATTACTATTAC TATAGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTGT TACCCTAATAGATTGATTTTAATATGGTAGTAGCTTAAATAATAATAGTAATAATAT GAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTAACCGT CGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTATCATTTAATTAAGTAGA CTTAATAAGCATTTTATGCTAGATATGCTACCACTAAAAAAAAAAAAAAAAAAAAA CCCTCCCCCAATTATATATATTATAGTAATAAATTTTTAACTCTTAACGGTGGATCA CTTGGCTCATGGATCGATGAAAAACGCACCTAGCTGCAATAAATATTGCGAATTGCA GACCCATTGAGCACAAAGATTTTGAATGCCATTGCACCATTGGGTTAATCTGAATT CGTCG

Table 15 (continued)

C8 Cat1	ATCGTGCTTCAAAAAAAAAAATAACACAACAATGATTGATTGATTTATTACTATTAC TATAGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTG TTACCCTAATAGATTGATTTTAATATGGTAGTAGCTTAAATAATAATAGTAATAAT ATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTAAC CGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTATCATTAAATTAAG TAGACTTAATAAGCATTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAAAAAA AAAAAACCTTACCCAAATTATATATATTATAGTAATAAATTTTAACTCTTAGCG GTGGATCACTTGGCTCATGGATCGATGAAAAACGCAGCTAGCTGCGATAAATAGTG CGAATTGCAAACGCATTGAGCACAAAGATTTGGAATGCACATTGCACCATTGGGTT AATCTGAATTCGTCG
C15 Cat2	TTATCGTGCTTCAAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTAT AGCTACCATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTT ATTAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATA ATAATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTAT CGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATT TAATTAAGTAGACTTAATAAGCATTATGCTAGATATGCTACCAACAAAAAAAAAAAA AAAAAAGACATACAAAAAAATTATATATATTATAGTAATAATAATAAAAAATTT TTTTTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCT AGCTGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTGGAATGCA CATTGCACCATTGGGTTAATCACGA
C19 Cat2	TTATCGTGCTTCAAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAGC TACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAATAAT AATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTA ACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTAAATTA GTAGACTTAATAAGCATTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAAAAGAC ATACAAAAAAATTATATATATATATTATAGTAATAATAATAAAAAATTTTTTTTAAAC TCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATA AATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTGGAATGCACATTGCACCAT TGGGTTAATCACGA
C22 Cat2	TTATCGTGCTTCAAAAAAAAAAATAACACAACAGTGATTGAATTTATTATTATTATAGC TACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAATAAT AATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGC CTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTAAAT TAAGTAGACTTAATAAGCATTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAAA GACATACAAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTAA CTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGAT AAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTGGAATGCACATTGCACCA TGGGTTAATCACGA

Table 15 (continued)

C30 Cat2	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAGC TACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAAAT AATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTA ACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTAA GTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAAAGAC ATACAAAAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTAACTC TTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATAAA TAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATTG GGTTAATCACGA
C36 Cat2	TTATCGTGCTTCAAAAAAAAAATACCCACCAATGATTGAATTTATTATTATTATAGC TCCCATATATATATATTATGATACTATATTAACAACATATTGTTGGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAATATGGTAGTGGCATAAATAATAATAATAAAT AATATGAATAACCGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTA ACCGTCGATACCAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTAA GTAGACTTAATAAGCATTTATGCTAGATATGCTCCACCAAAAAAAAAAAAAAAAAAGA CATACAAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTAACT CTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATAA ATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATT GGTTAATCACGA
C46 Cat2	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAGC TACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAAAT AATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTA ACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTAA GTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAAAGAC ATACAAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTAACTC TTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATAAA TAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATTG GGTTAATCACGA
C48 Cat2	TTATCGTGCTTCAAAAAAAAAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATT AGCTACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTA TTAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAAAT AATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGC CTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAAT TAAGTAGACTTAATAAGCATTTATGCTAGATATGCTCCCAACAAAAAAAAAAAAAAAA AAAGACATACAAAAAAATTATATATATTATAGTAATAATAATAAAAAATTTTTTTTAA ACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGA TAAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACC ATTGGGTAAATCACGA

Table 15 (continued)

C12 Cat3	TTATCGTGCTTCAAAAAAAAAATAGCACACAACGATTGAATTTATTATTATTATAGC TACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAAAT AATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTA ACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTAA GTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAAAAAA GACATACAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTTTAA CTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGAT AAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCA TTGGGTAAATCACGA
C23 Cat3	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAGC TACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAACAATAAT AATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTA ACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTAA GTAGACTTAATAAGCATTTATGCTAGGTATGCTACCAACAAAAAAAAAAAAAAAAAAGA CATACAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTTTAACTC TTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATAAA TAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATTG GGTAATCACGA
C30 Cat3	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAG CTACCATATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTA TTAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAAT AATAATATGAATAAACGGTGATATTCGTCGGTGTCTATACTTTATCCAAGTTATCGC CTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAAT TAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAAAA GACATACAAAAAATTATATATATATATTATAGTAATAATAATAAAAAATTTTTTTTTT AACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCG ATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCAC CATTGGGTAAATCTGAA
C31 Cat3	TTATCGTGCTTCAAAAAAAAAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATAA TAGCTACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTT ATTAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAGTAA TAATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCG CCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATGAATTTTACCATTTAA TTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAAAA AGACATACAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTTTAA CTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGAT AAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCA TTGGGTAAATCACGA

Table 15 (continued)

C54 Cat3	TTATCGTGCTTCAAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTAT AGCTACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTA TTAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAAT AATAATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTAT CGCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTA ATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAA AGACATACAAAAAATTATATATATATTATAGTAATAATAATAAAAAATCTTTTTTAA CTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGAT AAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCA TTGGGTAAATCACGA
C58 Cat3	TTATCGTGCTTCAAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATAGCTA CCATATATATATGTATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAATAAT AATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTA ACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTAA GTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAGA CATACAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTAACTCT TAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATAAAT AGTGCGAATTGCAGACGCATTGAGGACAAAGATTTTGAATGCACATTGCACCATTGG GTTAATCACGA
C62 Cat3	TTATCGTGCTTCAAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAGC TACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAATAAT AATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTA ACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTAA GTAGGCTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAGAA GACATACAAAAAGTTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTAA CTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGAT AAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCA TTGGGTAAATCACGA
C3 Cat4	TTATCGTGCTTCAAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTAT AGCTACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTG TTAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAAT AATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGC CTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAAT TAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAA AGACATACAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTAA ACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGA TAAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACC ATTGGGTAAATCACGA

Table 15 (continued)

C4 Cat4	TTATCGTGCTTCAAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATA GCTACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTAT TAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATA ATAATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATC GCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTA ATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAGG CATACAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTAACTC TTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATAAA TAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATTG GGTTAATCACGA
C28 Cat4	TTATCGTGCTTCAAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTAT AGCTACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTA TTAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAAAT AATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGC CTACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATT AAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAGAC ATACAAAACTATATATATATTATAGTAATAATAATAAAAAATTTTTTTAACTCTT AGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATAAATA GTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATTGGG TTAATCTGAATTCGTG
C33 Cat4	TTATCGTGCTTCAAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAGC TACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAAAT AATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTA ACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTA GTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAGAC GACATACAAAAAATTATATACATATTATAGTAATAATAATAAAAAATTTTTTTTAA CTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGAT AAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCA TTGGGTTAATCTGAATTCGTG
C38 Cat4	TTATCGTGCTTCAAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTAT AGCTACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTA TTAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAAAT AATAATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTAT CGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATT AATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAA GACATACAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTAAC TCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATA AATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCAT TGGGTTAATCTGAATTCGTG

Table 15 (continued)

C7 Cat5	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGGTTGAATTTATTATTATTATAGC TACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAAAT AATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTA ACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTAA GTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAAAGAC ATACAAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTTAACTC TTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATAAA TAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATTG GGTTAATCACGA
C8 Cat5	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAGC TACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAAAT AATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGC CTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAAT TAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAA AGACATACAAAAAGATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTAA CTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGAT AAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCA TTGGGTTAATCACGA
C9 Cat5	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATTA TAGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTACT AATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAGTAATAATAATAATAA TAATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCT AACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTAA AGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAAAGA CATACAAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTTAACTC TTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATAAA TAGTGCGAATTGCAGATGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATTG GGTTAATCTGAATTCGTCG
C13 Cat5	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAGC TACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATAAAT AATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTA ACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTAA GTAGACTTAATAAGCATTTACGCTAGATATGCTACCAACAAGAAAAAAAAAAAAAAAA GACATACAAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTTTAA CTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGAT AAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCA TTGGGTTAATCACGA

Table 15 (continued)

C17 Cat5	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATAGCTAC CATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTAATA GATTGATGTTAATAATTTTAAATATGGTAGTAGCATAAATAATAATAATAATAAT ATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTAACC GTGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTAAGTAG ACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAAAAGACAT ACAAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTAACTCTTA GCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCGGCTAGCTGCGATAAATAG TGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATTGGGT TAATCACGA
C36 Cat5	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAG CTACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATT GATAGATTGATGTTAATAATTTTAAATATGGTAGTAGCATAAATAATAATAATAA TAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCT AACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTA AGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAAA GACATACAAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTAA CTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGAT AAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCA TTGGGTAAATCTGAATTCGTCTG
C41 Cat5	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAGC TACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATTA ATAGATTGATGTTAATAATTTTAAATATGGTAGTAGCATAAATAATAATAATAAT AATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTA ACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTA GTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAAAAG ACATACAAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTAACT CTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGATAA ATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATT GGGTAAATCTGAATTCGTCTG
C2 Cat6	TATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATTATA GCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTACTA ATAGATTGATGTTAATAATTTTAAATATGGTAGTAGCATAAGTAATAATAATAATA TAATAATAATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATCCAAGTT ATCGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCA TTTAATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAA AAAAAAAAAAAAAAAAAAGTTATATATATATTATAGTAATAACAATA AAATTTTTTAACTCTTAGCGGTGGATCACTTGGCTCATGTATCGATGAAGAACGC AGCTAGCTGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAAATTTTCAA TGCACATTGCACCATTGGGTAAATCTGAATTCGTCTG

Table 15 (continued)

C5 Cat6	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATTAT AGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTACTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAGTAATAATAATAAAT AATAATAATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATCCAAGTTAT CGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTT AATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAA AAAAAACATACAAAAAAGTTATACATATATTATAGTAATAACAATAAAATTTTTTT TAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGC GATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAAATTTTGAATGCACATTGCA CCATTGGGTTAAGGGCGA
C6 Cat6	TATCGTGCTTCAAAAAAAAAATAACACAACAAGATTGAATTTATTATTATTATTAT AGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTACTA TAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAGTAATAATAATAA TAATAATAATAATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATCCA AGTTATCGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTT TACCATTTAATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAA AAAAAAAAAAAAAAAAAACTTCAAAAAAAGTTATATATATATTATAGTAATAAC AATAAAATTTTTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAG AACGCAGCTAGCTGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAAAT TTCGAATGCACATTGCACCATTGGGTTAATCTGAATTCGTCTG
C8 Cat6	TATCGTGCTTCAAAAAAAAAACACAACAATGATTGAATTTATTATTATTATTATAGC TACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTACTAAT AGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAGTAATAATAATAATA ATAATAATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATCCAAGTTAT CGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTT AATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAA AAAAAAAAAAAACTTACAAAAAAGTTATATATATATTATAGTAATAACAATAAAAT TTTTTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCT AGCTGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAAATTTTGAATGCA CATTGCACCATTGGGTTAATCTGAATTCGTCTG
C10 Cat6	TATCGTGCTTCAAAAAAAAAATAACACAACAAGATTGAATTTATTATTATTATTATA GCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTACTA ATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAGTAATAATAATAATA TAATAATAATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATCCAAGTT ATCGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCA TTTAATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAA AAAAAAAAAAAAACATACAAAAAAGTTATATATATATTATAGTAATAACAATAAAA TTTTTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGC TAGCTGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAAATTTTGAATGC ACATTGCACCATTGGGTTAATCTGAATTCGTCTG

Table 15 (continued)

C45 Cat6	GTTCGGTGTTCCAAAAAATATTACACATCAACGATAGAATTTTTTCATAATAAAGG CGCCGAAAAATTTACATATGCATCCTATATTACCAACAACGGGTAGTAGGTGCCTT TAATAAATTGTCCTAATTAATTTAAATATGGTGTAGCATAATTATTATTATCATT ATTTGGGGAGATAATCGGTGTTATTGGGGGGTTTTTTAACTTTTTTCAACTGACAC CTTAAAATCAGTTAACCATTGAGTCAAAATCGAAAAGGTTATTTAATTTACCAATT GAATAGAGTAGATTACCAACCATTACACCGTTTATTCATATTATAAATATAATT ACTTATGCTACTACCATATTTAAATTATTAACATCAATCTATTAGTAACACATACA ACAATATGTTGTTAATATAGTATCATAATATAATATGGTAGCTATAATAATAATA TAAATTCATCATTGTTGTGTTATTTTTTTGAAGCACGATAATGATCCTTCCGCA GGTTACCAAGGGCGA
C3 Cat7	TATCGGTGCTTCAAAAAAATAACACAACAATGATTGAATTTATTATTATTATTAT AGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTACT AATAGATTGATGTTAATAATTTTAAATATGGTAGTAGCATAAGTAATAATAATA ATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCTA ACCGTGCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTAATTA AGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAAAAA AACATACAAAAAAGTTATACATATATTATAGTAATAACAATAAAATTTTTTTAAC TCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGAT AAATAGTGCGAATTGCAGACGCATTGAGCACAAAAATTTTGAATGCACATTGCACC ATTGGGTAAATCTGAATTCGTGCG
C9 Cat7	TTATCGTGCTTCAAAAAAATAACACAACAATGATCGAATTTATTATTATTATTA TAGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTAC TAATAGATTGATGTTAATAATTTTAAATATGGTAGTAGCATAAGTAATAATAAAT AATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATCCAAGTTATCGCCT AACGTGCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTATCATTTAATT AAGTAGACTTAATAAGCATTTGTGCTAGATATGCTACCAACAAAAAAAAAAAAAAAA AAAAACATACAAAAAAGTTATACATATATTATAGTAATAACAATAAAATTTTTTTT AACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGC GATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAAATTTTGAATGCACATTGC ACCATTGGGTAAAGGGCGA
C18 Cat7	ATATCGTGCTTCAAAAAAATAACACAACAATGATTGAATTTATTATTATTATTA TTATAGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGT TACTAATAGATTGATGTTAATAATTTTAAATATGGTAGTAGCATAAGTAATAAAT AATAATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATCCAAGTTATCG CCTAACTGTGCGATAACAATGAAGATAAAGCGATAGCTTAATTAATCTTATCATTTA ATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAA AAAAAACATACAAAAAAGTTATATATATATTATAGTAATAACAATAAAATTTTTTT TAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTG CGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAAATTTTGAATGCACATTG CACCATTGGGTAAAGGGCGA

Table 15 (continued)

C22 Cat7	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATTA TAGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTAC TAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAGTAATAATAATAAT AATAATAATAATAATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATCC AAGTTATCGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTT TACCATTTAATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAA AAAAAAAAAAAAAAAAACATACAAAAAGTTATACATATATTATAGTAATAACAAT AAAATTTTTTTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAAC GCAGCTAGCTGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAAATTCG AATGCACATTGCACCATTGGGTAAAGGGCGA
C41 Cat7	TTATCGTGCTTTAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATTA TAGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTAC TAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAGTAATAATAATAAT AATAATAATAATATGAATGAACGGTGTTATTCGTTGGTGTCTATACTTTATCCAAG TTATCGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTAC CATTTAATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAA AAAAAAAAACATACAAAAAGTTATACATATATTATAGTAATAACAATAAAATTT TTTTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTA GCTGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAAATTCGAATGCAC ATTGCACCATTGGGTAAAGGGCGA

3.3 Identification and analysis of ITS1 nucleotide sequence data.

BLAST program was used for identification of 45 clones selected from feline *Brugia* spp. ITS1 nucleotide sequences in comparison to the previously reported data of *B. malayi*, *B. pahangi*, and *D. immitis* obtained from GenBank (Table 16a and 16b). Upon alignment using Clustal W, some nucleotide regions were deleted to generate the appropriate alignment and the sequences were manually corrected. The nucleotide sequences from 45 clones revealed that they were mainly classified as *B. malayi* or *B. pahangi*. The alignment of ITS1 region was shown in Table 17.

Table 16a Sources of *B. malayi* and *B. pahangi* from GenBank using in phylogenetic tree construction based on ITS1 region.

Samples	Geographical Area	References
<i>B. malayi</i> (AY499507)	Thailand	131
<i>B. malayi</i> (AY621464)	Thailand	131
<i>B. malayi</i> (AY621465)	Thailand	131
<i>B. malayi</i> (AY621466)	Thailand	131
<i>B. malayi</i> (AY621467)	Thailand	131
<i>B. malayi</i> (AY621468)	Thailand	131
<i>B. pahangi</i> (AY621469)	Thailand	131
<i>B. pahangi</i> (AY621470)	Thailand	131
<i>B. pahangi</i> (AY621471)	Thailand	131
<i>B. pahangi</i> (AY621472)	Thailand	131
Cat 1-5	Narathiwat, Thailand	In this study
Cat 6,7	Lad Krabang, Thailand	In this study

Table 16b Nucleotide sequences of ITS1 region of *B. malayi*, *B. pahangi*, and *D. immitis*.

AY621468Bm (<i>B. malayi</i>)	TTATCGTGCTTCAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAGC TACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATT AATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAATA ATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCGC CTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTAA TTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAA AAAAAGACATACAAAAAATTATATATATATTATAGTAATAAAAAATTTTTTTTAA CTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCGA TAAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCAC CATTGGGTTGATTCCCG
AY621472Bp (<i>B. pahangi</i>)	TTATCGTGCTTCAAAAAAATAACACAACAATGATTGAATTTATTATTATTATTA TAGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTAC TAATAGATTGATGTTGATAATTTTAATATGGTAGTAGCATAAGTAATAATAATAAT AATAATAATAATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATCCAAG TTATCGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTAC CATTTAATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAA AAAAAAAAAAAAAAAAACATACAAAAAAGTTATACATATATTATAGTAATAACAATAA AATTTTTTTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGC AGCTAGCTGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAAATTTCGAA TGCACATTGCACCATTGGGTTGATTCCCG
AY621469Bp (<i>B. pahangi</i>)	TTATCGTGCTTCAAAAAAATAACACAACAATGATTGAATTTATTATTATTATTA TAGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTAC TAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAGTAATAATAATAAT AATAATAATAATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATCCAAG TTATCGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTAC CATTTAATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAA AAAAAAAAAAAAAACATACAAAAAAGTTATACATATATTATAGTAATAACAATAA AATTTTTTTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGC AGCTAGCTGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAAATTTCGAA TGCACATTGCACCATTGGGTTGATTCCCG
AY621470Bp (<i>B. pahangi</i>)	TTATCGTGCTTCAAAAAAATAACACAACAATGATTGAATTTATTATTATTATTA TAGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTAC TAATAGATCGATGTTAATAATTTTAATATGGTAGTAGCATAAGTAATAATAATAAT AATAATAATAATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATCCAAG TTATCGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTAC CATTTAATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAA AAAAAAAAAAAAAACATACAAAAAAGTTATACATATATTATAGTAATAACAATAAAAT TTTTTTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGC TAGCTGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAAATTTTGAATGC ACATTGCACCATTGGGTTGATTCCCG

Table 16b (continued)

AY621471Bp (<i>B. pahangi</i>)	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATTA TAGCTACCATATTATATTATGATACTATATTAACAACATATTGTTGTATGTGTTAC TAATAGATTGATGTTAATAATTTTAAATATGGTAGTAGCATAAGTAATAATAATAAT AATAATAATAATATGAATAAACGGTGTATTTCGTTGGTGTCTATACTTTATCCAAG TTATCGCCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTAC CATTTAATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAGA AAAAAAAAAAAAACATACAAAAAAGTTATACATATATTATAGTAATAACAATAAA ATTTTTTTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCA GCTAGCTGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAAATTTTGAAT GCACATTGCACCATTTGGGTTGATTCCCG
AY499507Bm (<i>B. malayi</i>)	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATA GCTACCATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTATT AATAGATTGATGTTAATAATTTTAAATATGGTAGTAGCATAAATAATAATAATAATA ATAATATGAATAAACGGTGTATTTCGTTGGTGTCTATACTTTATCCAAGTTATCGC CTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTAA TTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAA AGACATACAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTTTTA ACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGCTGCG ATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCA CCATTGGGTTGATTCCCG
AY621465Bm (<i>B. malayi</i>)	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAG CTACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTAT TAATAGATTGATGTTAATAATTTTAAATATGGTAGTAGCATAAATAATAATAATAAT AATAATATGAATGAACGGTGTATTTCGTTGGTGTCTATACTTTATCCAAGTTGTGCG CCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTAA ATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAA AAAAGACATACAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTTT TTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGC TGCATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACAT TGCACCATTTGGGTTGATTCCCG
AY621464Bm (<i>B. malayi</i>)	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAG CTACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTAT TAATAGATTGATGTTAATAATTTTAAATATGGTAGTAGCATAAATAATAATAATAAT AATAATATGAATAAACGGTGTATTTCGTTGGTGTCTATACTTTATCCAAGTTATCG CCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTAA ATTAAGTAGACTTAATAAGCATTTATGCTAGATATGCTACCAACAAAAAAAAAAAAA AAAAAGACATACAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTTT TTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAGC TGCATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACAT TGCACCATTTGGGTTGATTCCCG

Table 16b (continued)

AY621467Bm (<i>B. malayi</i>)	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAG CTACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTAT TAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAAAT AATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCG CCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTA ATTAAGTAGACTTAATAAGCATTATGCTAGATATGCTACCAACAAAAAAAAAAAA AAAAAGACATACAAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTTT TTTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCTAG CTGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACA TTGCACCATTGGGTTGATTCCCG
AY621466Bm (<i>B. malayi</i>)	TTATCGTGCTTCAAAAAAAAAATAACACAACAATGATTGAATTTATTATTATTATAG CTACCATATATATATATTATGATACTATATTAACAACATATTGTTGTATGTGTTAT TAATAGATTGATGTTAATAATTTTAATATGGTAGTAGCATAAATAATAATAAAT AATAATATGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATCCAAGTTATCG CCTAACCGTCGATAACAATGAAGATAAAGCGATAGCTTAATTAATTTTACCATTTA ATTAAGTAGACTTAATAAGCATTATGCTAGATATGCTACCAACAAAAAAAAAAAA AAAAAGACATACAAAAAAATTATATATATATTATAGTAATAATAATAAAAAATTT TTTTTAACTCTTAGCGGTGGATCACTTGGCTCATGGATCGATGAAGAACGCAGCT AGCTGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCA CATTGCACCATTGGGTTGATTCCCG
AF217800Di(<i>D. immitis</i>)	ATACTACTATTAACATCATTATGCTGCTTATTTTCATTCTTTTTCAATAATGCAA GAATGAAATAGAATGAATGAATGATGTTTAATAGATTAATAGATGAATAGTTAGTA GTAGTTAGTAGTTAGTTAGATAGATAGATAAATGAAATGATGATGAAATATTTTTA TTCGATCAATTGAATATAAACGGTGATATTCGTTGGTGTCTATATTTTATCTAAGT TATCGCCTAACCGTCGATAGCGATGAAGATAAATGATAGCTTAATTGATGATGAT TGCTCAATTAAGTAGACTTAATAAGCATTATGCTAGTATGCTACCAACAAAATAA TACACACACATACATACAATAATATGATATAATTGTTATTTATAATAATTTTTTC AATAACTCTAAGCGGGGGATCACCTGGCTCGTGGATCGATGAAGAACGCAGCTAGC TGCGATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACAT TGCACCATCGGGTTGATTCCCGATGGTAC

Table 17 Nucleotide sequence alignment of the ITS1 region of *Brugia* spp. compared to *B. malayi*, *B. pahangi*, and *D. immitis*.

C10 Cat6	TATCG-TGCTTCAAAAAAAAA-----TAACAC-AACAAAGATTGA---ATTTATTATTATT 50
C6 Cat6	TATCG-TGCTTCAAAAAAAAA-----TAACAC-AACAAAGATTGA---ATTTATTATTATT 50
C8 Cat6	TATCG-TGCTTCAAAAAAAAA-----ACAC-AACAATGATTGA---ATTTATTATTATT 48
C2 Cat6	TATCG-TGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATTATT 50
C3 Cat7	TATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATTATT 51
C36 Cat5	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 50
C41 Cat5	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
C38 Cat4	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 52
C28 Cat4	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 52
C33 Cat4	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
C45 Cat6	GTTTCGGTGTTCAAAAAAATAT---TA-CAC-ATCAACGATAGA---ATTTTTCAAA---T 48
AF217800Di	ATACTAC-TATTAACATCATT---TG-CTG-CTTATTTTCATT---CTTTTTCAAA---T 49
C58 Cat3	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATT---T 47
AY621468Bm	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 48
AY621466Bm	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
AY621467Bm	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
AY621464Bm	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
AY621465Bm	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
AY499507Bm	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 50
C30 Cat3	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 50
C30 Cat2	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
C3 Cat4	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 52
C22 Cat2	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAGTATTGA---ATTTATTATT---T 49
C9 Cat5	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
C54 Cat3	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 52
C4 Cat4	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 51
C31 Cat3	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 53
C13 Cat5	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
C17 Cat5	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
C15 Cat2	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 51
C62 Cat3	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
C23 Cat3	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
C12 Cat3	TTATCGTGCTTCAAAAAAAAA-----TAGCAC-AACAACGATTGA---ATTTATTATT---T 49
C48 Cat2	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 52
C36 Cat2	TTATCGTGCTTCAAAAAAAAA-----TACCCC-ACCAATGATTGA---ATTTATTATT---T 49
C7 Cat5	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
C19 Cat2	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
C46 Cat2	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 49
C8 Cat5	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATT---T 50
C18 Cat7	ATATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATTATT 52
C9 Cat7	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATTATT 52
C22 Cat7	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATTATT 52
C41 Cat7	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATTATT 52
C5 Cat6	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATTATT 52
AY621470Bp	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATTATT 52
AY621471Bp	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATTATT 52
AY621469Bp	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATTATT 52
AY621472Bp	TTATCGTGCTTCAAAAAAAAA-----TAACAC-AACAATGATTGA---ATTTATTATTATT 52
C5 Cat1	TTTTGGTGTTCAAAAAAAA-----TACCCC-ACCAGGGTGGATTGATTTTTATTATT 56

Table 17 (continued)

C1	Cat1	TTATCGTGTTCAAAAAAAAA---TAACCC-AACAATGATTGATTGATTATTACTATT	56
C3	Cat1	TTATCGTGCTTCAAAAAAAAAA---TAACAC-ACCAATGATTGATTGATTATTACTATT	57
C7	Cat1	ATCGTGCTTCAAAAAAAAAA---TAACAC-AACAATGATTG---ATTGATTATTACT	52
C4	Cat1	TCTTTGCGTTCAAAAAAAAA---TAACACCGGCAATGATTGT---ATTGATTAACT	54
C6	Cat1	TCTGTGC-TTCAAAAAAAAAA---TAACAC-AACAATGATTG---ATTGATTATTACT	51
C2	Cat1	TCTGTGC-TTCAAAAAAAAAA---TAACAC-AACAATGATTG---ATTGATTATTACT	51
C8	Cat1	ATCGTGC-TTCAAAAAAAAAA---TAACAC-AACAATGATTG---ATTGATTATTACT	51
		* * * * * * * *	
C10	Cat6	ATTATAGCTACCATA----TTATATTATGATACTATATTA--ACAACATATTG-TTGTA	102
C6	Cat6	ATTATAGCTACCATA----TTATATTATGATACTATATTA--ACAACATATTG-TTGTA	102
C8	Cat6	ATTATAGCTACCATA----TTATATTATGATACTATATTA--ACAACATATTG-TTGTA	100
C2	Cat6	ATTATAGCTACCATA----TTATATTATGATACTATATTA--ACAACATATTG-TTGTA	102
C3	Cat7	ATTATAGCTACCATA----TTATATTATGATACTATATTA--ACAACATATTG-TTGTA	103
C36	Cat5	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	105
C41	Cat5	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C38	Cat4	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	107
C28	Cat4	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	107
C33	Cat4	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C45	Cat6	AATAAAGGCGCCGAAAA-ATTTACATATGCATCCTATATTA--CCAACA-ACGGGTAGTA	104
AF217800Di		AATGCAAGAATGAAATA-GAATGAATGAATGATGTTAATAGATTAAATAGATGAATAGTT	108
C58	Cat3	ATTATAGCTACCATATATATATGTATTATGATACTATATTA--ACAACATATTG-TTGTA	104
AY621468Bm		ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	103
AY621466Bm		ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
AY621467Bm		ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
AY621464Bm		ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
AY621465Bm		ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
AY499507Bm		ATTATAGCTACCATA--TATA--TTATGATACTATATTA--ACAACATATTG-TTGTA	103
C30	Cat3	ATTATAGCTACCATATATATATATATATTATGATACTATATTA--ACAACATATTG-TTGTA	107
C30	Cat2	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C3	Cat4	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	107
C22	Cat2	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C9	Cat5	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C54	Cat3	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	107
C4	Cat4	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	106
C31	Cat3	ATAATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	108
C13	Cat5	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C17	Cat5	A---TAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	101
C15	Cat2	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	106
C62	Cat3	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C23	Cat3	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C12	Cat3	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C48	Cat2	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	107
C36	Cat2	ATTATAGCTCCCATATA--TATATATTATGATACTATATTA--ACAACATATTG-TGGTA	104
C7	Cat5	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C19	Cat2	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C46	Cat2	ATTATAGCTACCATA--TATATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C8	Cat5	ATTATTATAGCTACCAT--ATTATATTATGATACTATATTA--ACAACATATTG-TTGTA	105
C18	Cat7	ATTATTATAGCTACCAT--ATTATATTATGATACTATATTA--ACAACATATTG-TTGTA	107
C9	Cat7	ATTAT---AGCTACCAT--ATTATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C22	Cat7	ATTAT---AGCTACCAT--ATTATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C41	Cat7	ATTAT---AGCTACCAT--ATTATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C5	Cat6	ATTAT---AGCTACCAT--ATTATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
AY621470Bp		ATTAT---AGCTACCAT--ATTATATTATGATACTATATTA--ACAACATATTG-TTGTA	104

Table 17 (continued)

AY621471Bp	ATTAT--AGCTACCAT--ATTATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
AY621469Bp	ATTAT--AGCTACCAT--ATTATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
AY621472Bp	ATTAT--AGCTACCAT--ATTATATTATGATACTATATTA--ACAACATATTG-TTGTA	104
C5 Cat1	CCTATAGCTCCCATA-----TTATTTTAGGATCCTATATTA--CCACCATATTG-TGGTA	108
C1 Cat1	ACTATAGCTACCATA-----TTATATTATGATACTATATTA--ACAACATATTG-TGGTA	108
C3 Cat1	ACTATAGCTCCCATA-----TTATATTATGATACTATATTA--ACAACATATTG-TTGTA	109
C7 Cat1	ATTACTATAGCT-ACCATATTATATTA-TGATA-CTATATTAACAACATATT--GTTGTA	107
C4 Cat1	ATTACCTCCTCCGAACATAGGGTAATAATGACAACCCTCTTCCCGATCAGTTTGGCTGTA	114
C6 Cat1	ATTACTATAGCT-ACCATATTATATTA-TGATA-CTATATTAACAACATATT--GTTGTA	106
C2 Cat1	ATTACTATAGCT-ACCATATTATATTA-TGATA-CTATATTAACAACATATT--GTTGTA	106
C8 Cat1	ATTACTATAGCT-ACCATATTATATTA-TGATA-CTATATTAACAACATATT--GTTGTA	106
	* * *	**
C10 Cat6	TGTGTTACTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAGTAATAATA	161
C6 Cat6	TGTGTTACTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAGTAATAATA	161
C8 Cat6	TGTGTTACTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAGTAATAATA	159
C2 Cat6	TGTGTTACTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAGTAATAATA	161
C3 Cat7	TGTGTTACTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAGTAATAATA	162
C36 Cat5	TGTGTTATTGATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	164
C41 Cat5	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
C38 Cat4	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	166
C28 Cat4	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	166
C33 Cat4	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
C45 Cat6	GGTGCCCTTAATAAATTGTCCTAATTAATTTA-AATATGGTGTTAGCAT-AATTATTATT	162
AF217800Di	AGTAGTAGTTAGTAGTTAGTTAGATAGATAGA-TAAATGAAATGATGATGAAATATTTT	167
C58 Cat3	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
AY621468Bm	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	162
AY621466Bm	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
AY621467Bm	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
AY621464Bm	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
AY621465Bm	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
AY499507Bm	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	162
C30 Cat3	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	166
C30 Cat2	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
C3 Cat4	TGTGTTGTTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	166
C22 Cat2	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
C9 Cat5	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
C54 Cat3	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	166
C4 Cat4	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	165
C31 Cat3	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	167
C13 Cat5	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
C17 Cat5	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	160
C15 Cat2	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	165
C62 Cat3	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
C23 Cat3	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
C12 Cat3	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
C48 Cat2	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	166
C36 Cat2	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTGGCATAAATAATAATA	163
C7 Cat5	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
C19 Cat2	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
C46 Cat2	TGTGTTATTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAATAATAATA	163
C8 Cat5	TGTGTTACTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAGTAATAATA	164
C18 Cat7	TGTGTTACTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAGTAATAATA	166
C9 Cat7	TGTGTTACTAATAGATTGATGTTAATAATTTT-AATATGGTAGTAGCATAAGTAATAATA	163

Table 17 (continued)

C22 Cat7	TGTGTTACTAATAGATTGATGTTAATAATTTT - AATATGGTAGTAGCATAAGTAATAATA	163
C41 Cat7	TGTGTTACTAATAGATTGATGTTAATAATTTT - AATATGGTAGTAGCATAAGTAATAATA	163
C5 Cat6	TGTGTTACTAATAGATTGATGTTAATAATTTT - AATATGGTAGTAGCATAAGTAATAATA	163
AY621470Bp	TGTGTTACTAATAGATCGATGTTAATAATTTT - AATATGGTAGTAGCATAAGTAATAATA	163
AY621471Bp	TGTGTTACTAATAGATTGATGTTAATAATTTT - AATATGGTAGTAGCATAAGTAATAATA	163
AY621469Bp	TGTGTTACTAATAGATTGATGTTAATAATTTT - AATATGGTAGTAGCATAAGTAATAATA	163
AY621472Bp	TGTGTTACTAATAGATTGATGTTGATAATTTT - AATATGGTAGTAGCATAAGTAATAATA	163
C5 Cat1	GGTGTGTTCCCTAA - - - - AAGATGGATTTT - AATAGGGTAGTGGCTTAAATAATAATG	162
C1 Cat1	TGTGTGTTACCCTAA - - - - TAGATTGATTTT - AATATGGTAGTAGCTTAAATAATAATA	162
C3 Cat1	TGTGTGTTACCCTAA - - - - TAGATTGATTTT - AATATGGTAGTAGCTTAAATAATAATA	163
C7 Cat1	TGTGTGTTA - - - - CCCTAATAGATTGATTTT - AATATGGTAGTAGCTTAAATAATAATA	161
C4 Cat1	TGGGTTTTTAC - - - - CCCTAATAGATTGATTTGGAATCTGGGAGGAGCTTTAATTATTTTA	171
C6 Cat1	TGTGTGTTA - - - - CCCTAATAGATTGATTTT - AATATGGTAGTAGCTTAAATAATAATA	160
C2 Cat1	TGTGTGTTA - - - - CCCTAATAGATTGATTTT - AATATGGTAGTAGCTTAAATAATAATA	160
C8 Cat1	TGTGTGTTA - - - - CCCTAATAGATTGATTTT - AATATGGTAGTAGCTTAAATAATAATA	160
	* * * * *	
C10 Cat6	ATAATAATAATAATAAT - - - ATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	218
C6 Cat6	ATAATAATAATAATAAT - - - ATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	218
C8 Cat6	ATAATAATAATAATAAT - - - ATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	216
C2 Cat6	ATAATAATAATAATAAT - - - ATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	218
C3 Cat7	ATAATAATA - - - - - TGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	210
C36 Cat5	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	215
C41 Cat5	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
C38 Cat4	ATAATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	220
C28 Cat4	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	217
C33 Cat4	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
C45 Cat6	ATC - - ATTATTTGGG - - - - - GAGATAATCGGTGTTATTCGTTGGGTTTTTAACTTTTTT	214
AF217800Di	ATTCGATCAATTGA - - - - - ATATAAACGGTGATATTCGTTGGTGTCTATATTTTATC	219
C58 Cat3	ATAATAATAATATG - - - - - AATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
AY621468Bm	ATAATAATAATATG - - - - - AATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	213
AY621466Bm	ATAATAATAATATG - - - - - AATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
AY621467Bm	ATAATAATAATATG - - - - - AATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
AY621464Bm	ATAATAATAATATG - - - - - AATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
AY621465Bm	ATAATAATAATATG - - - - - AATGAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
AY499507Bm	ATAATAATAATATG - - - - - AATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	213
C30 Cat3	ATAATAATAATATG - - - - - AATAAACGGTGATATTCGTCGGTGTCTATACTTTATC	217
C30 Cat2	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
C3 Cat4	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	217
C22 Cat2	ATAATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	217
C9 Cat5	ATAATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	217
C54 Cat3	ATAATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	220
C4 Cat4	ATAATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	219
C31 Cat3	GTAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	218
C13 Cat5	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
C17 Cat5	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	211
C15 Cat2	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	216
C62 Cat3	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
C23 Cat3	ACAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
C12 Cat3	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
C48 Cat2	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	217
C36 Cat2	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
C7 Cat5	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
C19 Cat2	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214
C46 Cat2	ATAATAATAATA - - - - - TGAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	214

Table 17 (continued)

C8 Cat5	ATAATAATAATATG-----AATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	215
C18 Cat7	ATAATAAT-----ATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	214
C9 Cat7	ATAATAAT-----ATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	211
C22 Cat7	ATAATAATAATAATAATAATATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	223
C41 Cat7	ATAATAATAATAATAAT--ATGAATGAACGGTGTTATTCGTTGGTGTCTATACTTTATC	220
C5 Cat6	ATAATAATAATAATAAT--ATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	220
AY621470Bp	ATAATAATAATAATAAT--ATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	220
AY621471Bp	ATAATAATAATAATAAT--ATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	220
AY621469Bp	ATAATAATAATAATAAT--ATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	220
AY621472Bp	ATAATAATAATAATAAT--ATGAATAAACGGTGTTATTCGTTGGTGTCTATACTTTATC	220
C5 Cat1	GT---ATTAATAGG-----ATTAACCGGGGATTTTGGTGGGTGTTTATATTTTATC	210
C1 Cat1	GT---AATAATAGG-----AATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	210
C3 Cat1	GT---AATAATATG-----AATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	211
C7 Cat1	GTAATAATAT-----GAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	209
C4 Cat1	GTTATAATAT-----GCAAAACCCGGGATTATCGTTGGTGGCTAAACTTTATC	219
C6 Cat1	GTAATAATAT-----GAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	208
C2 Cat1	GTAATAATAT-----GAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	208
C8 Cat1	GTAATAATAT-----GAATAAACGGTGATATTCGTTGGTGTCTATACTTTATC	208
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C10 Cat6	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	275
C6 Cat6	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	275
C8 Cat6	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	273
C2 Cat6	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	275
C3 Cat7	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	267
C36 Cat5	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	272
C41 Cat5	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
C38 Cat4	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	277
C28 Cat4	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	274
C33 Cat4	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
C45 Cat6	CAACTGACACCTTAAATCAGTTAACCA-TTGAGTCAAAATCGAAAAGGTTATTTAATT-	272
AF217800Di	TAAGTTATCGCCTAACCGTCGATAGCGA-TGAAGATAAAAT--GATAGCTTAATTGATGA	276
C58 Cat3	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
AY621468Bm	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	270
AY621466Bm	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
AY621467Bm	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
AY621464Bm	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
AY621465Bm	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
AY499507Bm	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	270
C30 Cat3	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	274
C30 Cat2	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
C3 Cat4	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	274
C22 Cat2	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	274
C9 Cat5	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	274
C54 Cat3	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	277
C4 Cat4	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	276
C31 Cat3	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATGAATTT	275
C13 Cat5	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
C17 Cat5	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	268
C15 Cat2	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	273
C62 Cat3	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
C23 Cat3	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
C12 Cat3	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
C48 Cat2	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	274

Table 17 (continued)

C36 Cat2	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
C7 Cat5	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
C19 Cat2	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
C46 Cat2	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	271
C8 Cat5	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	272
C18 Cat7	CAAGTTATCGCCTAACTGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATCT	271
C9 Cat7	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	268
C22 Cat7	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	280
C41 Cat7	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	277
C5 Cat6	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	277
AY621470Bp	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	277
AY621471Bp	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	277
AY621469Bp	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	277
AY621472Bp	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	277
C5 Cat1	CAAGTTATCGCTTACCCGTGGATAACAA-TGAAGATAAAGC--GAGAGCTTAATTAATTT	267
C1 Cat1	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	267
C3 Cat1	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	268
C7 Cat1	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	266
C4 Cat1	CAAGGTTTTACCCTATCGCCATTATAAATGGAGAAAAAGC--CAAGCTTAAATCACTTT	277
C6 Cat1	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	265
C2 Cat1	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	265
C8 Cat1	CAAGTTATCGCCTAACCGTCGATAACAA-TGAAGATAAAGC--GATAGCTTAATTAATTT	265
	** * * * * *	
C10 Cat6	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	332
C6 Cat6	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	332
C8 Cat6	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	330
C2 Cat6	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	332
C3 Cat7	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	324
C36 Cat5	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	329
C41 Cat5	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	328
C38 Cat4	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	334
C28 Cat4	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	331
C33 Cat4	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	328
C45 Cat6	TACCAATTGAATAGAGTAGATT-CACCAACCATTACACC-G-TTT-ATTC-----	319
AF217800Di	TGATTGCTCAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-TAT-GCTACCAACAAA-	332
C58 Cat3	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	328
AY621468Bm	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	327
AY621466Bm	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	328
AY621467Bm	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	328
AY621464Bm	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	328
AY621465Bm	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	328
AY499507Bm	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	327
C30 Cat3	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	331
C30 Cat2	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	328
C3 Cat4	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	331
C22 Cat2	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	331
C9 Cat5	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	331
C54 Cat3	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	334
C4 Cat4	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	333
C31 Cat3	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAAAA	332
C13 Cat5	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTACGCTAGATAT-GCTACCAACAAGA	328
C17 Cat5	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAA-A	324
C15 Cat2	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTTATGCTAGATAT-GCTACCAACAA-A	329

Table 17 (continued)

C62 Cat3	TACC-ATTTAATTAAGTAGGCT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	328
C23 Cat3	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGGTAT-GCTACCAACAAAA	328
C12 Cat3	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	328
C48 Cat2	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTCCCAACAAAA	331
C36 Cat2	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTCCCACCAAAA	328
C7 Cat5	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	328
C19 Cat2	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	328
C46 Cat2	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	328
C8 Cat5	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	329
C18 Cat7	TATC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	328
C9 Cat7	TATC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	325
C22 Cat7	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	337
C41 Cat7	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	334
C5 Cat6	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	334
AY621470Bp	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	334
AY621471Bp	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	334
AY621469Bp	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	334
AY621472Bp	TACC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACAAAA	334
C5 Cat1	TATC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTCCCACCAAAA	324
C1 Cat1	TATC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTCCCACCAAAA	324
C3 Cat1	TATC-ATTTAATTAAGTAGACT-TAATAAGCATTATGCTAGATAT-GCTCCCACCAAAA	325
C7 Cat1	TATCATTTAATTA-AGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACT---	320
C4 Cat1	TAACCATGGAATT-AGTAAACCACAAAAAGGCTTTTGTGCACATTGGTCCCAACC---	333
C6 Cat1	TATCATTTAATTA-AGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCCACA---	319
C2 Cat1	TATCATTTAATTA-AGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACA---	319
C8 Cat1	TATCATTTAATTA-AGTAGACT-TAATAAGCATTATGCTAGATAT-GCTACCAACA---	319
	* * * * *	
C10 Cat6	AAAAAAAAAAAAAAAAAA--CATACAAAAAAGTTATATATATA--TTATAGTAATAACAA	387
C6 Cat6	AAAAAAAAAAAAAAAAAA--CTTCCAAAAAAGTTATATATATA--TTATAGTAATAACAA	387
C8 Cat6	AAAAAAAAAAAAAAAAAA--CTTACAAAAAAGTTATATATATA--TTATAGTAATAACAA	387
C2 Cat6	AAAAAAAAAAAAAAAAAA--CTTACAAAAAAGTTATATATATA--TTATAGTAATAACAA	390
C3 Cat7	AAAAAAAAAAAAAAAAAA--CATACAAAAAAGTTATACATATA--TTATAGTAATAACAA	376
C36 Cat5	AAAAAAAAAAAAAAAAAA--GA--CATACAAAAAATTATATATATA--TTATAGTAATAATAA	382
C41 Cat5	AAAAAAAAAAAAAAAAAA--GA--CATACAAAAAATTATATATATA--TTATAGTAATAATAA	381
C38 Cat4	AAAAAAAA--GA--CATACAAAAA--TTATATATATA--TTATAGTAATAATAA	381
C28 Cat4	AAAAAAAA--GA--CATACAAAAA--CTATATATATA--TTATAGTAATAATAA	378
C33 Cat4	AAAAAAAAAAAAAAAAAA--GA--CATACAAAAAATTATATACATA--TTATAGTAATAATAA	382
C45 Cat6	ATATTATAAATAT---A---ATTACTTATGC-TACTAC-CATA--TTAAAATTAT--TAA	367
AF217800Di	ATAATACACACAC---A---CATACATACAA-TAATAT-GATA--TAATTGTTAT--TTA	380
C58 Cat3	AAAAAAAAAAAAAG--A---CATACAAAAA--TTATATATATA--TTATAGTAATAATAA	379
AY621468Bm	AAAAAAAAAAAAAAAAAA--GA--CATACAAAAAATTATATATATA--TTATAGTAATAATAA	378
AY621466Bm	AAAAAAAAAAAAAAAAAA--GA--CATACAAAAAATTATATATATA--TTATAGTAATAATAA	383
AY621467Bm	AAAAAAAAAAAAAAAAAA--GA--CATACAAAAAATTATATATATA--TTATAGTAATAATAA	381
AY621464Bm	AAAAAAAAAAAAAAAAAA--GA--CATACAAAAAATTATATATATA--TTATAGTAATAATAA	381
AY621465Bm	AAAAAAAAAAAAAAAAAA--GA--CATACAAAAAATTATATATATA--TTATAGTAATAATAA	380
AY499507Bm	AAAAAAAAAAAAAGA-----CATACAAAAA--TTATATATATA--TTATAGTAATAATAA	376
C30 Cat3	AAAAAAAAAAAAAGAC--A---TACAAAAAATTATATATATATA--TTATAGTAATAATAA	384
C30 Cat2	AAAAAAAAAAAA--GA--CATACAAAAAATTATATATATA--TTATAGTAATAATAA	379
C3 Cat4	AAAAAAAAAAAA--GA--CATACAAAAAATTATATATATA--TTATAGTAATAATAA	383
C22 Cat2	AAAAAAAAAAAA--GA--CATACAAAAAATTATATATATA--TTATAGTAATAATAA	382
C9 Cat5	AAAAAAAAAAAA--GA--CATACAAAAAAGATTATATATATA--TTATAGTAATAATAA	383
C54 Cat3	AAAAAAA-AA---GA--CATACAAAAA--ATTATATATATA--TTATAGTAATAATAA	383
C4 Cat4	AAAAA---AA---GG--CATACAAAAA--ATTATATATATA--TTATAGTAATAATAA	379

C31	Cat3	AAAAAAAAAAAAA- - - GA - - - CATACAAAAAA-ATTATATATATA- - TTATAGTAATAATAA	382
C13	Cat5	AAAAAAAAAAAAAAAAA- GA - - - CATACAAAAAAATTATATATATA- - TTATAGTAATAATAA	382
C17	Cat5	AAAAAAAAAAAAAAAAA- GA - - - CATACAAAAAAATTATATATATA- - TTATAGTAATAATAA	378
C15	Cat2	AAAAAAAAAAAAAAAAA- GA - - - CATACAAAAAAATTATATATATA- - TTATAGTAATAATAA	383
C62	Cat3	AAAAAAAAAAAAAAAAA- GA - - - CATACAAAAAAGTTATATATATA- - TTATAGTAATAATAA	382
C23	Cat3	AAAAAAAAAAAAAA- - - GA - - - CATACAAAAAA- TTATATATATA- - TTATAGTAATAATAA	379
C12	Cat3	AAAAAAAAAAAAAAAAA- GA - - - CATACAAAAAAATTATATATATA- - TTATAGTAATAATAA	382
C48	Cat2	AAAAAAAAAAAAAA- - - AA - - - GACATACAAAAAAATTATATATA- - TTATAGTAATAATAA	383
C36	Cat2	AAAAAAAAAAAAAA- - - GA - - - CATACAAAAAAATTATATATATA- - TTATAGTAATAATAA	380
C7	Cat5	AAAAAAAAAAAAAA- - - - GA - - - CATACAAAAAAATTATATATATA- - TTATAGTAATAATAA	379
C19	Cat2	AAAAAAAAAAAAAA- - - - GA - - - CATACAAAAAAATTATATATATATATTATAGTAATAATAA	381
C46	Cat2	AAAAAAAAAAAAAA- - - - GA - - - CATACAAAAAAATTATATATATA- - TTATAGTAATAATAA	379
C8	Cat5	AAAAAAAAAAAAAAG- - - - A - - - CATACAAAAAATTA- TATATATA- - TTATAGTAATAATAA	379
C18	Cat7	AAAAAAAAAAAAAAAAA- A - - - CATACAAAAAAGTTATATATATA- - TTATAGTAATAACAA	381
C9	Cat7	AAAAAAAAAAAAAAAAA- AA - - - CATACAAAAAAGTTATACATATA- - TTATAGTAATAACAA	379
C22	Cat7	AAAAAAAAAAAAAAAAA- AA - - - CATACAAAAAAGTTATACATATA- - TTATAGTAATAACAA	391
C41	Cat7	AAAAAAAAAA- - - - A- AA - - - CATACAAAAAAGTTATACATATA- - TTATAGTAATAACAA	384
C5	Cat6	AAAAAAAAAAAAAA- A- AA - - - CATACAAAAAAGTTATACATATA- - TTATAGTAATAACAA	387
AY621470Bp		AAAAAAAAAAAAAA- A- - A - - - CATACAAAAAAGTTATACATATA- - TTATAGTAATAACAA	386
AY621471Bp		GAAAAAAAAAAAAAA- AA - - - CATACAAAAAAGTTATACATATA- - TTATAGTAATAACAA	388
AY621469Bp		AAAAAAAAAAAAAAACAA- - - CATACAAAAAAGTTATACATATA- - TTATAGTAATAACAA	389
AY621472Bp		AAAAAAAAAAAAAA- - - - CATACAAAAAAGTTATACATATA- - TTATAGTAATAACAA	389
C5	Cat1	AAAAAAAAAA- - - - - - - - - AAAAAAAAAAG- - - CCTGCCCAAA- - TTATATATATTATAG	369
C1	Cat1	AAAAAAAAAA- - - - - - - - - AAAAAAAAAAAAAACATACACAAA- - TTATATATATTATAG	372
C3	Cat1	AAAAAAAAAA- - - - - - - - - AAAAAAAAAAAAAACATACACAAA- - TTATATATATTATAG	373
C7	Cat1	AAAAAAAAAAAAA- - - - - - - - - AAAAAAAAAAACCTCCCCCAATTATA- - - TATATT- A	365
C4	Cat1	TGAGGGCAATTATC- - - - - TTTAAAAAGAAGTCGTGCCCCCCCTTTCAAGTCATATTTG	387
C6	Cat1	AAAAAAAAAAAAA- - - - - - - - - AAAAAAAAAAAAAACCTACCCAAATTATA- TATATT- A	366
C2	Cat1	AAAAAAAAAAAAAA- - - - - A- - AAAAAAAAAACCATACCCAAATTATA- - - - TATATT- A	366
C8	Cat1	AAAAAAAAAAAAAA- - - - - A- - AAAAAAAAAACCTTACCCAAATTATA- - - - TATATT- A	366
		* * *	
C10	Cat6	TAAAATTTTTTTA- - - AACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	441
C6	Cat6	TAAAATTTTTTTA- - - AACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	441
C8	Cat6	TAAAATTTTTTTT- - - AACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	441
C2	Cat6	TAAAATTTTTTTA- - - AACTCTTAGCGGTGG- ATCACTTGGCTCATGTATCGAT- - GAAGA	444
C3	Cat7	TAAAATTTTTTTTT- - - AACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	431
C36	Cat5	TAAAATTTTTTTTTTAACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	439
C41	Cat5	TAAAATTTTTTTTTT- AACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	437
C38	Cat4	TAAAAATTTTTTTTTAACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	438
C28	Cat4	TAAAAATTTTTTTTTTAACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	435
C33	Cat4	TAAAAATTTTTTTTTTAACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	439
C45	Cat6	CATCAATCTATTAGTAACACATACAACAT- ATGTTGTTAATATAGTATCAT- - ATATA	424
AF217800Di		TAATAATTTTTTCAATAACTCTAAGCGGGG- ATCACTTGGCTCGTGGATCGAT- - GAAGA	437
C58	Cat3	TAAAATTTTTTTTT- TAACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	435
AY621468Bm		- - - AAATTTTTTTTTTAACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	432
AY621466Bm		TAAAATTTTTTTTTTAACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	440
AY621467Bm		TAAAATTTTTTTTTTAACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	438
AY621464Bm		TAAAATTTTTTTTTT- AACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	437
AY621465Bm		TAAAATTTTTTTTTTAACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	437
AY499507Bm		TAAAATTTTTTTTTTAACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	433
C30	Cat3	TAAAATTTTTTTTTTAACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	441
C30	Cat2	TAAAATTTTTTTTTTAACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	436
C3	Cat4	TAAAATTTTTTTTTTAACTCTTAGCGGTGG- ATCACTTGGCTCATGGATCGAT- - GAAGA	440

Table 17 (continued)

C22 Cat2	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	439
C9 Cat5	TAAAAATTTTTTTTT-AACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	439
C54 Cat3	TAAAAATCTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	440
C4 Cat4	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	436
C31 Cat3	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	439
C13 Cat5	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	439
C17 Cat5	TAAAAATTTTTTTTT-AACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	434
C15 Cat2	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	440
C62 Cat3	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	439
C23 Cat3	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	436
C12 Cat3	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	439
C48 Cat2	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	440
C36 Cat2	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	437
C7 Cat5	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	436
C19 Cat2	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	438
C46 Cat2	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	436
C8 Cat5	TAAAAATTTTTTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	436
C18 Cat7	TAAATTTTTTTT---AACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	435
C9 Cat7	TAAATTTTTTTT---TAACCTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	434
C22 Cat7	TAAATTTTTTTT---TAACCTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	446
C41 Cat7	TAAATTTTTTTT---TAACCTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	439
C5 Cat6	TAAATTTTTTTT---TAACCTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	442
AY621470Bp	TAAATTTTTTTT---TAACCTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	441
AY621471Bp	TAAATTTTTTTT---TAACCTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	443
AY621469Bp	TAAATTTTTTTT---TAACCTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	444
AY621472Bp	TAAATTTTTTTT---TAACCTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	444
C5 Cat1	TAATAAATTTTT---AACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	423
C1 Cat1	TAATAAATTTTT---AACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	426
C3 Cat1	TAATAAATTTTT---AACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAGA	427
C7 Cat1	TAGTAATAAATTTTTAACTCTTAACGGGTGG-ATCACTTGGCTCATGGATCGAT--GAAAA	422
C4 Cat1	CGCTAAAAATTTTTTGACCTTACCGGGGGGATCCCTGGGGCCTGGGGCCTTTTAAAAA	447
C6 Cat1	TAGTAATAAATTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAAA	423
C2 Cat1	TAGTAATAAATTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAAA	423
C8 Cat1	TAGTAATAAATTTTTAACTCTTAGCGGTGG-ATCACTTGGCTCATGGATCGAT--GAAAA	423
	* * * * *	
C10 Cat6	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	494
C6 Cat6	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	494
C8 Cat6	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	494
C2 Cat6	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	497
C3 Cat7	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	484
C36 Cat5	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	492
C41 Cat5	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	490
C38 Cat4	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	491
C28 Cat4	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	488
C33 Cat4	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	492
C45 Cat6	ATATGG--TAGCTAT--AATAATAATAATA-AATTCAATC--ATTGTTGTGTTATTTTT	476
AF217800Di	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	490
C58 Cat3	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGGACAAAGA	488
AY621468Bm	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	485
AY621466Bm	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	493
AY621467Bm	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	491
AY621464Bm	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	490

Table 17 (continued)

AY621465Bm	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	490
AY499507Bm	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	486
C30 Cat3	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	494
C30 Cat2	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	489
C3 Cat4	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	493
C22 Cat2	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	492
C9 Cat5	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	492
C54 Cat3	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	493
C4 Cat4	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	489
C31 Cat3	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	492
C13 Cat5	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	492
C17 Cat5	ACGCGGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	487
C15 Cat2	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	493
C62 Cat3	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	492
C23 Cat3	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	489
C12 Cat3	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	492
C48 Cat2	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	493
C36 Cat2	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	490
C7 Cat5	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	489
C19 Cat2	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	491
C46 Cat2	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	489
C8 Cat5	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--TGCATTGAGCACAAAGA	489
C18 Cat7	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	488
C9 Cat7	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	487
C22 Cat7	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	499
C41 Cat7	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	492
C5 Cat6	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	495
AY621470Bp	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	494
AY621471Bp	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	496
AY621469Bp	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	497
AY621472Bp	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAAA	497
C5 Cat1	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	476
C1 Cat1	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	479
C3 Cat1	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAGA--CGCATTGAGCACAAAGA	480
C7 Cat1	ACGCACC--TAGCTGC--AATAAATATTGCG-AATTGCAGA--CCCATTGAGCACAAAGA	475
C4 Cat1	ACTGATCAATATCTGTTTATTAATAATTTTCGCAATTGCCCTCCCTTTTGTACGAAGA	507
C6 Cat1	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAAA--CGCATTGAGCACAAAGA	476
C2 Cat1	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAAA--CGCATTGAGCACAAAGA	476
C8 Cat1	ACGCAGC--TAGCTGC--GATAAATAGTGCG-AATTGCAAA--CGCATTGAGCACAAAGA	476
	* ** ** *** * ***** **	
C10 Cat6	TTTCGAATGC-ACATTGCACCATTGGGTAAATCTGAATTCGTGC	537
C6 Cat6	TTTCGAATGC-ACATTGCACCATTGGGTAAATCTGAATTCGTGC	537
C8 Cat6	TTTCGAATGC-ACATTGCACCATTGGGTAAATCTGAATTCGTGC	537
C2 Cat6	TTTCGAATGC-ACATTGCACCATTGGGTAAATCTGAATTCGTGC	540
C3 Cat7	TTTCGAATGC-ACATTGCACCATTGGGTAAATCTGAATTCGTGC	527
C36 Cat5	TTTCGAATGC-ACATTGCACCATTGGGTAAATCTGAATTCGTGC	535
C41 Cat5	TTTCGAATGC-ACATTGCACCATTGGGTAAATCTGAATTCGTGC	533
C38 Cat4	TTTCGAATGC-ACATTGCACCATTGGGTAAATCTGAATTCGTGC	534
C28 Cat4	TTTCGAATGC-ACATTGCACCATTGGGTAAATCTGAATTCGTGC	531
C33 Cat4	TTTCGAATGC-ACATTGCACCATTGGGTAAATCTGAATTCGTGC	535
C45 Cat6	TTTGAAGCACGATAATGATCCTTCCGCAGGTTACCAAGGGCGA	520
AF217800Di	TTTCGAATGC-ACATTGCACCATCGGGTTGATTCCCGATGGTAC	533

Table 17 (continued)

C58 Cat3	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	524
AY621468Bm	TTTCGAATGC-ACATTGCACCATTGGGTGATTCCCG-----	521
AY621466Bm	TTTCGAATGC-ACATTGCACCATTGGGTGATTCCCG-----	529
AY621467Bm	TTTCGAATGC-ACATTGCACCATTGGGTGATTCCCG-----	527
AY621464Bm	TTTCGAATGC-ACATTGCACCATTGGGTGATTCCCG-----	526
AY621465Bm	TTTCGAATGC-ACATTGCACCATTGGGTGATTCCCG-----	526
AY499507Bm	TTTCGAATGC-ACATTGCACCATTGGGTGATTCCCG-----	522
C30 Cat3	TTTCGAATGC-ACATTGCACCATTGGGTTAATCTGAA-----	530
C30 Cat2	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	525
C3 Cat4	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	529
C22 Cat2	TTTCGAATGC-ACATTGCACCAT-GGGTTAATCACGA-----	527
C9 Cat5	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	528
C54 Cat3	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	529
C4 Cat4	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	525
C31 Cat3	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	528
C13 Cat5	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	528
C17 Cat5	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	523
C15 Cat2	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	529
C62 Cat3	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	528
C23 Cat3	TTTCGAATGC-ACATTGCACCATTGGGT-AATCACGA-----	524
C12 Cat3	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	528
C48 Cat2	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	529
C36 Cat2	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	526
C7 Cat5	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	525
C19 Cat2	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	527
C46 Cat2	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	525
C8 Cat5	TTTCGAATGC-ACATTGCACCATTGGGTTAATCTGAATTCGTCTG	532
C18 Cat7	TTTCGAATGC-ACATTGCACCATTGGGTTAAGGGCGA-----	524
C9 Cat7	TTTCGAATGC-ACATTGCACCATTGGGTTAAGGGCGA-----	523
C22 Cat7	TTTCGAATGC-ACATTGCACCATTGGGTTAAGGGCGA-----	535
C41 Cat7	TTTCGAATGC-ACATTGCACCATTGGGTTAAGGGCGA-----	528
C5 Cat6	TTTCGAATGC-ACATTGCACCATTGGGTTAAGGGCGA-----	531
AY621470Bp	TTTCGAATGC-ACATTGCACCATTGGGTGATTCCCG-----	530
AY621471Bp	TTTCGAATGC-ACATTGCACCATTGGGTGATTCCCG-----	532
AY621469Bp	TTTCGAATGC-ACATTGCACCATTGGGTGATTCCCG-----	533
AY621472Bp	TTTCGAATGC-ACATTGCACCATTGGGTGATTCCCG-----	533
C5 Cat1	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	512
C1 Cat1	TTTCGAATGC-ACATTGCACCATTGGGTTA-TCACGA-----	514
C3 Cat1	TTTCGAATGC-ACATTGCACCATTGGGTTAATCACGA-----	516
C7 Cat1	TTTCGAAT-GCCCATTCGACCATTGGGTTAATCTGAATTCGTCTG	518
C4 Cat1	TACTCATAGACTCTTGCGCTTGAGG---GGTGAAATAATCA	547
C6 Cat1	TTTCGAATGCAC-ATTGCACCATTGGGTTAATCTGAATTCGTCTG	519
C2 Cat1	TTTCGAATGCAC-ATTGCACCATTGGGTTAATCTGAATTCGTCTG	519
C8 Cat1	TTTCGAATGCAC-ATTGCACCATTGGGTTAATCTGAATTCGTCTG	519

** ** * * *

3.4 Phylogenetic tree construction of *Brugia* spp. based on ITS1 region

Phylogenetic tree construction based on ITS1 nucleotide sequences was analyzed by using PAUP program version 4.0 with Neighbor Joining (NJ) and DNA Parsimony (DNA PARS). For maximum parsimony analysis, the heuristic search strategy was utilized to find the most parsimonious trees using the parameters as followed; the number of substitution types = 2 (HKY85 variant), transition/ transversion ratio = estimate, distribution of rates at variable sites = gamma (discrete approximation) and shape parameter (alpha) = estimate. The bootstrap maximum parsimony was analyzed with 100 replicates, addition sequence = as-is and Branch-swapping algorithm = tree-bisection-reconnection (TBR), all minimal trees saved and zero branch lengths collapsed; all characters were assigned equal weight.

3.4.1 Neighbor Joining

A Neighbor Joining (NJ) distance analysis of these data is presented in Figure 15. According to the ITS1 NJ tree, 4 major groups of the parasites were obtained when rooted with *D. immitis* (outgroup). Group 1 contained feline *B. pahangi* from Thailand and 11 clones of cat 5, 6 and 7. Group 2 consisted of human *B. malayi* from Thailand and 24 clones of cat 2-5. Group 3 composed of 7 clones of cat 1. Lastly, group 4 comprised of 2 clones from cat 1 (C4) and cat 6 (C45).

3.4.2 DNA Parsimony

Similarly, The parsimony cladogram of ITS1 region exhibited 4 major groups. Group 1 comprised of *B. pahangi* and 11 clones of cat 6 and 7 with high bootstrap value (82%). Group 2 contained human *B. malayi* from GenBank with high bootstrap value (87%). Group 3 composed of 8 clone from cat 1 with high bootstrap value (94%). Lastly, group 4 consisted of 25 clones from cat 2-5 with low bootstrap value (51% and 52%)(Figure16).

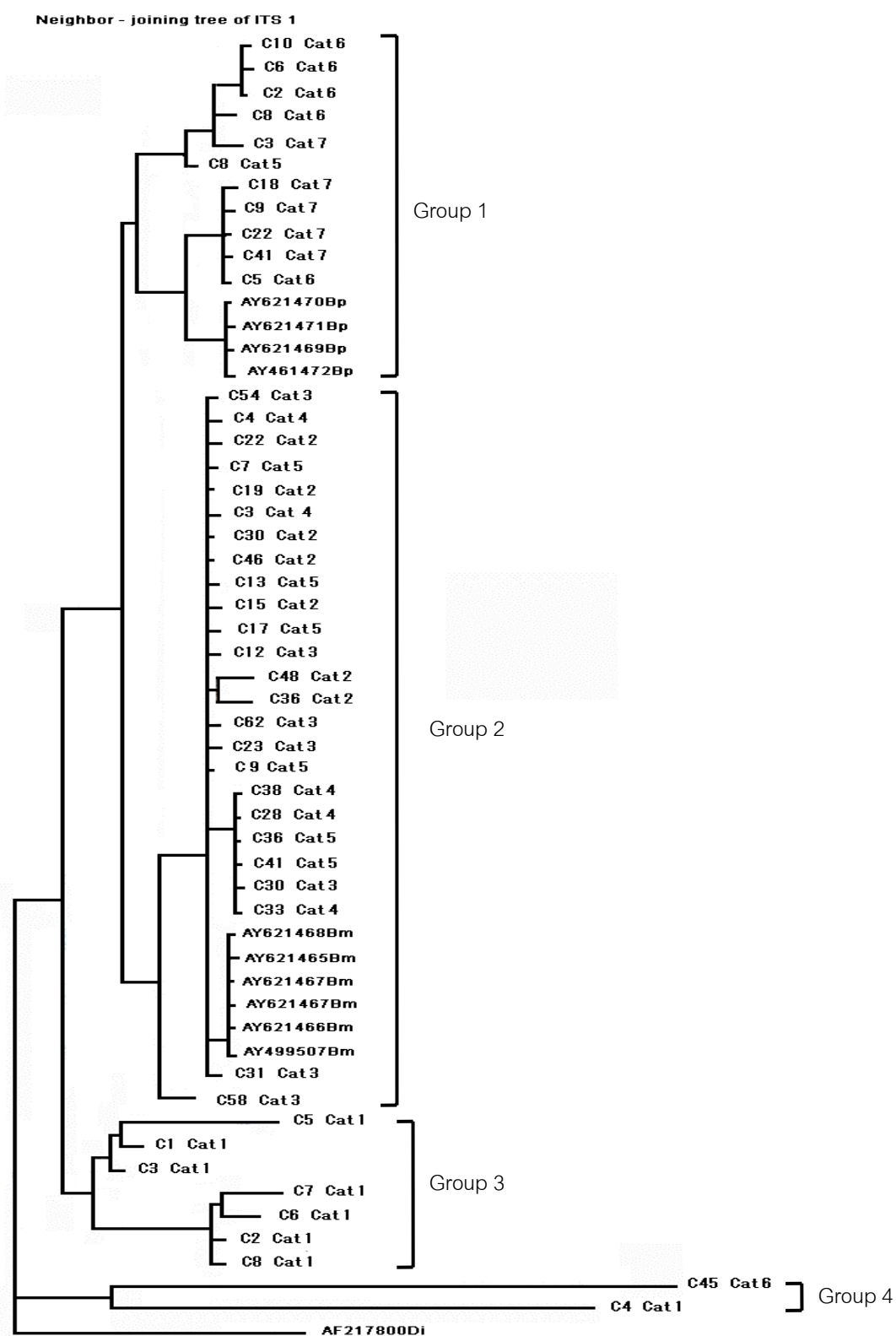


Figure 15 Phylogenetic relationship between 45 cloned of ITS1 region from feline *Brugia* spp. determined by neighbor-joining analysis.

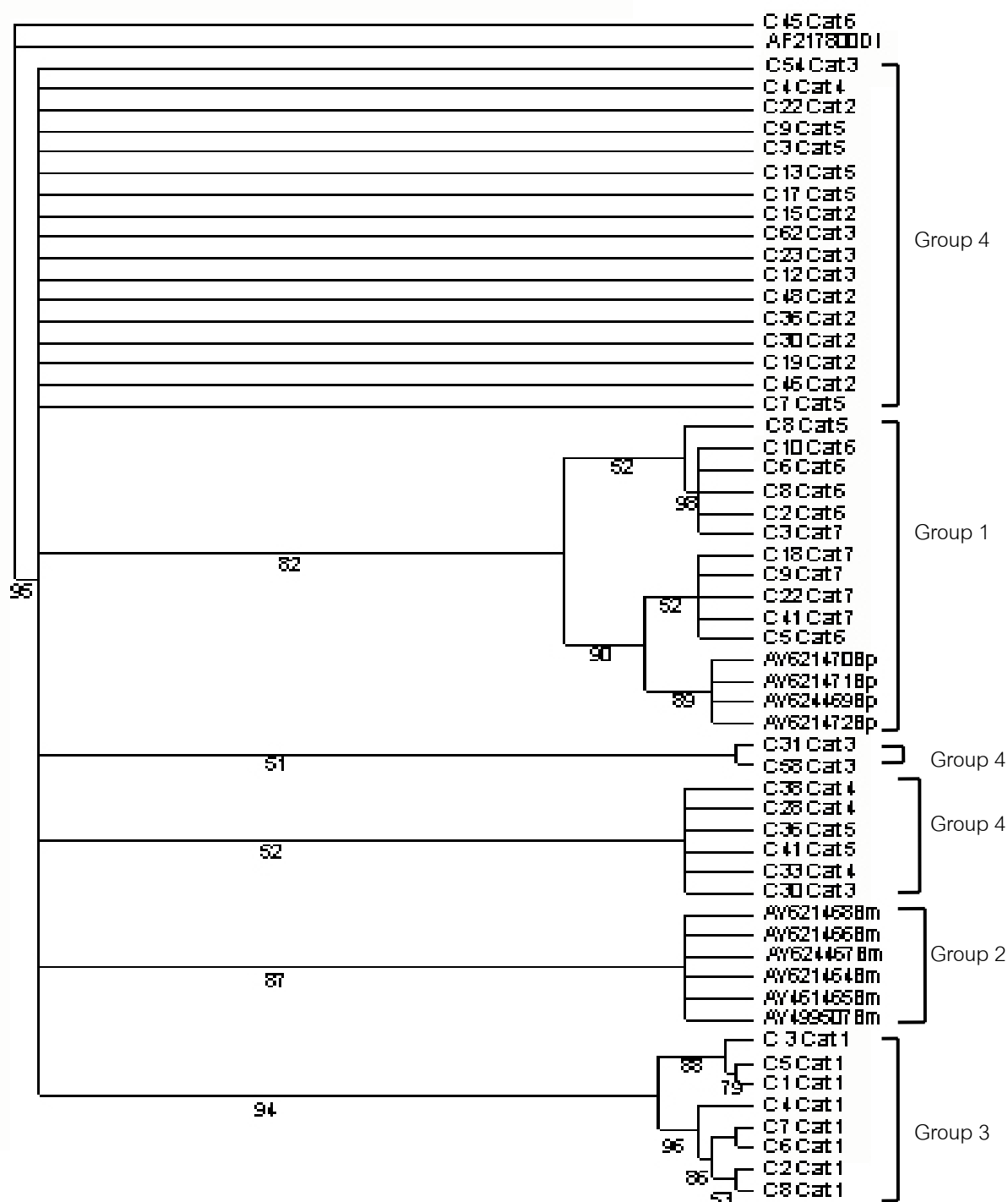


Figure 16 A pasimony cladogram of 45 clones of ITS1 region from feline *Brugia* spp. against *B. malayi*, *B. pahangi*, *B. timori*, and *D. immitis* (outgroup) produced by the heuristic search of PAUP version 4.0 and inferred from complete ITS1 region using a bootstrap resampling of the data set. The number at the nodes represent the percentage of times the group occurred out of 100 trees. Branches with less than 50% bootstrap support were collapsed. No significance is placed on the lengths of the branches connecting the species.

4. PCR amplification and DNA sequencing of ITS2 region

4.1 PCR amplification of ITS2 region

The PCR amplification was performed and analyzed according to the Materials and Methods 5. Figure 17 showed that the PCR product of approximately 660 bp in size was observed when ITS2F and ITS2R were used as primers.

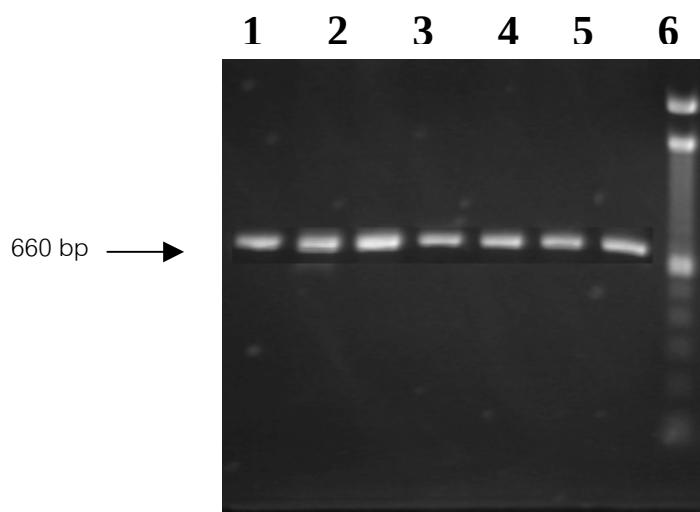


Figure 17 The PCR amplification profile of ITS2 from purified *Brugia* spp. DNA of cats in Narathiwat and Lad krabang. The PCR product of 660 bp in size was observed on 1.2% agarose gel electrophoresis using ITS2F and ITS2R as primer

Lane M = 100 bp DNA ladder marker

Lane 1 = PCR product of *Brugia* spp. from cat1

Lane 2 = PCR product of *Brugia* spp. from cat2

Lane 3 = PCR product of *Brugia* spp. from cat3

Lane 4 = PCR product of *Brugia* spp. from cat4

Lane 5 = PCR product of *Brugia* spp. from cat5

Lane 6 = PCR product of *Brugia* spp. from cat6

Lane 7 = PCR product of *Brugia* spp. from cat7

4.2 DNA sequencing of ITS2 region

PCR products of ITS2 gene from PCR amplification using ITS2F and ITS2R were used for cloning and DNA sequencing. Among ITS2 clones, 45 of them were randomly selected for proceeding to DNA sequencing (Table 18). The nucleotide sequence data of ITS2 were shown in Table 19.

Table 18 Summary of 45 clones of *Brugia* spp. ITS2 region from 7 cat reservoirs.

Cat	clone
Cat 1	C2, C4, C10, C28, C32
Cat 2	C2, C4, C5, C6, C8, C52
Cat 3	C2, C3, C6, C13, C39, C45
Cat 4	C2, C7, C24, C26, C34, C35, C37
Cat 5	C6, C9, C10, C28, C34, C57, C62
Cat 6	C3, C5, C6, C8, C9, C16
Cat 7	C4, C8, C9, C24, C37, C45, C54, C56

Table 19 Nucleotide sequence data of 45 clones of *Brugia* spp. ITS1 region from cat reservoirs.

C2 Cat1	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATC AAATAATTTTTGTTTGTTTGTTAAAAAGATTATTTGATGATAATG AATGAAAAAGATGATTGAATCAATGATTAGATACAAAATGCATC AGGTGATTTAGTAACAGAGAGAGTGAGAATGAAAAATCTCAAAA TAAATCCCCTGATAAGTAATAATAGATATGAGTAATATTTTTACC TTATTTAACATATTGAATATATATGTATATATATATATATATA TTAAAAAGTAATCTTTCATGAATAAATAATAAAGAAAGATTACAA TTATTTATTTATTATGCATTGATTTACTTTATTGTTTGTTTGTTT TGTTGTTAAATGTTTCAAATTATAATGCAAGTTATTTGAAACATT AAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGA ATGATAATTTCAATATGTTTTATATCATTTTTTT
C4 Cat1	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATC AAATAATTTTTGTTTGTTTGTTAAAAAGATTATTTGATGATAATG AATGAAAAAGATGATTGAATCAATGATTAGATACAAAATGCATC AGGTGATTTAGTAACAGAGAGAGTGAGAATGAAAAATCTCAAAA TAAATCCCCTGATAAGTAATAATAGATATGAGTAATATTTTTACC TTATTTAACATATTGAATATATATGTATATGTATATATATATATA TATTA AAAAGTAATCTTTCATGAATAAATAATAAAGAAAGATTAC AATTATTTATTTATTATGCATTGATTTACTTTATTGTTTGTTTGT TTTGTTGTTAAATGTTTCAAATTA AATGCAAGTTATTTGAAACA TTAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATAT GAATGATAATTTCAATATGTTTTATATCATTTTTTT
C10 Cat1	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATC AAATAATTTTTGTTTGTTTGTTAAAAAGATTATTTGATGATAATG AATGAAAAAGATGATTGAATCAATGATTAGATACAAAATGCATC AGGTGATTTAGTAACAGAGAGAGTGAGAATGAAAAATCTCAAAA TAAATCCCCTGATAAGTAATAATAGATATGAGTAATATTTTTACC TTATTTAACATATTGAATATATATGTATATGTATATATATATATA TATATTA AAAAGTAATCTTTCATGAATAAATAATAAAGAAAGATT ACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTGTTT GTTTTGTTGTTAAATGTTTCAAATTA AATGCAAGTTATTTGAAA CATTA AAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATAT ATGAATGATAATTTCAATATGTTTTATATCATTTTTTT

Table 19 (continued)

C28 Cat1	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTTGTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATATATTA AAAAGTAATCTTTTCATGAATAAATAATA AGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTG TTTGTTTGTGTTTAAATGTTTCAAATTAATGCAAGTTATTTGAAACAT TAAATAAACAAATAAATAAGGTAAAAAATTAGTATATATATATGAATGAT AATTTCAATATGTTTTATATCATTTTTTT
C32 Cat1	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTTGTGTTAAAAAGATTATTTGATGATAATGAATGAAACAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATATATATATTA AAAAGTAATCTTTTCATGAATAAA TAATAAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTAT TGTTTGTGTTTGTGTTTAAATGTTTCAAATTAATGCAAGTTATTTG AAACATTAATAAATAAATAAATAAGGTAAAAAATTAGCATATATATATG AATGATAATTTCAATATGTTTTATATCATTTTTTT
C2 Cat2	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCCATAAT TTTTGCTTGCTTGTTAAAAAGATTATTTGATGATTATGGATGAAAAAGAT GATTGAATCCATGATTAGATACCAAATGCCTCCGGTGATTTAGTAACAGAC AGAGTGAGAATGAAAAATCTCTCCATTAATCCCCTGATCAGTAATAATAG ATATTAGTAATATTTTTACCTTATCTAACCATTGAATATCTATCGGTCTA CATATATCTCTTA AAAAGGCATCTTTTCATGAATGCATATTTCTGCCATGAT CCCGTAAAGATCACATCATGTTCTCTTATTTACATATGAGACTACCACT CGATGACTGTGTTGTATCCCGTGCTCCAAAGTTGTTACATCTATAATGTCC CAGTGTTTGCTTCCCCTTTTGCTACACACCCCGAATAGAAAGAAAAGTAAT AGGCATAATTTGTGGAATGAGCGCTTCCCGCATGTGTCTATATTCACCTT TTT
C4 Cat2	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTTGTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATTA AAAAGTAATCTTTTCATGAATAAATAATAAGAA AGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTGTGTTG TTTTGTTGTTTAAATGTTTCAAATTAATGCAAGTTATTTGAAACATTAATA ATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATGATAATT TCAATATGTTTTATATCATTTTTTT

Table 19 (continued)

C5 Cat2	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTGTTTGTGTTTAAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATGTATATATATTAAGTAATCTTTTCATGAATAAATAAT AAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTT TGTTTGTGTTTGTGTTAAATGTTTCAAATTAATGCAAGTTATTTGAAAC ATTAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATG ATAATTTCAATATGTTTTATATCATTTTTTT
C6 Cat2	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTGTTTGTGTTTAAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATATATATATTAAGTAATCTTTTCATGAATAAA TAATAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTAT TGTTTGTGTTTGTGTTAAATGTTTCAAATTAATGCAAGTTATTTG AAACATTAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATG AATGTAATTTCAATATGTTTTATATCATTTTTTT
C8 Cat2	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTGTTTGTGTTTAAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT ATATGTATATATATATATATTAAGTAATCTTTTCATGAATAAATAATAA AGAAAGATTACAATTATTTATCTATTATGCATTGATTTACTTTATTGTTG TTTGTGTTTGTGTTAAATGTTTCAAATTAATGCAAGTTATTTGAAACAT TAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATGAT AATTTCAATATGTTTTATATCATTTTTTT
C52 Cat2	TAACAGTAATAATTGTATATGCATAGAAAAAATTTATGATTATCAAATAA AAAGAGTTTGTGAGTTAAAAGGATTATTTGAGGTTAATGAATGAAAAATGA GGTTCGAATCACTTCTGGGATTCAAATGCATCGGGTGTGTTAGTGACAGA GTGTGTGAGAATGTCACATTCTCAGTATTAATCGCTTGGTGAGTTATTTA GCTTTGTGTAATATTTTGACTTTATTTGACTTTGTGAATATATATGTATAT ATATATATATATGTATTAATCGTGATTTTTCATTAATAAATAATAAGAA AGATTACAATTATTCATTTATTATGCATTGATTTACTTTATTGTTTGTGTTG TTTCGTTGTTAAATGTTTCAAATTAATGCAAGTTGTTTGAACATTAATA ATAAACAAACGAGTAAAGGAAAAAATTAGCATATATGTGAATGACAATTC AATATGTTTTATATCATTTTTTT

Table 19 (continued)

C2 Cat3	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATTTAAAAAGTAATCTTTTCATGAATAAATAATAAG AAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTGTT TGTTTTGTTGTTAAATGTTTCAAATTTAAATGCAAGTTATTTGAAACATTA AAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATGATAA TTTCAATATGTTTTATATCATTTTTTTT
C3 Cat3	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT ATATATATATATATATATATATATTTAAAAAGTAATCTTTTCATGAATAATA ATAAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTG TTTGTTTGTTTGTTGTTAAATGTTTCAAATTTAAATGCAAGTTATTTGAA ACATTAATAATAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAA TGATAATTTCAATATGTTTTATATCATTTTTTTT
C6 Cat3	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATGTATATATATATATATATATTTAAAAAGTAATCTTTTCATGAATAA TAATAAAGAAAGATTACAATTATTTATTTTAAAAAGTAATCTTTTCATGAAT AAATAATAAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTT TATTGTTTGTTTGTTTGTTGTTAAATGTTTCAAATTTAAATGCAAGTTAT TTGAAACATTAATAATAACAAATAAATAAGGTAAAAAATTAGCATATATAT ATGAATGATAATTTCAATATGTTTTATATCATTTTTTTT
C13 Cat3	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACGGA GAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATATTTAAAAAGTAATCTTTTCATGAATAAATAATA AGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTG TTTGTTTTGTTGTTAAATGTTTCAAATTTAAATGCAAGTTATTTGAAACAT TAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATGAT AATTTCAATATGTTTTATATCATTTTTTTT

Table 19 (continued)

C39 Cat3	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATATATATATATATATTA AAAAGTAATCTTTCATGAATA AATAATAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTT ATTGTTTGTGTTTGTGTTGTTAAATGTTTCAAATTA AAATGCAAGTTATT TGAAACATTAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATA TGAATGATAATTTCAATATGTTTTATATCATTTTTTT
C45 Cat3	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT ATATATATATATATATATTA AAAAGTAATCTTTCGTAATAAATAATAAAG AAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTGT TGTTTTGTTGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAAACATTA AAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATGATAA TTTCAACATGTTTTATATCATTTTTTT
C2 Cat4	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATATTA AAAAGTAATCTTTCATGAATAAATAAT AAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTT TGTTTTGTTGTTGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAAAC ATTAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATG ATAATTTCAATATGTTTTATATCATTTTTTT
C7 Cat4	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAGGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATTA AAAAGTAATCTTTCATGAATAAATAATAAAG AAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTGT TGTTTTGTTGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAAACATTA AAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATGATAA TTTCAATATGTTTTATATCATTTTTTT

Table 19 (continued)

C24 Cat4	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT ATATATATATATTA AAAAGTAATCTTTCATGAATAAATAATAAGAAAGAT TACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTGTGTTT GTTGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAAACATTAAATAA ACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATGATAATTTCAA TATGTTTTATATCATTTTTTTT
C26 Cat4	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT ATATATATATATATTA AAAAGTAATCTTTCATGAATAAATAATAAGAAAG ATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTGTGTTT TTGTTGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAAACATTAAAT AAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATGATAATTTCA AATATGTTTTATATCATTTTTTTT
C34 Cat4	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATATATATATTA AAAAGTAATCTTTCATGAATAAATA ATAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTG TTTGTGTTGTTTGTGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAA ACATTAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAA TGATAATTTCAATATGTTTTATATCATTTTTTTT
C35 Cat4	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGACTTAGTAACAGA TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATGATGAATGAAAAAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATATATATATATATGCATTGATTTACTTTATTGTTTGT TTGTTTTGTTGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAAACATT AAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATGATA ATTTCAATATGTTTTATATCATTTTTTTT

Table 19 (continued)

C37 Cat4	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATATATATTA AAAAGTAATCTTT CATGAATAAATAAT AAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTT TGTTTGTGTTTGTGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAAAC ATTAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATG ATAATTTCAATATGTTTTATATCATTTTTTT
C6 Cat5	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATGATGAATGAAAAAAG ATGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTGTAACAGA GAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATAATATATATGTA TGTATATATATATATATATATATATATTA AAAAGTAATCTTT CATGAATAA ATAATAAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTA TTGTTTGTGTTTGTGTTAAATGTTTCAAATTA AAATGCAAGTTATTT GAAACATTA AAATAAACAAATAAATAAGGTAAAAAATTAGCATATATGTGA ATGATAATTTCAATATGTTTTATATCATTTTTTT
C9 Cat5	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTGATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATATATTA AAAAGTAATCTTT CATGAATAAATAATA AGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTG TTTGTGTTTGTGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAAACAT TAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATGAT AATTTCAATATGTTTTATATCATTTTTTT
C10 Cat5	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT ATATATATATTA AAAAGTAATCTTT CATGAATAAATAATAAAGAAAGATTA CAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTGTGTTTGT TGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAAACATTA AAATAAAC AAATAAATAAGGTAAAAAATTAGCATATATATATGAATGATAATTTCAATA TGTTTTATATCATTTTTTT

Table 19 (continued)

C28 Cat5	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT ATATATATATATATTA AAAAGTAATCTTTCATGAATAAATAATAAGAAAG ATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTGTGTT TTGTTGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAAACATTAAAT AAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATGATAATTC AATATGTTTTATATCATTTTTTT
C34 Cat5	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT ATATATATATATTA AAAAGTAATCTTTCATGAATAAATAATAAGAAAGAT TACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTGTGTTT GTTGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAAACATTAAATAA ACAAATAAATAAGGTAAAAAATTAGCATATATATATGAATGATAATTTCAA TATGTTTTATATCATTTTTTT
C57 Cat5	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATATATATTA AAAAGTAATCTTTCATGAATAAATA ATAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTG TTTGTGTTGTTTGTGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAA ACATTAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAA TGATAATTTCAATATGTTTTATATCATTTTTTT
C62 Cat5	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTAAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT GTATATATATATATATATATATATTA AAAAGTAATCTTTCATGAATAAATA ATAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTG TTTGTGTTGTTTGTGTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAA ACATTAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATATATGAA TGATAATTTCAATATGTTTTATATCATTTTTTT

Table 19 (continued)

C3 Cat6	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTTAAAAGATTATTTGATGATGATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTGTAACAGAG AGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATAG ATATGAGTAATATTTTTACCTTATTTAACATATTGAATAATATATATATAT ATATATATATATATATTA AAAAGTAATCTTTCATGAATAAATAATAAGAA AGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTGTGTTG TTTTGTTGTTAAATGTTTCAAATTA AATGCAAGTTATTTGAAACATTA A ATAACAAATAAATAAGGTAAAAAATTAGCATATATGTGAATGATAATTC AATATGTTTTATATCATTTTTTT
C5 Cat6	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTTAAAAGATTATTTGATGATAATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTAGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATATATATGTATAT ATATATATATATATATTA AAAAGTAATCTTTCATGAATAAATAATAAGAA AGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTGTGTTG TTTTGTTGTTAAATGTTTCAAATTA AATGCAAGTTATTTGAAACATTA A ATAACAAATAAATAAGGTAAAAAATTAGCATATATATGAATGATAATT TCAATATGTTTTATATCATTTTTTT
C6 Cat6	TAAAAGTAATAATTGATTTGCCTTGATTTATATTTATTATTATCCAATAA TTTTTGTGTTGTTGTTTAAAAGATTATTTGATGATGATGAATGAAAAAGA TGATTGAATCCATGATTAGATACCAAATGCCTCCGGTGATTTGTAACAGAG AGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATAG ATATGAGTAATATTTTTACCTTATTTAACATATTGAATAATATATATGTAT GTATATATATATATATATATTA AAAAGTAATCTTTCATGAATAAATAATAA AGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTTTG TTTGTTTTGCTGTTAAATGTTTCAAATTA AATGCAAGTTACTTTGAAACA TTAAAATAAACAAATAACTAACGTAAAAAATTAGCATATATGTGAATGATC ATTTCAACATGTTTTACATCATTTTTTT
C8 Cat6	TAAAAGTAATAATTGATTCGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTTAAAAGATTATTTGATGATGATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTGTAACAGAG AGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATAG ATATGAGTAATATTTTTACCTTATTTAACATATTGAATAATATATATGTAT GTATATATATATATATATATATTA AAAAGTAATCTTTCATGAATAAATAAT AAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGTT TGTTTGTGTTTGTGTTAAATGTTTCAAATTA AATGCAAGTTATTTGAAAC ATTA AATAAACAAATAAATAAGGTAAAAAATTAGCATATATGTGAATGAT AATTTCAATATGTTTTATATCATTTTTTT

Table 19 (continued)

C9 Cat6	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTTAAAAGATTATTTGATGATGATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTGTAACAGAG AGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATAG ATATGAGTAATATTTTTACCTTATTTAACATATTGAATAATATATATGTAT GTATATATATATATATATATATATTA AAAAGTAATCTTTCATGAATAAATAAT AAAGAAAGATTACAATTATTTATTTATTATGCGTTGATTTACTTTATTGTT TGTTTGTTTGTTGTTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAAAC ATTA AAATAAACAAATAAATAAGGTAAAAAATTAGCATATATGTGAATGAT AATTTCAATATGTTTTATATCATTTTTTT
C16 Cat6	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTTAAAAGATTATTTGATGATGATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTGTAACAGAG AGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATAG ATATGAGTAATATTTTTACCTTATTTAACATATTGAATAATATATATATAT GTATATATATATATATATATATATATTA AAAAGTAATCTTTCATGAATAAATA ATAAAGAAAGATTACAATTATTTATTTTAAAAAGTAATCTTTCATGAATAA ATAATAAAGAAAGATTACAATTATTTATTTATTATGCAATTGATTTACTTTA TTGTTTGTTTGTTTGTTGTTTAAATGTTTCAAATTA AAATGCAAGTTATTT GAAACATTAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATGTGA ATGATAATTTCAATATGTTTTATATCATTTTTTT
C4 Cat7	AAAAAGTAATAATGGTATCCGCATGGATTTAATTTATTTATTATCAAATAT TTTTTGTGTTGTTGTTTAAAAGATTATTTGATGATGATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTGTAACAGAG AGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATAG ATTTGAGTAATATTTTTACCTTTTTTTAACATATTGAATAATATATATGTGT GTATATATATATATATATATATATTA AAAAGTAATCTTTCATGAATAAATAAT AAAGAAAGATTACAATTATTTATTTATTATGCAATTGATTTACTTTATTGTT TGTTTGTTTGTTGTTTAAATGTTTCAAATTA AAATGCAAGTTATTTGAAAC ATTA AAATAAACAAATAAATAAGGTAAAAAATTAGCATATATGTGAATGAT AATTTCAATATGTTTTATATCATTTTTTT
C8 Cat7	TAAAAGTAATAATTGATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGTTGTTGTTTAAAAGATTATTTGATGATGATGAATGAAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTGTAACAGAG AGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATAG ATATGAGTAATATTTTTACCTTATTTAACATATTGAATAATATATATGTAT GTATATATATATATATATATTTTAAAAAGATCTCTTCGTGTATATATTATAG AGAGAGATCACTTTTATTTTTTTAATGCGCAGAGATACACTATAGTGTGTG TGTGTTGTGGTGAAAAGTGTCTCAAATTAATGTGCGTGTTTTTTGACATTT TAATATACACATATATATGGGGTAAAAATTTTCGCATATGTGAGAGAGAAAA TCTCAATGTGTTATATAACATTTTTTG

Table 19 (continued)

C54 Cat7	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGGTTTGTGTTTAAAAGATTATTTGATGATGATGAATGAAAAAAG ATGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTGTAACAGA GAGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATA GATATGAGTAATATTTTTACCTTATTTAACATATTGAATAATATATATGTA TGTATATATATATATATATATATATTAATAAGTAATCTTTCATGAATAAATAA TAAAGAAAGATTACAATTATTTATTTATTATGCATTGATTTACTTTATTGT TTGTTTGTGGTTGTTAAATGTTTCAAATTAATAATGCAAGTTATTTGAAA CATTAAATAAACAAATAAATAAGGTAAAAAATTAGCATATATGTGAATGA TAATTTCAATATGTTTTATATCATTTTTTT
C56 Cat7	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTATCAAATAA TTTTTGTGGTTTGTGTTTAAAAGATTATTTGATGATGATGAATGAAAAAGA TGATTGAATCAATGATTAGATACAAAATGCATCAGGTGATTTGTAACAGAG AGAGTGAGAATGAAAAATCTCAAAATAAATCCCCTGATAAGTAATAATAG ATATGAGTAATATTTTTACCTTATTTAACATATTGAATAATATATATGTAT GTGTATATATATATATATATTAATAAGTAATCTTCCTGAATAAATAATAA AGAAAGATTACCATTTTTTATTTTTTATGCATTGATTTACTTTATTGCTTG TTTGTGTTGTTGTTAAAGTTTCCAATTTAAATGCACGTTATTTGAAACCT TTAAATAAACCAATAAATAAGGGAAAAAATTTTTCCTATATGTGAACGATA ATTTCCATAATGTTTTATATAACATTTTTT

4.3 Identification and analysis of ITS2 nucleotide sequence data.

BLAST program was used for identification of 45 clones selected from feline *Brugia* spp. ITS2 nucleotide sequences in comparison to the previously reported data of *B. malayi*, *B. pahangi*, *B. timori*, and *D. immitis* obtained from GenBank (Table 20a and 20b). Upon alignment using Clustal W, some nucleotide regions were deleted to generate the appropriate alignment and the sequences were manually corrected. The nucleotide sequences from 45 clones revealed that they were mainly classified as *B. malayi* or *B. pahangi*. The alignment of ITS2 region was shown in Table 21.

Table 20a Sources of *B. timori*, *B. malayi*, and *B. pahangi* from GenBank using in phylogenetic tree construction based on ITS2 region.

Sample	Geographical Areas	References
<i>B. malayi</i> (AY988599)	unpublished	132
<i>B. malayi</i> (AF499130)	Sulawesi, Indonesia	133
<i>B. pahangi</i> (AY988600)	unpublished	132
<i>B. timori</i> (AF499132)	Alor Island, Indonesia	133
Cat 1-5	Narathiwat, Thailand	In this study
Cat 6,7	Lad Krabang, Thailand	In this study

Table 20b GenBank accession number of ITS2 region of *B. malayi*, *B. pahangi*, *B. timori*, and *D. immitis*.

AF217800Di (<i>D. immitis</i>)	TACTACTACTACTAATACTAATACTAATACTACTATTAACATC ATTATGCTGCTTATTTTCATTCTTTTCAAATAATGCAAGAAT GAAATAGAATGAATGAATGATGTTTAATAGATTAATAGATGAA TAGTTAGTTAGTTAGTAGTTAGTTAGATAGATAGATAAATGAA ATGATGATGAAATATTTTATTCGATCAATTGAAATAAACGGT GATATTCGTTGGTGTCTATTTTTATCTAAGTTATCGCCTAAC CGTCGATAGCGATGAAGATAAAATGATAGCTTAATTGATGATG ATTGCTCAATTAAGTAGACTTAATAAGCATTTTAGCTAGTATG TACCAACAAAATAATACACACACACATACATAACAATAATATGA TATAATTGTTATTTATAATAATTTTTCAATAACTCTAAGCGGG GGATCACCTGGCTCGTGGATCGATGAAGAACGCAGCTAGCTGC GATAAATAGTGCGAATTGCAGACGCATTGAGCACAAAGATTTTC GAATGCACATTGCACCATCGGGTTGATTCCCGATGGTACGTCT GGTTGAGGGTCAATATCGATCAGATTATCAAATAATATACCAAA
AF988599Bm (<i>B. malayi</i>)	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTA TCAAATAATTTTTGTTTGTTTGTTAAAAAGATTATTTGATGAT AATGAATGAAAAAGATGATTGAATCAATGATTAGATACAAAA TGCATCAGGTGATTTAGTAACAGAGAGAGTGAGAATGAAAAAA TCTCAAAATAAATCCCCTGATAAGTAATAATAGATATGAGTAA TATTTTTACCTTATTTAACATATTGAATATATATGTATATGTA TATATATATATATATATTAATAAGTAATCTTTCATGAATAAAT AATAAAGAAAGATTACAATTATTTATTTATTATGCATTGATTT ACTTTATTGTTTGTTTGTTTGTTTGTTAAATGTTTCAAATTA AATGCAAGCTATTTGAAACATTAATAAATAAATAAATAAAGG TAAAAAATTAGCATATATATATGAATGATAATTTCAATATGTT TTATATCATTTTTTT
AF988600Bp (<i>B. pahangi</i>)	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTTATT ATTATCAAATAATTTTTGTTTGTTTGTTAAAAAGATTATTTGAT GATGATGAATGAAAAAGATGATTGAATCAATGATTAGATACA AAAATGCATCAGGTGATTTGTAACAGAGAATGAGAATGAAAAA ATCTCAAAATAAATCCCCTGATAAGTAATAGATATGAGTAATA TTTTTACCATATTTAACATATTGAATATATATATATATATATA TAT ATATATATATATTAATAAATAATCTTTCATGAATAATTATTTA TAAATAATAAAGAAAGATTATAATTATTCATTTATTATGCATT GATTTACTATATTGTTTGTTTGTTTGTTTGTTGTTGTTAAATGTT TCAAATTAATAAGCAAGTTATATTTGAAACATTAATAAATAAACA AATAAATAGAGTAAAAAATTAGCATATATATGTGAATGATAA TTTCAATATGTTTTATATCATTTCCTT

Table 20b (continued)

AF499132Bt (<i>B. timori</i>)	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTA TCAAATAATTTTCATTCAAACAAGATTATTTTCTTTATGCAA ATAATTTTTGTTTGTTTATTTAAAAGATTATTTGATGATGATGA ATGAAAAAAGATGATTGAATCAATGATTAGATACAAAATGCAT CAGGTGATTTGTAACAGAGAGTGAGAATGAAAAAATCTCAAAA TGAATCCCCTGATAAGTAATAGATATGAGTGATATTTTTACCT TATTTAACTTATTGAATATATATATTTAAAAGTAATCTTTCAT GAATAAATATTCATAAATAATAAAGAAAGATTACAATTATTCA TTTATTATGCATTGATTTACTTTATTGTTTGTTTGTTTCGTTG TTAAATGTTTCAAATTTAAAATGCAAGTCGTTTGAAACATTAAA ATAAACAAACGAGTAAAGGAAAAAATTAGCATATATGTGAATG ACAATTTCAATATGTTTTATATCATTTTTTTT
AF499130Bm (<i>B. malayi</i>)	TAAAAGTAATAATTGTATTTGCATTGATTTATATTTATTATTA TCAAATAATTTTCATTCAAACAAGATTATTTTCTTTATGCAA ATAATTTTTGTTTGTTTATTTAAAAGATTATTTGATGATGATGA ATGAAAAAAGATGATTGAATCAATGATTAGATACAAAATGCAT CAGGTGATTTGTAACAGAGAGTGAGAATGAAAAAATCTCAAAA TGAATCCCCTGATAAGTAATAGATATGAGTGATATTTTTACCT TATTTAACTTATTGAATATATATATTTAAAAGTAATCTTTCAT GAATAAATATTCATAAATAATAAAGAAAGATTACAATTATTCA TTTATTATGCATTGATTTACTTTATTGTTTGTTTGTTTCGTTG TTAAATGTTTCAAATTTAAAATGCAAGTTGTTTGAAACATTAAA ATAAACAAACGAATAAAGGAAAAAATTAGCATATATGTGAATG ACAATTTCAATATGTTTTATATCATTTTTTTT

Table 21 Nucleotide sequence alignment of the ITS2 of *Brugia* spp. compared to *B. malayi*, *B. pahangi*, *B. timori*, and *D. immitis*.

C2 Cat4	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C35 Cat4	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C37 Cat4	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C62 Cat5	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C57 Cat5	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C34 Cat4	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C5 Cat2	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C4 Cat2	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C7 Cat4	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C4 Cat1	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C2 Cat3	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C10 Cat1	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
AY988599Bm	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C9 Cat5	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C28 Cat1	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C13 Cat3	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C8 Cat2	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C6 Cat3	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C54 Cat3	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C2 Cat1	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C6 Cat5	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C34 Cat5	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C24 Cat4	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C10 Cat5	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C26 Cat4	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C28 Cat5	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C39 Cat3	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C32 Cat1	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C6 Cat2	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C3 Cat3	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C52 Cat2	TAACAGTAATAATTGTATATGCATTAGAA - AAAAATTTATG -----	39
AY988600Bp	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATTATT -----	43
C3 Cat6	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C6 Cat6	TAAAAGTAATAATTGATTTGCCTTGAT - TTATATTTATT -----	39
C16 Cat6	TAAAAGTAATAATTGATTTGCATTGAT - TTATATTTATT -----	39
C4 Cat7	AAAAAGTAATAATGGTATCCGCATGGAT - TTA - ATTTATT -----	39
C8 Cat6	TAAAAGTAATAATTGTATTCGCATTGAT - TTA - TATTTATT -----	39
C24 Cat7	TAAAAGTAATAATTGTATTTGCATTGAT - TTATATTTATT -----	39
C37 Cat7	TAAAAGTAATAATTGTATTTGCATTGAT - TTATATTTATT -----	39
C9 Cat6	TAAAAGTAATAATTGTATTTGCATTGAT - TTATATTTATT -----	39
C54 Cat7	TAAAAGTAATAATTGTATTTGCATTGAT - TTATATTTATT -----	39
C5 Cat6	TAAAAGTAATAATTGTATTTGCATTGAT - TTATATTTATT -----	39
C45 Cat7	TAAAAGTAATAATTGTATTTGCATTGAT - TTATATTTATT -----	39
C9 Cat7	TAAAAGTAATAATTGTATTTGCATTGAT - TTATATTTATT -----	39
C56 Cat7	TAAAAGTAATAATTGTATTTGCATTGAT - TTATATTTATT -----	39
C8 Cat7	TAAAAGTAATAATTGTATTTGCATTGAT - TTATATTTATT -----	39
AF499132Bt	TAAAAGTAATAATTGTATTTGCATTGAT - TTATATTTATTATTATCAAATAATTTTCATT	59
AF499130Bm	TAAAAGTAATAATTGTATTTGCATTGAT - TTATATTTATTATTATCAAATAATTTTCATT	59
C2 Cat2	TAAAAGTAATAATTGTATTTGCATTGAT - TTATATTTATT -----	39
AF217800Di	TACTACTACTACTAATACTAATACTACTATTAACATC -----	43
	* * ** ** * ** * * **	

Table 21 (continued)

C2 Cat4	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C35 Cat4	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C37 Cat4	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C62 Cat5	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C57 Cat5	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C34 Cat4	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C5 Cat2	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C4 Cat2	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C7 Cat4	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C4 Cat1	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C2 Cat3	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C10 Cat1	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
AY988599Bm	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C9 Cat5	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C28 Cat1	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C13 Cat3	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C8 Cat2	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C6 Cat3	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C54 Cat3	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C2 Cat1	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C6 Cat5	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C34 Cat5	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C24 Cat4	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C10 Cat5	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C26 Cat4	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C28 Cat5	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C39 Cat3	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C32 Cat1	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C6 Cat2	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C3 Cat3	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C52 Cat2	-----ATTAT-----CAAATAAAAAGAGTTGTGAGTTAAAAAGATTATTT	80
AY988600Bp	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	83
C3 Cat6	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C6 Cat6	-----ATTAT-----CCAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C16 Cat6	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C4 Cat7	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C8 Cat6	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C24 Cat7	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C37 Cat7	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C9 Cat6	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C54 Cat7	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C5 Cat6	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C45 Cat7	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C9 Cat7	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C56 Cat7	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
C8 Cat7	-----ATTAT-----CAAATAATTTTGTGTTGTTGTTAAAAAGATTATTT	80
AF499132Bt	CAAACAAGATTATTTTCTTTATGCAAATAATTTTGTGTTGTTATT-AAAAGATTATTT	118
AF499130Bm	CAAACAAGATTATTTTCTTTATGCAAATAATTTTGTGTTGTTATT-AAAAGATTATTT	118
C2 Cat2	-----ATTAT-----CCATAATTTTGTCTGCTTGTAAAAAGATTATTT	79
AF217800Di	-----ATTAT-----GCTGCTTATTTTCATT--CTTTTCAAATAATGCAAG	83
	***** * *	

Table 21 (continued)

C2 Cat4	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C35 Cat4	GTGAC - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C37 Cat4	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C62 Cat5	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C57 Cat5	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C34 Cat4	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C5 Cat2	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C4 Cat2	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C7 Cat4	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C4 Cat1	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C2 Cat3	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C10 Cat1	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
AY988599Bm	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C9 Cat5	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C28 Cat1	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C13 Cat3	GTGAT - - TTAGTAACGAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C8 Cat2	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C6 Cat3	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C54 Cat3	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C2 Cat1	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C6 Cat5	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C34 Cat5	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C24 Cat4	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C10 Cat5	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C26 Cat4	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C28 Cat5	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C39 Cat3	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C32 Cat1	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C6 Cat2	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C3 Cat3	GTGAT - - TTAGTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C52 Cat2	GTGTG - - TTAGTGACAGAGTGTGTGAGAATGTCACATTCTCAGTATTAATCGCTT - GGTG	194
AY988600Bp	GTG - A - - TTTGTAACAGAGAAT - - GAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	195
C3 Cat6	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	193
C6 Cat6	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	193
C16 Cat6	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	193
C4 Cat7	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	193
C8 Cat6	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	193
C24 Cat7	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	193
C37 Cat7	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	193
C9 Cat6	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	193
C54 Cat7	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C5 Cat6	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	194
C45 Cat7	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	193
C9 Cat7	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	193
C56 Cat7	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	193
C8 Cat7	GTGAT - - TT - GTAACAGAGAGAGTGAGAATGAAAAAATCTCAAAATAAATCCCCT - GATA	193
AF499132Bt	GTGAT - - TT - GTAACAGAGAG - - TGAGAATGAAAAAATCTCAAAATGAATCCCCT - GATA	229
AF499130Bm	GTGAT - - TT - GTAACAGAGAG - - TGAGAATGAAAAAATCTCAAAATGAATCCCCT - GATA	229
C2 Cat2	GTGAT - - TTAGTAACAGACAGAGTGAGAATGAAAAAATCTCTCCATTAATCCCCT - GATC	193
AF217800Di	TTAGTAGTTAGTTAGATAGATAG - ATAAATGAAATGATGATGAAATATTTTTATTTCGATC	201
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Table 21 (continued)

C2 Cat4	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C35 Cat4	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C37 Cat4	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C62 Cat5	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C57 Cat5	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C34 Cat4	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C5 Cat2	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C4 Cat2	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C7 Cat4	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C4 Cat1	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C2 Cat3	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C10 Cat1	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
AY988599Bm	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C9 Cat5	AGTA-----ATAATAGATATGAGTGATATTTTACCTTATTTAACATATT	239
C28 Cat1	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C13 Cat3	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C8 Cat2	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C6 Cat3	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C54 Cat3	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C2 Cat1	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C6 Cat5	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C34 Cat5	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C24 Cat4	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C10 Cat5	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C26 Cat4	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C28 Cat5	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C39 Cat3	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C32 Cat1	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C6 Cat2	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C3 Cat3	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C52 Cat2	AGT-----TATTTTAGCTTTGTGTAATATTTTGACTTTATTTGACTTTGT	239
AY988600Bp	AGTAATAGATATGAGTAATATTTTACCATATTTAACATATTGAATATATATATATAT	255
C3 Cat6	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	238
C6 Cat6	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	238
C16 Cat6	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	238
C4 Cat7	AGTA-----ATAATAGATTTGAGTAATATTTTACCTTTTTAACATATT	238
C8 Cat6	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	238
C24 Cat7	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	238
C37 Cat7	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	238
C9 Cat6	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	238
C54 Cat7	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C5 Cat6	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	239
C45 Cat7	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	238
C9 Cat7	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	238
C56 Cat7	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	238
C8 Cat7	AGTA-----ATAATAGATATGAGTAATATTTTACCTTATTTAACATATT	238
AF499132Bt	AGTA-----ATAGATATGAGTGATATTTTACCTTATTTAACCTTATT	271
AF499130Bm	AGTA-----ATAGATATGAGTGATATTTTACCTTATTTAACCTTATT	271
C2 Cat2	AGTA-----ATAATAGATATTAGTAATATTTTACCTTATCTAACCCATT	238
AF217800Di	AATTGAATATAA-----ACGGTGATATTCGTTGGTGTCTATATTTTATCTAAGTTATC	254
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Table 21 (continued)

C2 Cat4	GAATA-TATATGTATATGTATATATATATATATATATT-----	278
C35 Cat4	GAATA-TATATGTATATGTATATATATATATATATAT-----	277
C37 Cat4	GAATA-TATATGTATATGTATATATATATATATATATATT-----	278
C62 Cat5	GAATA-TATATGTATATGTATATATATATATATATATATAT-----	279
C57 Cat5	GAATA-TATATGTATATGTATATATATATATATATATATAT-----	279
C34 Cat4	GAATA-TATATGTATATGTATATATATATATATATATATAT-----	279
C5 Cat2	GAATA-TATATGTATATGTATATATATATGTATATATAT-----	277
C4 Cat2	GAATA-TATATGTATATGTATATATATAT-----ATAT-----	271
C7 Cat4	GAATA-TATATGTATATGTATATATATAT-----ATATAT-----	273
C4 Cat1	GAATA-TATATGTATATGTATATATATAT-----ATATAT-----	273
C2 Cat3	GAATA-TATATGTATATGTATATATATAT-----ATATAT-----	273
C10 Cat1	GAATA-TATATGTATATGTATATATATAT-----ATATATAT-----	275
AY988599Bm	GAATA-TATATGTATATGTATATATATAT-----ATATATAT-----	275
C9 Cat5	GAATA-TATATGTATATGTATATATATAT-----ATATATAT-----	275
C28 Cat1	GAATA-TATATGTATATGTATATATATAT-----ATATATAT-----	275
C13 Cat3	GAATA-TATATGTATATGTATATATATAT-----ATATATAT-----	275
C8 Cat2	GAATA-TATATGTATATATATGTATATAT-----ATATATAT-----	275
C6 Cat3	GAATA-TATATGTATATGTATATGTATAT-----ATATATATATATATTTAAAAAGTAATCTTT	296
C54 Cat3	GAATA-TATATGTATATATATATATATAT-----ATATAT-----	273
C2 Cat1	GAATA-TATATGTATATATATATATATAT-----ATAT-----	271
C6 Cat5	GAATA-TATATGTATATATATATATATAT-----ATAT-----	271
C34 Cat5	GAATA-TATATGTATATATATATATATAT-----	267
C24 Cat4	GAATA-TATATGTATATATATATATATAT-----	267
C10 Cat5	GAATA-TATATGTATATATATATATAT-----	265
C26 Cat4	GAATA-TATATGTATATATATATATATAT-----AT-----	269
C28 Cat5	GAATA-TATATGTATATATATATATATAT-----AT-----	269
C39 Cat3	GAATA-TATATGTATATGTATATATATATATATATATATATAT-----	283
C32 Cat1	GAATA-TATATGTATATGTATATATATATATATATATATATAT-----	281
C6 Cat2	GAATA-TATATGTATATGTATATATATATATATATATATATAT-----	281
C3 Cat3	GAATA-TATATGTATATATATATATATATATATATATATAT-----	279
C52 Cat2	GAATA-TATATGTATATATATATATATATATGTAT-----	271
AY988600Bp	ATATA-TAT-----	313
C3 Cat6	GAATA--ATATATATATATATATATATATATAT-----	271
C6 Cat6	GAATA--ATATATATGTATGTATATATATATATATAT-----	275
C16 Cat6	GAATAATATATATATATGTATATATATATATATATATATATATTTAAAAAGTAATCTTTCATG	298
C4 Cat7	GAATAATATATATGTGTGTATATATATATATATATATAT-----	277
C8 Cat6	GAATAATATATATGTATGTATATATATATATATATATAT-----	277
C24 Cat7	GAATAATATATATGTATGTATATATATATATATATATAT-----	277
C37 Cat7	GAATAATATATATGTATGTATATATATATATATATATAT-----	277
C9 Cat6	GAATAATATATATGTATGTATATATATATATATATATAT-----	277
C54 Cat7	GAATAATATATATGTATGTATATATATATATATATATAT-----	278
C5 Cat6	GAATAATATATATGTATGTATATATATATATATATATATAT-----	282
C45 Cat7	GAATAATATATATGTATGTATATATATATATATATATAT-----	277
C9 Cat7	GAATAATATATATGTATGTATATATATATATATATATATAT-----	283
C56 Cat7	GAATAATATATATGTATGTGTATATATATATATATAT-----	275
C8 Cat7	GAATAATATATATGTATGTATATATATATATATATTT-----	275
AF499132Bt	GAATA-----TATATAT-----	283
AF499130Bm	GAATA-----TATATAT-----	283
C2 Cat2	GAATA-TCTATCGGTCTACATATATCTCT-----	266
AF217800Di	GCCTA-ACCGTCGATAGCGATGAAGATAAAATGATAGCTTAATTGATGATGATTGCTCAA	313

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Table 21 (continued)

C2 Cat4	-----AAAAAGTAAT-CTTTCATGA	297
C35 Cat4	-----	
C37 Cat4	-----AAAAAGTAAT-CTTTCATGA	297
C62 Cat5	-----TAAAAAGTAAT-CTTTCATGA	299
C57 Cat5	-----TAAAAAGTAAT-CTTTCATGA	299
C34 Cat4	-----TAAAAAGTAAT-CTTTCATGA	299
C5 Cat2	-----TAAAAAGTAAT-CTTTCATGA	297
C4 Cat2	-----TAAAAAGTAAT-CTTTCATGA	291
C7 Cat4	-----TAAAAAGTAAT-CTTTCATGA	293
C4 Cat1	-----TAAAAAGTAAT-CTTTCATGA	293
C2 Cat3	-----TAAAAAGTAAT-CTTTCATGA	293
C10 Cat1	-----TAAAAAGTAAT-CTTTCATGA	295
AY988599Bm	-----TAAAAAGTAAT-CTTTCATGA	295
C9 Cat5	-----TAAAAAGTAAT-CTTTCATGA	295
C28 Cat1	-----TAAAAAGTAAT-CTTTCATGA	295
C13 Cat3	-----TAAAAAGTAAT-CTTTCATGA	295
C8 Cat2	-----TAAAAAGTAAT-CTTTCATGA	295
C6 Cat3	CATGAATAAATAATAAGAAAGATTACAATTATTTATTTTAAAAAGTAAT-CTTTCATGA	355
C54 Cat3	-----TAAAAAGTAAT-CTTTCATGA	293
C2 Cat1	-----TAAAAAGTAAT-CTTTCATGA	291
C6 Cat5	-----TAAAAAGTAAT-CTTTCATGA	291
C34 Cat5	-----TAAAAAGTAAT-CTTTCATGA	287
C24 Cat4	-----TAAAAAGTAAT-CTTTCATGA	287
C10 Cat5	-----TAAAAAGTAAT-CTTTCATGA	285
C26 Cat4	-----TAAAAAGTAAT-CTTTCATGA	289
C28 Cat5	-----TAAAAAGTAAT-CTTTCATGA	289
C39 Cat3	-----TAAAAAGTAAT-CTTTCATGA	303
C32 Cat1	-----TAAAAAGTAAT-CTTTCATGA	301
C6 Cat2	-----TAAAAAGTAAT-CTTTCATGA	301
C3 Cat3	-----TAAAAAGTAAT-CTTTCATGA	299
C52 Cat2	-----TAAATCGTGAT-TTTTCATTA	291
AY988600Bp	-----TAAAAAATAAT-CTTTCATGA	333
C3 Cat6	-----TAAAAAGTAAT-CTTTCATGA	291
C6 Cat6	-----TAAAAAGTAAT-CTTTCATGA	295
C16 Cat6	AATAAATAATAAAGAAAGATTACAATTATTTATT - - - TAAAAAGTAAT-CTTTCATGA	353
C4 Cat7	-----TAAAAAGTAAT-CTTTCATGA	297
C8 Cat6	-----TAAAAAGTAAT-CTTTCATGA	297
C24 Cat7	-----TAAAAAGTAAT-CTTTCATGA	297
C37 Cat7	-----TAAAAAGTAAT-CTTTCATGA	297
C9 Cat6	-----TAAAAAGTAAT-CTTTCATGA	297
C54 Cat7	-----TAAAAAGTAAT-CTTTCATGA	298
C5 Cat6	-----TAAAAAGTAAT-CTTTCATGA	302
C45 Cat7	-----TAAAAAGTAAT-CTTTCCTGA	297
C9 Cat7	-----TAAAAAGTAAT-CTTTCATGA	303
C56 Cat7	-----TAAAAAGTAAT-CCTTCCTGA	295
C8 Cat7	-----TAAAAAGATCT-CTTTCGTGT	295
AF499132Bt	-----TAAAAAGTAAT-CTTTCATGA	303
AF499130Bm	-----TAAAAAGTAAT-CTTTCATGA	303
C2 Cat2	-----TAAAAAGGCAT-CTTTCATGA	286
AF217800Di	TTAAGTAGACTTAATAAGCATTTTAGCTAGTATGCTACCAACAAAATAATACACACACAC	373

Table 21 (continued)

C2 Cat4	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	339
C35 Cat4	-----ATTATGCA	285
C37 Cat4	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	339
C62 Cat5	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	341
C57 Cat5	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	341
C34 Cat4	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	341
C5 Cat2	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	339
C4 Cat2	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	333
C7 Cat4	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	335
C4 Cat1	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	335
C2 Cat3	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	335
C10 Cat1	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	337
AY988599Bm	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	337
C9 Cat5	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	337
C28 Cat1	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	337
C13 Cat3	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	337
C8 Cat2	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATC--TATTATGCA	337
C6 Cat3	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	397
C54 Cat3	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	335
C2 Cat1	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	333
C6 Cat5	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	333
C34 Cat5	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	329
C24 Cat4	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	329
C10 Cat5	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	327
C26 Cat4	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	331
C28 Cat5	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	331
C39 Cat3	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	345
C32 Cat1	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	343
C6 Cat2	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	343
C3 Cat3	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	341
C52 Cat2	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTCATT--TATTATGCA	333
AY988600Bp	ATAATTATTTATAA-ATAATAAAG-AAAGATTATA---ATTATTCATT--TATTATGCA	385
C3 Cat6	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	333
C6 Cat6	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	337
C16 Cat6	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	395
C4 Cat7	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	339
C8 Cat6	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	339
C24 Cat7	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	339
C37 Cat7	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	339
C9 Cat6	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCG	339
C54 Cat7	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	340
C5 Cat6	ATAA-----ATAATAAAG-AAAGATTACA---ATTATTTATT--TATTATGCA	344
C45 Cat7	ATAA-----ATAATAAAG-AAAGATTACC---ATTATTTATT--TATTATGCA	339
C9 Cat7	ATAA-----ATAATAAAG-AAAGATTACA---A-----	327
C56 Cat7	ATAA-----ATAATAAAG-AAAGATTACC---ATTTTTTTATT--TTTTATGCA	337
C8 Cat7	ATAT-----ATTATAGAG-AGAGATCACT---TTTATTTTTT--TAATGCGCA	337
AF499132Bt	ATAAATATTCATAA-ATAATAAAG-AAAGATTACA---ATTATTCATT--TATTATGCA	355
AF499130Bm	ATAAATATTCATAA-ATAATAAAG-AAAGATTACA---ATTATTCATT--TATTATGCA	355
C2 Cat2	ATGCATATTCCTGCCATGATCCCGTAAAGATCACATCATGTTCCCTCTTA--TTTCACATA	344
AF217800Di	ATACATACAATAAT-ATGATATAATTGTTATTTATAATAATTTTCAATAACTCTAAGCG	432

Table 21 (continued)

C2 Cat4	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	388
C35 Cat4	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	334
C37 Cat4	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	388
C62 Cat5	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	390
C57 Cat5	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	390
C34 Cat4	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	390
C5 Cat2	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	388
C4 Cat2	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	382
C7 Cat4	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	384
C4 Cat1	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	384
C2 Cat3	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	384
C10 Cat1	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	386
AY988599Bm	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	386
C9 Cat5	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	386
C28 Cat1	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	386
C13 Cat3	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	386
C8 Cat2	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	386
C6 Cat3	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	446
C54 Cat3	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	384
C2 Cat1	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	382
C6 Cat5	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	382
C34 Cat5	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	378
C24 Cat4	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	378
C10 Cat5	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	376
C26 Cat4	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	380
C28 Cat5	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	380
C39 Cat3	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	394
C32 Cat1	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	392
C6 Cat2	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	392
C3 Cat3	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	390
C52 Cat2	TTGATTTACT--TTATTGTTTGT-TTGTTT----CGTTGTTAAATGTTTCAAAT----TA	382
AY988600Bp	TTGATTTACT--ATATTGTTTGT-TTGTTTGTTCGTTGTTAAATGTTTCAAAT----TA	438
C3 Cat6	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	382
C6 Cat6	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGCTGTTAAATGTTTCAAAT----TA	386
C16 Cat6	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	444
C4 Cat7	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	388
C8 Cat6	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	388
C24 Cat7	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	388
C37 Cat7	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	388
C9 Cat6	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	388
C54 Cat7	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	389
C5 Cat6	TTGATTTACT--TTATTGTTTGT-TTGTTT----TGTTGTTAAATGTTTCAAAT----TA	393
C45 Cat7	TTGATTTACT--TTATTGGTTGG-TTGGTT----TGGTGGTAAATGTTTCAAAT----TA	388
C9 Cat7	-----TTAT-TTATTT-----	337
C56 Cat7	TTGATTTACT--TTATTGCTTGT-TTGTTG----TGTTGTTAAAAGTTTCCAAT----TT	386
C8 Cat7	GAGATACACT--ATAGTGTGTGT-GTGTTG----TGGTGAAAAGTGTCTCAAAT----TA	386
AF499132Bt	TTGATTTACT--TTATTGTTTGT-TTGTTT----CGTTGTTAAATGTTTCAAAT----TA	404
AF499130Bm	TTGATTTACT--TTATTGTTTGT-TTGTTT----CGTTGTTAAATGTTTCAAAT----TA	404
C2 Cat2	TGAGACTACCACTCGATGACTGTGTGTATCCCGTGCTCCAAAGTTGTTACATC----TA	400
AF217800Di	GGGGATCACC--TGGCTCGTGGATCGATGAAGAACGCAGCTAGCTGCGATAAATAGTGCG	490

Table 21 (continued)

C2 Cat4	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	437
C35 Cat4	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	383
C37 Cat4	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	437
C62 Cat5	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	439
C57 Cat5	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	439
C34 Cat4	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	439
C5 Cat2	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	437
C4 Cat2	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	431
C7 Cat4	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	433
C4 Cat1	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	433
C2 Cat3	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	433
C10 Cat1	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	435
AY988599Bm	AAATG----CAAGCTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	435
C9 Cat5	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	435
C28 Cat1	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	435
C13 Cat3	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	435
C8 Cat2	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	435
C6 Cat3	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	495
C54 Cat3	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	433
C2 Cat1	TAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	431
C6 Cat5	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	431
C34 Cat5	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	427
C24 Cat4	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	427
C10 Cat5	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	425
C26 Cat4	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	429
C28 Cat5	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	429
C39 Cat3	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	443
C32 Cat1	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	441
C6 Cat2	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	441
C3 Cat3	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	439
C52 Cat2	AAATG----CAAGTTGT--TTGAAACATTAATAAAACAAACGA--GTAAAG-GAAAA--	431
AY988600Bp	AAATG----CAAGTTATATTTGAAACATTAATAAAACAAATAA--ATAGAGTAAAAA--	490
C3 Cat6	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	431
C6 Cat6	AAATG----CAAGTTAC-TTTGAAACATTAATAAAACAAATAA--CTAACG-TAAAA--	436
C16 Cat6	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	493
C4 Cat7	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	437
C8 Cat6	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	437
C24 Cat7	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	437
C37 Cat7	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	437
C9 Cat6	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	437
C54 Cat7	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	438
C5 Cat6	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	442
C45 Cat7	AAATG----CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	437
C9 Cat7	---TG---CAAGTTAT--TTGAAACATTAATAAAACAAATAA--ATAAGG-TAAAA--	383
C56 Cat7	AAATG----CACGTTAT--TTGAAACCTTTAATAAACCAATAA--ATAAGGGAAAAA--	436
C8 Cat7	ATGTG----CGTGT---TTGACATTTTAAATACACATATAT--ATGGGG-TAAAA--	435
AF499132Bt	AAATG----CAAGTCGT--TTGAAACATTAATAAAACAAACGA--GTAAAG-GAAAA--	453
AF499130Bm	AAATG----CAAGTTGT--TTGAAACATTAATAAAACAAACGA--ATAAAG-GAAAA--	453
C2 Cat2	TAATGTCC-CAGTGTGTTGCTTCCCTTTTGCTACACACCC-CGA--ATAGAAAGAAAAGT	456
AF217800Di	AATTGCAGACGCATTGAGCACAAAGATTTTGAATGCACATTGCACCATCGGGTTGATTCC	550

Table 21 (continued)

C2 Cat4	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	490
C35 Cat4	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	436
C37 Cat4	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	490
C62 Cat5	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	492
C57 Cat5	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	492
C34 Cat4	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	492
C5 Cat2	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	490
C4 Cat2	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	484
C7 Cat4	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	486
C4 Cat1	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	486
C2 Cat3	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	486
C10 Cat1	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	488
AY988599Bm	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	488
C9 Cat5	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	488
C28 Cat1	AATTAGTATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	488
C13 Cat3	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	488
C8 Cat2	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	488
C6 Cat3	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	548
C54 Cat3	AATTAGCATATATATATGAATGA-TAATTTCAACA-TGT-TTTATAT--CATTTTTTTT	486
C2 Cat1	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	484
C6 Cat5	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	484
C34 Cat5	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	480
C24 Cat4	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	480
C10 Cat5	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	478
C26 Cat4	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	482
C28 Cat5	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	482
C39 Cat3	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	496
C32 Cat1	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	494
C6 Cat2	AATTAGCATATATATATGAATG--TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	493
C3 Cat3	AATTAGCATATATATATGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	492
C52 Cat2	AATTAGCATATAT--GTGAATGA-CAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	482
AY988600Bp	AATTAGCATATATATGTGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTCTTT	543
C3 Cat6	AATTAGCATATAT--GTGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	482
C6 Cat6	AATTAGCATATAT--GTGAATGA-TCATTTCAACA-TGT-TTTACAT--CATTTTTTTT	487
C16 Cat6	AATTAGCATATAT--GTGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	544
C4 Cat7	AATTAGCATATAT--GTGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	488
C8 Cat6	AATTAGCATATAT--GTGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	488
C24 Cat7	AATTAGCATATAT--GTGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	488
C37 Cat7	AATTAGCATATAT--GTGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	488
C9 Cat6	AATTAGCATATAT--GTGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	488
C54 Cat7	AATTAGCATATAT--GTGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	489
C5 Cat6	AATTAGCATATAT--GTGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	493
C45 Cat7	AATTAGCATATAT--GTGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	488
C9 Cat7	AATTAGCATATAT--GTGAATGA-TAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	434
C56 Cat7	ATTTTCCTATAT--GTGAACGA-TAATTTCCATAATGT-TTTATATAACATTTTTTTT	490
C8 Cat7	TTTTCGCATATGT--GAGAGAGA-AAATCTCAATG-TGT-TATATAA--CATTTTTTTG	486
AF499132Bt	AATTAGCATATAT--GTGAATGA-CAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	504
AF499130Bm	AATTAGCATATAT--GTGAATGA-CAATTTCAATA-TGT-TTTATAT--CATTTTTTTT	504
C2 Cat2	AATAGGCATAATTTGTGGAATGAGCGCTTCCCGCGATGTGTCTATATT-CACCTTTTT	513
AF217800Di	CGATGGTACGTCTGGTTGAGGGT-CAATATCGATCAGATTATCAAATAATATACCAA	607
	* ** *	

4.4 Phylogenetic analysis of *Brugia* spp. based on ITS 2 region

Phylogenetic tree construction based on ITS2 nucleotide sequences was analyzed using PAUP program version 4.0 with Neighbor Joining (NJ) and DNA Parsimony (DNA PARS). For maximum parsimony analysis, the heuristic search strategy was utilized to find the most parsimonious trees using the parameters as followed; the number of substitution types = 2 (HKY85 variant), transition/ transversion ratio = estimate, distribution of rates at variable sites = gamma (discrete approximation) and shape parameter (alpha) = estimate. The bootstrap maximum parsimony was analyzed with 100 replicates, addition sequence = as-is and Branch-swapping algorithm = tree-bisection-reconnection (TBR), all minimal trees saved and zero branch lengths collapsed; all characters were assigned equal weight.

4.4.1 Neighbor Joining

A Neighbor Joining (NJ) distance analysis of these data was presented in Figure 18. NJ tree of ITS2 region revealed that one major group of human *B. malayi* (AY 988599) and 29 clones of cat 1-5. The rest of the clones mainly from cat 6 and 7, were distantly separated. One clone, C 52 cat 2, was categorized within *B. pahangi* group (AY 988600).

4.4.2 DNA Parsimony

According to the ITS2 tree, one major groups human *B. malayi* (AY 988599) and 29 clones of cat 1-5 were observed with moderate bootstrap value (69%) as shown in Figure 19. The 12 and 2 clones from cat 6 and 7 were separately categorized with moderate bootstrap value at less than 50% and 66%, respectively. Among them, clone C52 cat 2 was classified in a group as feline *B. pahangi* with high bootstrap value (81%).

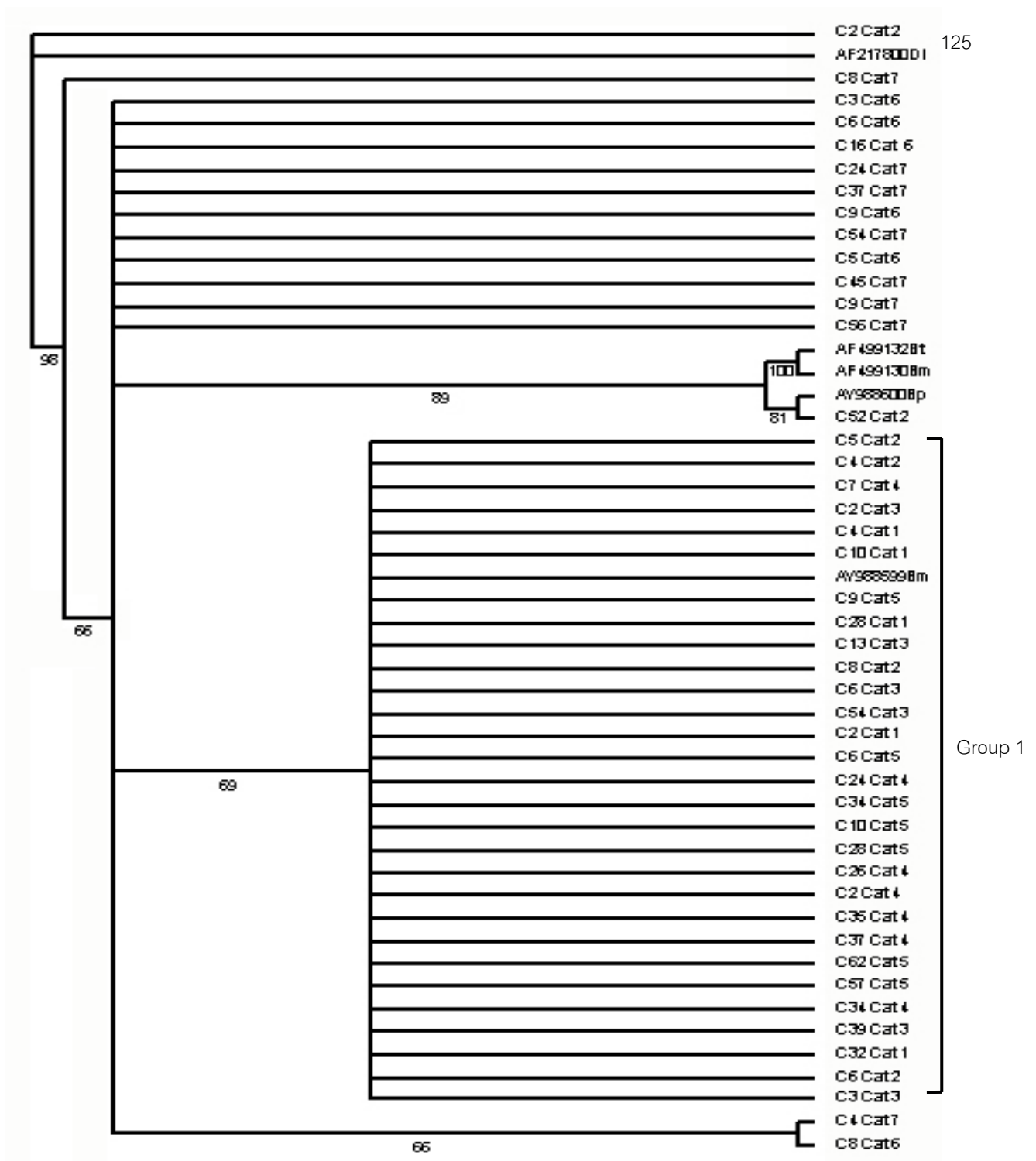


Figure 19 A pasimony cladogram of 45 clones of ITS2 region from feline *Brugia* spp. against *B. malayi*, *B. pahangi*, *B. timori*, and *D. immitis* (outgroup) produced by the heuristic search of PAUP version 4.0 and inferred from complete ITS2 region using a bootstrap resampling of the data set. The number at the nodes represent the percentage of times the group occurred out of 100 trees. Branches with less than 50% bootstrap support were collapsed. No significance is placed on the lengths of the branches connecting the species.

CHAPTER V

DISCUSSION

The molecular phylogenetic analysis for the specific identification of microfilaria of *Brugia* species based on small subunit ribosomal (18S rDNA) and internal transcribed spacers genes (ITSs) were achieved.

Analysis of 18S rDNA among *Brugia* spp.

The nucleotide sequences of 18S rDNA gene showed that all of the cat reservoirs contained mixed infection of *B. malayi* and *B. pahangi* whereas morphological characters could not clearly provide a mean of distinguishing *Brugia* spp. Nucleotide sequence alignment of the 18S rDNA of *Brugia* spp. compared to *B. malayi* (AF036588) and *W. bancrofti* (AY843438). (Region1 and Region2) revealed that each region is highly conserved. However, some variation of nucleotide sequences due to nucleotide insertion, deletion and SNPs were observed which may fall within coding sequences (CDS) and noncoding regions of genes (i.e. introns), or between genes (intergenic regions). Positions of insertion, deletion and SNPs within a CDS may or may not change the amino acids of the protein sequences. These data indicated that *B. malayi* and *B. pahangi* are genetically closely related. They also showed that the 18S rDNA is not informative for studying genetic diversity of *Brugia* spp. based on phylogenetic tree construction. Despite their high homology of 18S rDNA of *B. malayi* and *B. pahangi* the single nucleotide polymorphisms (SNPs) in some positions have been observed. These SNPs are enable to classify between two species of *Brugia* parasites but are not sufficient for studying genetic variation within each *Brugia* spp. Similarly, the nucleotide sequence comparison of various genes from *B. malayi* and *B. pahangi* such as *Hha I* repetitive region, trans-spliced leader exon 1, glutathione peroxidase, antigen larval transcript-1, cuticle gene-1, cytidine deaminase-1 and sheat proteins revealed that they are homology for more than 95%. However, the PCR-RFLP of these genes could differentiate *B. malayi* and *B. pahangi*.^(130,134) In 2005, Nuchprayoon and coworker demonstrated that the PCR-RFLP of ITS1 region could distinguish

human *B. malayi* from feline *B. pahangi*.⁽¹³¹⁾ Nevertheless, these PCR-RFLP of the genes mentioned above could not illustrated the genetic diversity of *Brugia* spp. within specific host.

Analysis of ITS regions among *Brugia* spp.

The phylogenetic relationship of *Brugia* spp. based on ITS1 and ITS2 regions of 7 cats from endemic areas in Thailand were compared to those of *B. malayi*, *B. pahangi* and *D. immitis* from GenBank. The cladogram of ITS1 and ITS2 regions exhibited the variation of nucleotide sequences and was enable to show the relationship among 45 clones of ITS region obtained for cat reservoirs. Phylogenetic tree construction based on ITS1 and ITS2 nucleotide sequences was analyzed by using the methods of Neighbor Joining (NJ) and DNA Parsimony (DNA PARS). Types of infection in cat reservoirs based on ITS1 and ITS2 nucleotide sequences was summarized in Table 22. Phylogenetic tree of ITS1 and ITS2 were in agreement that cat 3, and 4 contained *B. malayi*. The ITS1 trees revealed that cat 1 was most likely to contain new variant of *Brugia* spp. whereas the ITS2 trees indicated that they were *B. malayi*. To assure these, more clones from cat 1 should be harvest to reach the significant data. According to ITS1 tree, cat 6 and 7 were classified to be infected with *B. pahangi* whereas the ITS2 tree could not clearly classified the clones. However, both tree succussfully demonstrated the genetic variation within *B. malayi* and *B. pahangi*.

Referring to the ITS tree, mix infection of *B. malayi* and *B. pahangi* has been found in cat 2 (ITS2 data) and cat 5 (ITS1 data). To confirm these, more clones should be investigated and analyzed. However, to date, the genetic diversity of *Brugia* spp. in specific host has not been reported. Hence, the data obtained from this study are the first evidences that clearly demonstrated the genetic diversity in cat reservoirs based on ITS regions.

In conclusion, the genetic variation of *B. malayi* and *B. pahangi* have been found in cat reservoirs based on ITS tree whereas the 18S rDNA data was not informative for phylogenetic analysis. Hence it can be proposed that the ITS region could be used as the informative data or identification, classification and studing genetic variation of *Brugia* spp. However, the mix-infection of both species has been found in cat 2 (ITS2 data) and 5 (ITS1 data). However, clones from cat 1 were catagorized as *B. malayi* when ITS2 data was used. This revealed that the ITS1 and ITS2 nucleotide sequences are informative for studying on genetic diversity of

Brugia spp. in cat reservoirs than those of 18S rDNA. Hence, it can be proposed that the ITS region could be used as the genetic markers for classification of *Brugia* spp.

Table 22. Summary of *Brugia* spp. in cat reservoirs based on Neighbor Joining and parsimony trees of ITS1 and ITS2 regions.

Cats	ITS1	ITS2
1	?	<i>B. malayi</i>
2	<i>B. malayi</i>	<i>B. malayi, B. pahangi</i>
3	<i>B. malayi</i>	<i>B. malayi</i>
4	<i>B. malayi</i>	<i>B. malayi</i>
5	<i>B. malayi, B. pahangi</i>	<i>B. malayi</i>
6	<i>B. pahangi</i>	?
7	<i>B. pahangi</i>	?

CHAPTER VI

CONCLUSION

In this study the following conclusion have been reached.

1. Analysis of 18S rDNA among *Brugia* spp. revealed that each region is highly conserved. However, some variation of nucleotide sequences due to nucleotide insertion, deletion and SNPs were observed which may fall within coding sequences (CDS) and noncoding regions of genes (i.e.), or between genes (intergenic regions). These data indicated that *B. malayi* and *B. pahangi* are genetically closely related. They also showed that the 18S rDNA is not informative for studying genetic diversity of *Brugia* spp. based on phylogenetic tree construction. Despite their high homology of 18S rDNA of *B. malayi* and *B. pahangi* the single nucleotide polymorphisms (SNPs) in some positions have been observed. The data are not sufficient for studying genetic variation within each *Brugia* spp.

2. Analysis of ITS1 regions among *Brugia* spp. showed the variation of nucleotide sequences and was enable to show the relationship among 45 clones from cat reserviors. It could be concluded that most of them were a single species infection of either *B. malayi* (cat 2, 3 and 4) or *B. pahangi* (cat 6 and 7). However, the mix-infection of both species has been found in cat 5. *Brugia* spp. of cat 1 were not clearly classified as *B. malayi* or *B. pahangi* when they were analysed using ITS1 data. However, the ITS1 trees revealed that cat 1 was most likely to contain new variant of *Brugia* spp. whereas the ITS2 trees indicated that they were *B. malayi*. To assure these, more clones from cat 1 should be harvest to reach the significant data.

3. Analysis of ITS2 regions among *Brugia* spp. exhibited the variation of nucleotide sequences and was enable to show the relationship among 45 clones from cat reserviors. It could be concluded that most of them were a single species infection of *B. malayi* (cat 1, 3, 4 and 5). However, the mix-infection of both species has been found in cat 2. However, the ITS1 tree revealed that cat 6 and 7 were classified to be infected with *B. pahangi* whereas the ITS2 tree could not clearly classified the clones. However, both tree succussfully demonstrated the genetic variation within *B. malayi* and *B. pahangi*.

4. The mix-infection of *B. malayi* and *B. pahangi* has been found in cat 2 (ITS2 data) and cat 5 (ITS1 data). In this case, more use clones of cat 2 and cat 5 should be investigated.

5. It can be proposed that ITS regions could be used for investigation of genetic diversity *Brugia* spp. in cat reservoirs which will be beneficial for epidemiological studying and for the control and eradication of the filarial disease in endemic area.

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APPENDICES

Materials

Absolute Ethanol		Merck
Agarose		Seakem
Bacto agar		GibcoBRL
Bacto TM peptone		BDH
Boric acid		Merck
Deep-frozen tube		Nunc
DE 52 DEAE cellulose		Whatman
Deoxynucleotide triphosphates (dNTPs)		Gibco BRL
100 bp DNA Ladder		Gibco BRL
EDTA.Na ₂ .2H ₂ O Ultrapure		BSU
Glucose		BDH
Glycerol		Sigma
Heparin		Leo
Hydrochloric acid	HCl	Merck
Isoamyl alcohol		Carlo erba
Kanamycin		Sigma
Lambda DNA – <i>HindIII</i> Marker		Promega
Magnesium Chloride	MgCl ₂	Gibco BRL
10x PCR Buffer		Gibco BRL
Phenol		Ultrapure
Phenol/Chloroform/Isoamyl alcohol. PH 7.8		Research organics
Phosphoric acid	H ₃ PO ₄	Merck
Proteinase K		BRL
SDS (Sodium dodecyl sulfate)		Sigma
Sodium chloride	NaCl	Merck
Sodium di hydrogen phosphate	(2H ₂ O) NaH ₂ PO ₄ .2H ₂ O	Univar
Sodium hydrogen phosphate	Na ₂ HPO ₄ .H ₂ O	Merck
<i>Thermus aquaticus</i> (Taq) DNA polymerase		Gibco BRL
Tris (Tris(hydroxymethy))		Serva
Tris-acetate EDTA buffer		Sigma
Yeast extract		Gibco BRL

Reagent

1. Phosphate buffered saline (PBS buffer)

NaCl	8 g
KCl	0.2 g
Na ₂ HPO ₄	1.44 g
KH ₂ PO ₄	0.24 g
H ₂ O (distilled water)	800 ml
Adjust pH 7.4 with HCl	
H ₂ O (distilled water) adjust volume to	1000 ml

2. LB broth

Bacto TM peptone	10 g
Yeast extract	5 g
NaCl	10 g
H ₂ O (distilled water) adjust volume to	1000 ml

3. LB-ampicillin agar plate

Bacto TM peptone	10 g
Yeast extract	5 g
NaCl	10 g
Agar	15 g
H ₂ O (distilled water)	1000 ml
Ampicillin	100 µg/ml

4. IPTG 200 mg/ml

IPTG (Isopropyl-β-D-thiogalactopyranoside, dioxane free)	1 g
H ₂ O (distilled water) (sterile)	5 ml

5. X-Gal 20 mg/ml

X-Gal (5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside)	100 mg
N, N-dimethylformamide	5 ml

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