GENETIC AND PHYLOGENETIC STUDIES OF TOLL-LIKE RECEPTOR 5 (TLR5) IN RIVER BUFFALO (*BUBALUS BUBALIS*)

A Dissertation

by

BRITTANY CHANELLE JONES

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

DOCTOR OF PHILOSOPHY

Approved by:

Chair of Committee,	James Womack
Committee Members,	James Derr
	Loren Skow
	Patricia Holman
Head of Department,	Linda Logan

December 2012

Major Subject: Veterinary Microbiology

ABSTRACT

River buffalo are economically important to many countries and only recently has their genome been explored for the purpose of mapping genetic variation in traits of economic and biologic interest. The purpose of this research is to characterize the genetic and evolutionary profile of Toll-like receptor 5 (TLR5), which mediates the mammalian innate immune response to bacterial flagellin.

This study is comprised of three parts: 1) generating a radiation hybrid (RH) map of river buffalo chromosome 5 (BBU5) where the TLR5 gene is located and building a comparative map with homologous cattle chromosomes; 2) conducting a single-nucleotide polymorphism (SNP) survey of the TLR5 gene to reveal variation within river buffalo and other species; and 3) performing an evolutionary study by inferring phylogenetic trees of TLR5 across multiple taxa and determining the possible evolutionary constraints within the TLR5 coding region.

River buffalo chromosome 5 is a bi-armed chromosome with arms corresponding to cattle chromosomes 16 and 29. A BBU5 RH map was developed using the previously published river buffalo RH mapping panel and cattle-derived markers. The RH map developed in this study became an integral part of the first river buffalo whole genome RH map.

Genetic variation of the TLR5 gene was evaluated in a small domestic herd of river buffalo. Sequencing of the TLR5 coding region and partial associated 5'- and 3'-untranslated regions yielded 16 novel SNPs. Six SNPs were identified as non-synonymous with one predicted to potentially code for a functionally altered product.

For the evolutionary study of the TLR5 coding region, phylogenetic trees were inferred based on TLR5 variation across multiple orders and another for artiodactyla. Species that are closely related to river buffalo appear to have undergone negative selection in TLR5 while those that diverged from river buffalo earlier may be retaining alleles that river buffalo are removing from the population.

In conclusion, putative chromosomal rearrangements were identified between river buffalo and cattle, the variation that was uncovered in the TLR5 coding region could potentially lead to differential immunity across species, and there appears be some evolutionary flexibility in the DNA sequence of the TLR5 coding region.

DEDICATION

To my mother, brother, and sister. You’re the best.

ACKNOWLEDGEMENTS

I would like to extend much thanks and gratitude to Dr. James Womack. He taught me how to be an ethical and capable scientist and I cannot thank him enough for his steady mentorship. I also thank my committee members; Dr. James Derr, Dr. Loren Skow, and Dr. Patricia Holman, for keeping me on the straight and narrow and for introducing me to new ideas that broadened my horizons. Jan Elliot and Elaine Owens of the Womack lab also are very deserving of my thanks. They patiently guided me around the lab and made me feel welcome when I was but a spore in the field of veterinary microbiology. I would also like to thank Dr. Elisabete Amaral and Dr. Ence Yang for their guidance and help with this research. Their contributions are invaluable.

My acknowledgements could not be complete without the many friends that I have made here at Texas A&M University. My experiences were enriched by my time working in the Graduate Student Council. So thank you Stefanie Baker for being an advisor to me outside of my research. I shared many late nights, triumphs and failures with my partners in the lab, Erin Flores and Catherine Busch. The Axis will remain, my friends. I would also be remiss if I failed to thank my friend, Matthew Kelsey. Miles away and the magic of MSN Messenger made it possible to have late nights discussing our graduate school shenanigans. Thanks, buddy, for sharing the graduate school experience with me!

I also want to thank the entire A&E Department at Abilene Christian University. I received so much from each and every person there. I would like to specifically mention Dr. Foy Mills, Jr. I owe my graduate school experience to him. The respect and admiration I have for him is beyond my ability to state it and so I thank you, Dr. Mills, for what the department allowed me to accomplish.

Finally, all this would not have possible if not for the loving support offered by mother, Alice Jones; my brother, Adonis Jones; and my sister, Amber Thompson. Thank you for the years of helping me move and watching me leave for college. I know you missed me and I missed you, but you encouraged me and gave me the tools I needed to succeed. Thank you for being the best family this side of families!

TABLE OF CONTENTS

Page

LIST OF FIGURES

LIST OF TABLES

Page

Page

CHAPTER I

INTRODUCTION

Economic and Research Comparisons of Cattle and Buffalo

Cattle are the predominant livestock species in the United States and many parts of the world, where the sheer number of head illustrates their importance both economically and socially. Worldwide, the number of cattle was estimated to be about 1.4 billion in 2010 (FAO, 2012). Thirty-six percent of the cattle population reside in the Americas (North and South), with 94 million produced in the United States of America. Thirty-three percent of cattle are found in Asia, twenty percent in Africa, and the rest spread across Europe and Oceania (FAO, 2012). These numbers are important factors in the investment in scientific research worldwide, as the sheer volume of cattle consumes many resources in terms of time, money, and energy. Because cattle are dominant among the ruminant agricultural species, they are also the predominant ruminant livestock species in terms of research investment.

Cattle have also served as model organisms in several areas of biomedical research. Cattle and other large animal models have proven useful in the areas of modern vaccination programs (smallpox), reproduction technologies (in vitro embryo production, sperm conservation, and artificial insemination), and neurodegenerative disease (bovine spongiform encephalopathy), to name a few (Polge *et al.*, 1949; Foote, 1982; Barquet & Domingo, 1997; Hasler, 1998; Dalton *et al.*, 2001; Watts *et al.*, 2006).

As a consequence, cattle genetic resources have been developed in the biomedical research community as well as in the agricultural research community.

The economic burden on producers of livestock is immense and failure to efficiently manage production, breeding, and disease can devastate an industry. It is for this reason that the potential for possible outbreaks of diseases, such as bovine respiratory disease, brucellosis, and bovine spongiform encephalitis, to name a few, cause lasting harm to a region after an outbreak even years after the issue has been resolved. As an example, if foot and mouth disease is found within the population, that country is prohibited from exporting livestock (USDA, 2012). Thus, host response to pathogens remains an important area of genetic research in cattle and other livestock species.

It is useful to examine cattle statistics in the context of other economically important livestock. While cattle reign supreme and impact the economies of many nations, water buffalo are also economically important to many regions of the world, particularly Asia. Ninety-seven percent of the water buffalo population, or about 188 million head, reside in Asia. Two percent of water buffalo are found in Africa. The remaining populations of water buffalo are spread across Europe, the Americas, and Oceania (FAO, 2012). Despite the fact that there are more head of cattle worldwide than there are water buffalo, more people worldwide rely on water buffalo for a larger variety of activities. Not only are water buffalo utilized as a food source, as both dairy and meat, they are also used for draught power in many parts of the world because they are capable of moving heavier loads than cattle (Michelizzi *et al.*, 2010).

Because water buffalo, specifically river buffalo, are an important livestock species worldwide, understanding and examining their genetics can potentially have a positive impact on the agricultural productivity of many developing nations. Studying the genetics of river buffalo also has the potential to benefit the cattle industry through comparative studies because of their close evolutionary relationship. Therefore, the focus of this research is the river buffalo and the genetics of Toll-like receptor 5, a gene of importance to the innate immune system of mammals.

Water Buffalo: Economic and Production Importance

Water buffalo are a member of the order Artiodactyla, sub-order Ruminantia, family Bovidae, sub-family Bovinae, tribe Bovini (Borghese & Mazzi, 2005). The tribe Bovini includes the following genera: *Bos, Bison, Bubalus,* and *Syncera* (MacEachern *et al.*, 2009). Water buffalo is a single species, comprised of two economically important sub-species: river buffalo, *Bubalus bubalis bubalis*, and swamp buffalo, *Bubalus bubalis carabanesis* (Michelizzi *et al.*, 2010). River buffalo have been differentiated into breeds, while swamp buffalo largely remain as a single breed (Michelizzi *et al.*, 2010). The wild Asian buffalo (*Bubalus bubalis arnee)* is also considered a sub-species of water buffalo, but it is on the IUCN's (International Union for Conservation of Nature and Natural Resources) endangered species list as there are estimated to be less than 4,000 left in the wild and their population is rapidly declining (IUCN, 2011). Buffaloes, as a whole, are not to be confused with the American bison (*Bison bison*). It is common, especially in the United States, for the two names to be used interchangeably, but they are separated on the genus level.

The two sub-species of water buffalo are used for different tasks. River buffalo are most often used as a meat and dairy source, while swamp buffalo are best used for draught power. Water buffalo are able to better utilize less digestible feeds for growth and nourishment than cattle, which make them particularly valuable to developing countries (Michelizzi *et al.*, 2010). The small producer is able to use and sustain buffalo as a food source and for draught power while utilizing cheaper food sources, thus requiring fewer economic resources.

Buffalo meat also has advantages as a food source. It is lower in saturated fat than beef and pork (Borghese, 2005a). In addition, buffalo meat has, so far, not been linked to mad cow disease (Borghese, 2005a).

While milk production for the buffalo lags significantly behind cattle dairy breeds, buffalo milk has higher total solids (18-23 percent) than cattle (13-16 percent) (FAO, 2000). Buffalo milk also has high casein to total protein ratio (81-84 percent) as opposed cattle milk (78 percent) (Tripaldi *et al.*, 1997; Tripaldi *et al.*, 2003). The general demand for buffalo milk is also increasing. Fourteen percent of the buffalo milk that is produced in Italy is exported to Germany, France, the UK, Switzerland, the US, and Japan (Borghese, 2005b).

Anecdotally, water buffalo are healthier, on average, than cattle. Their wallowing behavior, which is due to the fewer number of sweat glands, exposes them to a large variety of pathogens. Though water buffalo are afflicted by many of the same pathogens as other large ungulates, cattle in particular, disease effects on the animal and productivity are sometimes not as apparent as in cattle (Fagioli *et al.*, 2005).

Despite the many advantages that water buffalo boast, their reproductive efficiency is sub-optimal. Female water buffalo also express estrus weakly, so artificial insemination techniques have not had the impact they have generally had on cattle breeding and management programs (Barile, 2005).

This study focuses on the immunology of river buffalo, specifically the gene coding Toll-like receptor 5, which is important to innate immunity as it functions in recognizing broad motifs in pathogens or pathogen-associated molecular patterns (PAMPs) in mammals. Studying innate immunity is important because a poorly functioning immune system can negatively impact animal health which in turn can lead to monetary loss for producers.

Buffalo Genetics: Asiatic and African

To properly understand the important differences as discussed in the previous section (nutritional, fertilization, and hardiness disparities) between river buffalo and other large ungulates, these differences need to be examined first on a genetic level. There are two main species of buffalo: Asiatic (*B. bubalis*), which has two sub-species, the river (*B. b. bubalis*) and swamp (*B. b. carabanesis*) buffalo; and African, which is comprised of cape buffalo (*Syncerus caffer caffer)* and African forest buffalo (*Syncerus caffer nanus*). Cytogenetically, river buffalo have 50 chromosomes. River buffalo have 19 pairs of autosomal acrocentric chromosomes, 5 pairs of metacentric or submetacentric autosomal chromosomes, and X and Y chromosomes (Iannuzzi, 2007). Swamp buffalo diverge from river buffalo in that they possess a diploid number of 48 chromosomes. This difference between river and swamp buffalo is the result of a river buffalo chromosomal fusion between *B. bubalis* (BBU) 4 and BBU9 in swamp buffalo (Iannuzzi, 2007; Amaral *et al.*, 2008). Hybrids between the two sub-species are possible, but the resultant offspring possess 49 chromosomes and may suffer from reduced fertility (Iannuzzi, 2007).

Bos taurus are also different from water buffalo in that they possess 60 chromosomes, 29 acrocentric autosomal chromosome pairs and the X and Y chromosome pair (Zimin *et al.*, 2009). To further illustrate the genetic differences between river buffalo and cattle, river buffalo have 5 bi-armed chromosomes, the remaining chromosomes cytogenetically correspond to *Bos taurus* acrocentric chromosomes (Amaral *et al.*, 2008). The fusion of BTA chromosomes 1 and 27 form BBU chromosome 1, BTA2 and BTA23 form BBU2, BTA8 and BTA19 form BBU3, BTA5 and BTA28 form BBU4, and BTA16 and BTA29 form BBU5 (El Nahas *et al.*, 2001; Iannuzzi *et al.*, 2003). River buffalo x cattle hybrids have not been observed, but inter-species fertilization is possible *in vitro* (Kochhar *et al.*, 2002).

In contrast, African buffalo have more chromosomes than their Asian counterparts. Cape buffalo have 52 chromosomes, with four being bi-armed. African forest buffalo have 54 chromosomes, with three being bi-armed. Crosses between Asian and African buffalo have not been reported and are unlikely to succeed owing to the fact that they share no bi-armed chromosomes, which would yield unbalanced chromosome numbers in possible offspring (Iannuzzi, 2007).

Innate immune genes are not well studied in river buffalo. There have been studies performed in river buffalo describing the differential expression of TLR5 in river buffalo (Vahanan *et al.*, 2008), but to the best of the author's knowledge, no further discussion about possible evolutionary origins for the differential expression within river buffalo. This research represents the first detailed investigation of the TLR5 gene in river buffalo.

Toll-Like Receptor (TLR) Characteristics

The *Drosophila melanogaster* protein, Toll, was discovered by embryologist Christiane Nüsslein-Volhard of the Max Planck Institute in Tübingen, Germany in an analysis of mutations in fruit flies. In 1985, she saw abnormal fly larva in which the ventral portion of the body was underdeveloped. The protein product of the Toll gene was found to cause ventralization, and normal functional activity of Toll is necessary for dorsoventral polarity in the fly (Steward & Nusslein-Volhard, 1986). It is said that when researchers saw this, they were so surprised that they shouted in German, "Das war ja toll!" which translates as "That's weird!" (Hansson & Edfeldt, 2005). There seems to be some dispute as to the proper translation of "toll". German-to-English dictionaries indicate that "toll" can mean amazing, fantastic, great, wonderful, mad, crazy, or wild.

Building upon this study, it was reported that Toll not only controls dorsoventral polarity, but also has a role in the immune defense in *D. melanogaster*. It was discovered that flies with mutated Toll did not survive fungal infection. Toll activation triggers an NF-kB cascade, which mounts the defense against fungi. The association with host defense became clearer based on the fact that the protein that induces ventralization, Spätzle, also initiates the NF-kB cascade. Spätzle is the binding ligand for Toll (Lemaitre *et al.*, 1996).

The first reported cloning of the mammalian homologue of Toll, now called Toll-like receptors (TLR), occurred in 1997. Researchers were able to show that the pathway is conserved between Drosophila to humans. It was also discovered that the human homologue, which is known to be Toll-like receptor 4 (TLR4) had the ability to induce both adaptive and innate immunity. The construction of a constitutively active mutant determined that TLR induces NF-kB activation in a comparable way as ligation of the interleukin (IL)-1 receptor, which is analogous to Drosophila Toll (Medzhitov *et al.*, 1997).

The members of the TLR family are type I transmembrane proteins and are evolutionarily conserved between insects and mammals (Anderson, 2000). They tend to recruit other intra-and extracellular proteins to the TLR-MyD88 complex, which initiates signaling cascades and will be discussed later in this chapter (Takeuchi *et al.*, 2000). Mammalian Toll-like receptors are expressed in neutrophils, monocytes, macrophages and dendritic cells (Akira *et al.*, 2001; O'Mahony *et al.*, 2008). Many TLRs are also expressed on epithelial cells since the epithelial layer is the first point of entry for pathogens (Iwasaki & Medzhitov, 2004). They are also major players in cell death, innate-adaptive immunity crosstalk, and inflammatory conditions (Hansson & Edfeldt, 2005).

Toll-like receptors function within the innate immune system and recognize pathogen-associated molecular patterns (PAMPs). Toll-like receptors generally function as homodimers, but a few also form heterodimers. Ten TLRs have been identified and sequenced in humans and bovids, with thirteen found in the mouse (Kawai & Akira, 2006). Toll-like receptor 2 (TLR2) forms a heterodimer with TLR1 to recognize diacyl lipopeptides and another heterodimer with TLR6 to recognize triacyl lipopeptides (Kawai & Akira, 2006; Kurokawa *et al.*, 2012). TLR3 forms a homodimer to recognize double-stranded ribonucleic acid (RNA) (Alexopoulou *et al.*, 2001; Kawai & Akira, 2006). TLR4 forms a heterodimer to recognize bacterial endotoxin (Poltorak *et al.*, 1998; Kawai & Akira, 2006). TLR5 forms a heterodimer to recognize bacterial flagellin (Hayashi *et al.*, 2001; Kawai & Akira, 2006). Toll-like receptor 7 and TLR8 recognize single-stranded RNA (Hemmi *et al.*, 2002; Heil *et al.*, 2004; Kawai & Akira, 2006). TLR9 forms a homodimer to recognize unmethylated CpG islands (Hemmi *et al.*, 2000; Kawai & Akira, 2006). Toll-like receptors 1, 2, 4, 5, and 6 are located on the cell surface, while TLRs 3, 7, 8, and 9 are located within the cell on specialized organelles (Kawai & Akira, 2006).

The Toll-like family of receptors has been catalogued in water buffalo using reverse transcriptase PCR (RT-PCR). Mononuclear cells express all TLRs except TLR1.

Neutrophils express all TLRs except TLR3. The spleen, liver, and lungs express all TLRs. The heart lacked only TLR10 expression, while the kidneys expressed only TLRs 2, 5, 7, and 9. The uterus expressed all TLRs except TLRs 1, 3, 4, and 6, and the ovaries expressed all TLRs except TLR1 (Vahanan *et al.*, 2008). TLRs 2, 5, 7, and 9 were represented in all tissues surveyed. These TLRs are stimulated by lipoprotein, bacterial flagellin, single-stranded RNA, and unmethylated CpG islands respectively.

A comparable expression profile study was performed in goat using quantitative real-time PCR (qPCR). Data were normalized to glyceraldehyde phosphate dehydrogenase (GAPDH). Tissues surveyed included the lung, skin, uterus, jejunum, lymph node, spleen, and peripheral blood mononuclear cells (PBMNC). A threshold of greater than or equal to 0.5 was used to determine whether there was high expression. All tissues expressed all TLRs. Lungs expressed high levels of all TLRs except TLR4 and TLR10. The skin expressed high levels of TLRs 5, 6, and 7. The uterus expressed high levels of all TLRs except TLRs 3, 4, and 10. The jejunum expressed high levels of all TLRs except TLRs 3, 4, and 10. The lymph nodes expressed high levels of all TLRs. The spleen expressed high levels of all TLRs except TLR4 and TLR10. Finally, PBMNC expressed high levels of all TLRs except TLR10 (Tirumurugaan *et al.*, 2010). TLRs 1, 5, 6, and 7 were both expressed in all tissues and met the threshold of highly expressed.

The expression profile for TLRs has also been catalogued for humans using qPCR (Zarember & Godowski, 2002). For direct comparison, only the tissues that the two studies have in common will be discussed. The study used expression levels for the spleen to normalize data. The heart, ovary, spleen, liver, lungs, kidney, and peripheral blood leukocytes (PBLs) express all TLRs. To compare the goat and human expression profile studies that utilized qPCR, I arbitrarily used the goat metric of 0.5 to determine what can be considered “highly expressed” in humans. By using the 0.5 threshold, no TLR could be considered highly expressed in the heart; TLR5 is the only TLR highly expressed in the ovaries; TLRs 3, 5, and 7 were highly expressed in the kidneys; PBLs highly expressed all TLRs except TLRs 3, 7, 9 and 10; no TLRs were considered highly expressed for the liver; the lungs highly expressed TLRs 1, 2, 3, 5, 7, and 8; and the spleen highly expressed all TLRs.

The expression (in terms of presence or absence) differential between humans and water buffalo could be due to the fact that Vahanan *et al.* 2008 did not perform qPCR; therefore, it is possible that TLR expression in the buffalo was so low that presence or absence could not be detected by agarose gel electrophoresis, but would be detected by real-time PCR. In addition, river buffalo samples were collected from the slaughterhouse so animal health would not have been definitively known, which might also be a source of discrepancies between expression profiles.

It can be concluded that diverse TLR representation will generally be found in tissues that are involved in immunity such as lymph nodes and PBLs or those tissues that are generally the sites of invasion (expected to encounter microbes) such as the skin, gut and the lungs.

Toll-Like Receptor 5 (TLR5)

While the family of Toll-like receptors is of great interest and value to immunology in general, this study specifically focuses on TLR5, which recognizes bacterial flagellin. Bacterial flagellin allows bacteria to be motile. Bacterial flagellin has four domains that are connected: D0, D1, D2, and D3. The N-terminal begins at D0 and goes through D1, D2, and D3. Then the C-terminal begins by following N-terminal D3 with D2 and D1 and ends in D0 (Yonekura *et al.*, 2003). Toll-like receptor 5 features a leucine-rich repeat (LRR) domain that serves as the recognition site for bacterial flagellin, a transmembrane domain, and the Toll-like/ interleukin-1 (IL-1) receptor (TIR) domain, which is on the inside of the cell and transduces the cytokine storm to activate the immune response (Letunic *et al.*, 2009). Toll-like receptor 5 activity is stimulated by the N-terminal D1 domain on flagellin, but it also requires the D2-D3 and the C-terminal D1 domain (Andersen-Nissen *et al.*, 2005). TLR5 signals through MyD88, which has an N-terminal death domain, a C-terminal Toll/Interleukin-1 receptor (TIR) and a short connecting linker (Bonnert *et al.*, 1997). The intracellular TIR domain of TLR5 engages the TIR domain of MyD88 to initiate the signaling cascade for an effective immune response (Figure 1.1) (Cell Signaling Technologies, 2012). Toll-like receptor 5 is active in the urinary tract, the respiratory tract, and the intestinal tract of the river buffalo (Andersen-Nissen *et al.*, 2007; Vijay-Kumar *et al.*, 2007; Morris *et al.*, 2009).

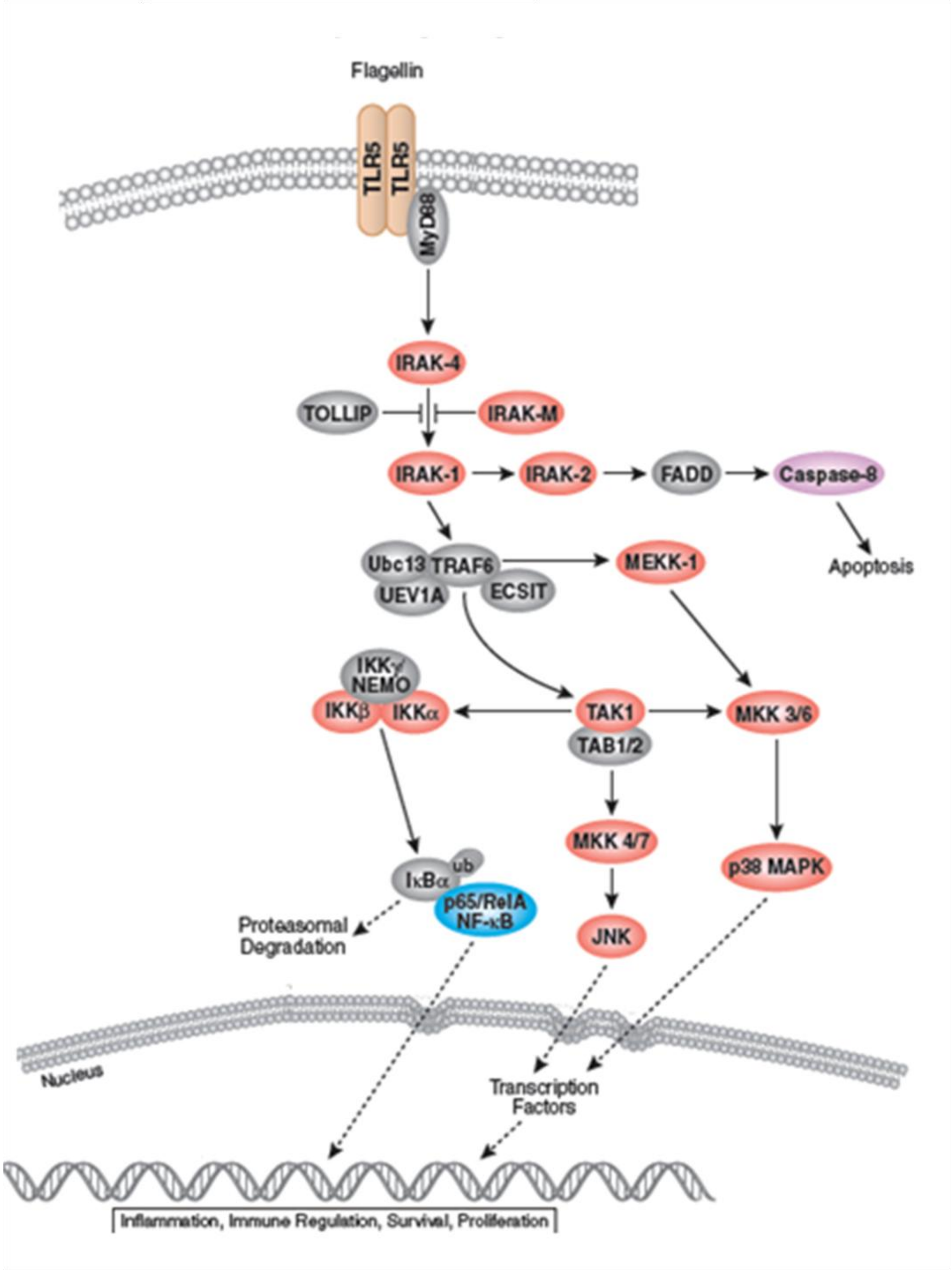


Figure 1.1 Toll-like receptor 5 (TLR5) signaling. TLR5 has three domains: extracellular LRR domain that recognizes bacterial flagella of gram negative and positive bacteria, a transmembrane domain that allows it to cross the cell membrance, and the intracellular TIR domain that interacts with the TIR domain of MyD88 to begin the immune response against flagellated bacteria.
Modified from Cell Signaling Technologies® www.cellsignal.com

What happens in the absence of TLR5 gene expression is paramount to elucidating functionality and importance of TLR5 in regards to innate and adaptive immunity. Knock-out mice were developed to answer this question (Andersen-Nissen *et al.*, 2007). Mice without TLR5 activity have a reduced ability to manage their commensal load; therefore they suffer from an increased burden of commensal bacteria (Andersen-Nissen *et al.*, 2007). Generally, within the gastro-intestinal tract flagellated bacteria, both helpful and harmful, will be found. Examples of pathogens that stimulate TLR5 activity are *Escherichia coli, Salmonella typhimurium, Pseudomonas aeruginosa,* and *Listeria monocytogenes.* In addition to a decreased ability to maintain a balanced commensal load, TLR5 knockout mice were shown to develop spontaneous colitis. Though they appeared to be healthy and there were no observable phenotypic alterations to their small intestines, they tended to be smaller than their age-matched, sex-matched wild type littermates. Rectal prolapse, enlarged spleens, exacerbated gut pathology in Salmonella gastreoenteritis, and reduced ability to begin the signal cascade (Figure 1.1) when TLR5 is stimulated were also common in these mice (Andersen-Nissen *et al.*, 2007).

Toll-Like Receptor 5 and Ipaf

The immune system as a construct of human health is riddled with complex relationships between large numbers of system actors. Even when researchers reduce the size and scope of study from the two arms of the immune system (innate and adaptive) and focus on one arm, the complexity remains. This dissertation focuses on TLR5, which is heavily involved in innate immunity as stated previously. Because the innate immune system is vast and complex, the TLR family works in conjunction with other innate immune actors. One example of this cooperation is between the TLR family and the NLR (Nod-like receptor) family. Specifically this section discusses how TLR5 works with its NLR counterpart, Ipaf.

Toll-like receptors are found on the cell surface, or they localize on specialized cell organelles. Invaders such as *Yersinia pseudotuberculosis* have developed ways to evade TLRs by passing through the endothelium and infiltrating the cytosol, where TLRs are not present and cannot initiate a cytokine cascade (Cossart & Sansonetti, 2004). In response to a pathogen's ability to infiltrate the cytosol, organisms have developed a countermeasure: the Nod-like receptor family, which are cytosolic pattern recognition receptors (PRRs).

Like TLRs, NLRs possess a leucine-rich repeat (LRR) domain that forms the ligand-binding site, which is the feature that allows the NLR (and TLR) to recognize and bind a particular PAMP (Fritz & Girardin, 2005). The first NLRs to be discovered were NOD1 and NOD2, which recognize the products resulting from the degradation of peptidoglycan (PG) (Fritz & Girardin, 2005). Peptidoglycan is a major component of gram positive cell wall and is only a thin layer in the periplasmic space of gram negative bacteria (Fritz & Girardin, 2005). Specifically, NOD1 responds to dipeptide D-Glu-*meso*-DAP that is found in most gram-negative bacteria and a few gram positive bacteria (*Bacillus* spp.) and is a naturally occurring product of peptidoglycan degradation. Some members of the NLR family, which include NOD1 and NOD2, induce tumor necrosis factor (TNF), Interleukin-6 (IL-6), and IL-12 (Kobayashi *et al.*, 2005). Other family members, including Ipaf, induce caspase-1, which acts upon IL-1ß and IL-18. These two cytokines require a signal from a TLR to begin transcription and translation of their precursor, and then an NLR to induce caspase-1 to activate their processing and secretion functions (Sahoo *et al.*, 2011). Such a combined response provides the immune system the ability to detect flagellated bacteria both outside and inside the cell and serves to lessen the impact of a key evasion tactic of microbes.

Toll-like receptor 5 and Ipaf work together to recognize bacterial flagellin. Ipaf responds to intracellular threats that possess both flagellin and specific virulence factors, while TLR5 recognizes extracellular bacteria flagellin only (Miao *et al.*, 2007). Redundancies, such as this one, ensure that there are numerous checkpoints (if one fails) to detect and neutralize invasion by microbes. It also demonstrates the complexity of the system and reveals potential targets of therapeutics.

Evasion of Toll-Like Receptor 5

As with many biological processes, there is adaptation on both sides of the equation between pathogen and host. Adaptation represents the constant struggle to come to equilibrium that will allow both pathogen and host to successfully propagate. It is generally accepted that the mitochondrion began as an infectious agent. The circular nature of mitochondrial DNA and its mode of replication and propagation are clues that provide evidence that it more than likely began as an infectious agent. Mitochondrial presence within organisms is an example of how, over time, an organism will adapt to best ensure its own survival. In this case, the host received an efficient means of energy production, and the pathogens, mitochondria, successfully incorporated themselves into their preferred host, thus ensuring their continued survival (Cavalier-Smith, 1987). The Toll-like family of receptors and its agonists are no different.

Many infectious organisms have devised ways to evade TLR5 stimulation. The general concept of the innate immune system is to recognize broad classes of motifs. The response is consistent. The innate immune system can prime adaptive immunity so that the host can eventually tailor a response to infection. Because the innate immune system recognizes broad motifs (PAMPs), it is particularly difficult for a pathogen to change or mutate these motifs to evade detection (Andersen-Nissen *et al.*, 2005). Usually, such changes result in the reduced ability to successfully invade and infect a host (Andersen-Nissen *et al.*, 2005).

However, there are examples of organisms that have successfully found ways to evade the system. Members of the alpha and epsilon (based on ribosomal RNA sequence) proteobacteria (all gram negative) possess flagellin not recognized by TLR5 despite being motile organisms. These organisms were able to successfully mutate the TLR5 recognition site. This class of bacteria also seems to have a compensatory amino acid change within the flagellin monomer surface that results in retention of filament formation (Andersen-Nissen *et al.*, 2005). Notable members important in human disease are: *Campylobacter jejuni* (rod-shaped, non-spore forming, epsilon class, found in animal feces, infection leads to enteritis); *Helicobacter pylori* (helix-shaped, epsilon class, found in stool or vomit and has been found in saliva; causes chronic low level inflammation of stomach lining and has been strongly associated with gastric ulcers and stomach cancer); and *Bartonella bacilliformis* (rod-shaped, transmitted by sandflies; causes acute Carrion's disease or chronic Verruga Peruana). In addition, successful evasion may also result in an asymptomatic carrier-state, which is a boon to bacteria as it almost ensures successful proliferation within populations (Andersen-Nissen *et al.*, 2005).

Previous studies have also shown other evasion tactics besides mutating the TLR5 recognition site. *Listeria monocytogenes* is able to down-regulate flagellin expression at 37°C (Kathariou *et al.*, 1995). *Escherichia coli* and *Pseudomonas* spp. also down-regulate their flagellin during the process of biofilm formation, which aids bacteria survival in hostile environments; and, as evidenced by *P. aeruginosa* infection, can allow bacterial species to evade host detection and exhibit resistance to antimicrobials (Costerton *et al.*, 1999; Prigent-Combaret *et al.*, 1999; Whiteley *et al.*, 2001).

Other Functions of Toll-Like Receptor 5

Toll-like receptor 5 also has many other roles in addition to recognizing bacterial flagellin. Toll-like receptor 5 has been proven to be an important actor in autoimmune disease, such as Crohn's disease (Gewirtz *et al.*, 2006). However, there are conflicting data as to the nature of the role TLR5 plays in mediating response in the disease. Crohn's is a disease of the gastrointestinal tract. Some data suggest a link between Crohn's disease and an adaptive immune response against flagellin, but there are also data that suggest the problem is in the innate immune response. Toll-like receptor 5 is also an attractive target for immunotherapies because it has been linked to protective functions, e.g. increased TLR5 in humans resulted in elevated antibody production against some *E.coli* flagella (Hugot *et al.*, 2001; Lodes *et al.*, 2004; Hawn *et al.*, 2005; Sitaraman *et al.*, 2005; Gewirtz *et al.*, 2006; Strober *et al.*, 2007; Vijay-Kumar *et al.*, 2007; Vijay-Kumar *et al.*, 2008).

Discussion of Crohn's disease is important because of a similar disease in livestock called Johne's disease, which causes a chronic inflammation of the intestines. *Mycobacterium avium paratuberculosis* (MAP) is the causative agent of Johne's disease (Pierce, 2009). Numerous studies have attempted to link MAP with Crohn's disease. However, while there is some evidence that MAP is involved with Crohn's disease, it is still not widely accepted as the causative agent (Scanu *et al.*, 2007; Pierce, 2009; 2010). Regardless, large animal models of Johne's disease can serve to elucidate the etiology of Crohn's disease, especially in light of the fact that there is evidence of MAP being present in some Crohn's patients and that both Crohn's and Johne's disease are associated with immune dysregulation (Scanu *et al.*, 2007; Mendoza *et al.*, 2009; Pierce, 2009; 2010).

Toll-like receptor 5 engagement modulates tumor development and growth in the mouse xenograft model of human colon cancer (Rhee *et al.*, 2008). In the study, expression of MyD88 or TLR5 was stably knocked down in human colon cancer cells. The lack of expression of MyD88 or TLR5 resulted in enhanced tumor growth and inhibited tumor necrosis, whereas TLR5 activation by a bacterial flagellin solution that was administered by researchers around the tumor site increased tumor necrosis (Rhee *et al.*, 2008). Thus, TLR5-dependent signaling could be a potential immunotherapeutic target to modulate colonic tumors.

Toll-like receptor 5 also has a role in the innate immune response to acute *Pseudomonas aeruginosa* pneumonia (Morris *et al.*, 2009). *P. aeruginosa* is an opportunistic pathogen and a leading cause of hospital-acquired pneumonia. TLR5 is highly expressed in human and murine lung tissue by airway epithelial cells, neutrophils, and alveolar macrophages. TLR5 signals through MyD88, which is an adapter protein and is key to pathogen clearance (Morris *et al.*, 2009).

Research Goals

The water buffalo, due to its economic and social importance to a large portion of the world's population, is an organism that is in need of enhanced research efforts to improve its health and productivity. The river buffalo was specifically chosen for this study, as opposed to the swamp buffalo, because of its prominence with producers. Within the context of improved animal health, TLR5 was chosen as a gene of potential importance because of its role in the innate immune system.

This study is comprised of three parts: 1) generating a radiation hybrid map of river buffalo chromosome 5 (BBU5) where the TLR5 gene is located and building a comparative map with homologous cattle chromosomes; 2) conducting a single-nucleotide polymorphism (SNP) survey of the TLR5 gene to reveal variation within river buffalo and across multiple species;and 3) performing an evolutionary study by inferring a phylogenetic trees of TLR5 across multiple taxa and across bovids and determining the possible selective constraints within the coding region of TLR5 over a segment of evolutionary history.

The mapping effort produced a map of an entire chromosome in a species for which whole-genome sequence is not yet available. The goal of the SNP study was to explore the extent of genetic variation in this gene in breeding populations of river buffalo. While a comprehensive SNP chip for buffalo awaits an investment in sequencing, the identification of SNPs in putative candidate genes for host-resistance might provide a first step in the study of association of genetic variation with disease phenotypes.

A SNP chip of candidate genes could reduce the time and monetary investment in association studies since it would only be necessary to sequence DNA across targeted genes and not across the whole genome. The SNP survey afforded the opportunity to evaluate Toll-like receptor 5 within an evolutionary context. By expanding the number of species, the divergence over time of sequences for the TLR5 gene could be observed and adaptive changes in the gene between species could be postulated. Understanding the genomic differences between species (chromosomal rearrangements, sequence variability, and evolutionary departures) provides avenues of future study.

The goal of this research was to highlight some of those differences in river buffalo and to put that into context with other species by constructing an RH map to reveal possible rearrangements between river buffalo and cattle, examining sequence variation and haplotype and protein domain coding structure in the TLR5 gene, and performing a phylogenetic analysis across multiple species based on this single gene of importance in innate immunity.

CHAPTER II

A RADIATION HYBRID MAP OF RIVER BUFFALO (*BUBALUS BUBALIS*) CHROMOSOME 5 (BBU5)

Introduction

There are approximately 194 million river buffalo (*Bubalus bubalis*) in the world (FAO, 2012). While economically important to many countries, roughly 97 percent of the river buffalo population are located in Asian countries, where it is used for food, fuel, fertilizer, and as draught power (FAO, 2000). Buffalo milk is higher in total solids (protein, fat, minerals) than cow milk; and the meat is also leaner than beef (Tripaldi *et al.*, 1997; FAO, 2000; Tripaldi *et al.*, 2003). Buffalo also have the ability to grow better on less digestible feeds than cattle (Tripaldi *et al.*, 1997; FAO, 2000; Tripaldi *et al.*, 2003).

Despite the fact that the river buffalo is economically important to many Asian countries and in other parts of the world, only recently has its genome been explored for the purpose of mapping genetic variation in the traits of economic and biologic interest. There are few genetic resources available for river buffalo other than the somatic cell and cytogenetic maps (El Nahas *et al.*, 1996; Iannuzzi *et al.*, 2003). Consequently, comparative mapping and exploration of genetic variation in river buffalo is lagging behind other livestock (Womack, 2005).

To generate a radiation hybrid (RH) panel, fibroblast cells from river buffalo were lethally irradiated at 5000 centiRays (CrR) to fragment chromosomes and were then fused with Chinese Hamster cells, which are thymidine kinase deficient (Cox *et al.*, 1990). The degree of chromosomal fragmentation is dependent on how much the cells were irradiated and determines the resolution of resultant maps. The newly fused cell line was then grown in selective medium that contained hypoxanthine, aminopterin, and thymidine (HAT) so that only cells that contained donor chromosomal fragments were able to grow (Cox *et al.*, 1990). Clones of hybrid cells were then picked and propagated (Cox *et al.*, 1990). A radiation hybrid mapping panel of 90 clones was constructed for river buffalo using the above method (Amaral *et al.*, 2007) and was kindly provided for use in the current study by other students and staff in the J.E. Womack Laboratory at Texas A&M University. The utility of the panel was previously demonstrated by deriving RH maps of chromosomes 3 and 10, 6, and 1 (Amaral *et al.*, 2007; Miziara *et al.*, 2007; Stafuzza *et al.*, 2007). In this current study, this RH panel was used to construct a map of river buffalo chromosome 5 (BBU5), which is included in the recent publication of the first generation river buffalo whole-genome radiation hybrid map (Amaral *et al.*, 2008). This study seeks to describe the chromosomal arrangement of BBU5 via constructing a radiation hybrid map since a comprehensive map of this chromosome has not been previously produced.

Cattle (*Bos taurus*, BTA) and river buffalo (*Bubalus bubalis*, BBU) chromosomes can be matched arm for arm at the cytogenetic level. However, the river buffalo has five bi-armed chromosomes, which appear to be fusions of single-armed cattle chromosomes. The fusion of BTA chromosomes 1 and 27 form BBU chromosome 1, BTA2 and BTA23 form BBU2, BTA8 and BTA19 form BBU3, BTA5 and BTA28 form BBU4, and BTA16 and BTA29 form BBU5 (El Nahas *et al.*, 2001; Iannuzzi *et al.*, 2003). Even though chromosome 5 is the smallest of the bi-armed chromosomes, previous mapping of 10 potentially economic important quantitative trait loci (QTL) markers to BTA16 and BTA29 make BBU5 a potentially important chromosome for traits of biologic and economic interest.

Materials and Methods

The RH map of BBU5 was generated using cattle-derived markers (Table 2.1). Three markers were chosen that had been previously placed on the river buffalo cytogenetic map to aid in the orientation of the RH map (Iannuzzi *et al.*, 2003). Other markers were chosen based on their place on cattle chromosomes 29 and 16 (Jann *et al.*, 2006). Markers were amplified from DNA from a panel of 90 RH cell lines, plus a river buffalo control and hamster DNA by PCR using PE Applied Biosystems GeneAmp® PCR System 9700 and Techne Touchgene® Gradient TC-512 in 96-well PCR plate. Markers were initially optimized by performing a gradient PCR across cattle, river buffalo and hamster controls to find the optimal annealing temperature that would allow for the best possible amplification from cattle and river buffalo but not hamster DNA. Each 10 µl PCR contained the following: 50 ng DNA, 1.5 mM $MgCl_2$, 0.2 mM each of dNTP, 0.2 mM each of the forward and reverse primer (Table 2.1), and 0.5 U of AmpliTaq Gold DNA polymerase (Applied Biosystems). The gradient PCR reaction was as follows: initial denaturation for 10 s at 94ºC, followed by 35 cycles of 30 s at 94ºC, 30 s at 58ºC Δ 17ºC, and 30 s at 72ºC, with a final extensions of 5 min at 72ºC for 35 cycles. Gradient PCR reactions were conducted on the TouchGene TC-512 (Techne) thermocycler. The resulting amplicons were electrophoresed through an ethidium bromide (EtBr) stained 2% agarose gel in 1X TBE buffer and viewed under ultraviolet transillumination to visualize the bands. Optimal primer temperatures were assessed via success of amplification of the template. The criteria were strong bands with the appropriate band size with no smear or extra bands at other band sizes and no amplification of the negative control.

After the annealing temperature was optimized for the primers, a PCR was carried out using the radiation hybrid panel DNA as the template and the appropriate annealing temperatures for each primer as determined above. The PCR program was as follows and was performed using the ABI GeneAmp PCR 9700 (Applied Biosystems) or the TouchGene TC-512 (Techne) thermocyler: initial denaturation for 10 s at 94ºC, followed by 35 cycles of 10 s at 94ºC, annealing temperatures ranging from 54ºC to 65ºC depending on the data from the gradient PCR, 30 s at 72ºC, and a final extension of 5 min at 72ºC, with a final hold of 4ºC.

The resulting amplicons were electrophoresed through a 2% agarose gel in 1X TBE buffer and markers were scored (1 for a strong positive, 2 for an ambiguous result, and 0 indicated a negative) independently. All markers were typed twice across the RH panel DNA and scored at least twice. Discrepancies were resolved by a third repetition. Retention frequencies were then calculated by dividing the number of positives by the number of clones across the panel.

To compute the RH map, the software packages rh_tsp_map 3.0 and CONCORDE were used with the maximum likelihood criterion (MLE) (Agarwala *et al.*, 2000; Applegate *et al.*, 2006; Schaffer *et al.*, 2007). The map was constructed according to the steps given in the rh_tsp_map tutorial as previously described (Miziara *et al.*, 2007). However, the pairwise LOD score threshold for making linkage groups was increased to 7.0 because the increasing number of typed markers makes spurious high LOD scores between markers on different chromosomes more likely to occur.

Table 2.1
Cattle-derived markers used to construct the BBU5 RH map.

Marker	Type	RF (%)	Location (cR)	Tm (°C)	Forward Primer (5’-3’)	Reverse Primer (5’-3’)	UniSTS ID	Accession
ILSTS081[2]	MS	34.4	0.0	57	AGTCAGACAACGACTGTGCG	TTTCGAACAGGCTTTTGGGG	16092	L37276
S68957[3]	GENE	35.6	31.13	57	CTTCCCTTGCAGATGCCCAGAG	CTTCCCTTGCAGATGCCCAGAG	278462	S68957
BMC6004[2]	MS	35.6	46.8	55	GATTCCCTGATAGAAATGGCA	GGTGAGATGAGGATGCGATC	46306	G19099
RME33[2]	MS	40.0	80.26	53	TTAGAGGCACCACCTAACGG	GCTTCTCAGTTGTTCTGCCC	U15435	251429
AW461519[3]	EST	41.1	92.6	57	GGGGAGAAGAAAAGGCATTC	GGTCTGTGGTTCCCCTTACA	278070	AW461519
BZ932751[3]	EST	41.1	138.7	65	GGCGGCGAACGAGTCTGG	AGAGCGGGAGGTGGTGGTC	477149	BZ932751
BMC3224[2]	MS	38.9	148.49	56	CCATCACTGCTATTCTACCTCC	CACAGCCAATTTCTGATTTCA	279690	279690
RM040[2]	MS	34.4	158.55	58	TGGAGGACTACAATCCATGAGG	TAAGTGCAGTAAGATGCCATGG	251356	U10386
BZ900418[3]	EST	33.3	183.57	61	GCTGGCAGGTGTGGGTGTTC	GTCGGATTCTCCCTCTGACCACA	477145	BZ900418
BZ905352[3]	EST	27.8	209.71	57	TGTCTTTCAGAGTATCATCACCC	TTCAACCATAGGCAACTTCAA	477143	BZ905352
BMS1600[2]	MS	34.4	226.22	55	TGTGGGAATCTGAAGCTCTATAT	GACATGACTGAGCAACTTTTACC	75448	G18676
BZ946384[3]	EST	37.8	233.71	58	CAGGAAAGACTGAGCAGTAAGTG	AATAGCCTTCACTTTGCCTTCAC	477140	BZ946384
BZ933262[3]	EST	41.1	263.44	57	ATCCTCAGGCTTTTATCTTTGTG	AGATTCCTATGAGCTGATAAGTC	477137	BZ933262
ILSTS089[2]	MS	40.0	Placed	60	AATTCCGTGGACTGAGGAGC	AAGGAACTTTCAACCTGAGG	6537	L37239
BMC8012[1,2]	MS	41.1	283.52	57	AATTCCATGCACAGAGGACC	GATTCCAGAAAGTTCCCCCA	6526	G18773
BZ951039[3]	EST	44.4	306.57	57	TGGCAATGATTACAGGTGCATT	TTGAAAAGCACAACTCATATTC	477131	BZ951039
ILSTS019[2]	MS	46.7	Placed	58	AAGGGACCTCATGTAGAAGC	ACTTTTGGACCCTGTAGTGC	251117	L23492
BZ901563[3]	EST	43.3	318.22	60	CTTAGTCAAGTCTACCACACA	AACCTTTTCTCCAGGCAG	477130	BZ901563
ILSTS057[2]	MS	41.1	Placed	58	GGAACTGTTCTAAGAAGTGG	TGCTGTTCATTCTATGTGGG	51298	L37265
BZ930457[3]	EST	41.1	337.78	60	GTCTTCAAGTGCCAAATCCA	ACTTTCTCCATAGTTGCCTGTA	477127	BZ930457
CC447793[3]	EST	45.6	347.35	57	GATGTGTTTTGGTGAAGAAGCAGAG	TGAGACAAATGAGAATATGCAGGTG	477125	CC447793
BZ919428[3]	EST	51.1	369.74	63	TGATGGTCTCTTGCTCAGGATGG	GGGCTGAATGGCTCTTTGTTCTG	477123	BZ919428
BZ919809[3]	EST	54.4	376.6	57	CCATTGCCAGATTCAGTCTCATC	AGATCCTCAAGCAGTGTGATGG	477121	BZ919809
BZ938148[3]	EST	48.9	Placed	57	AGTAAGATAATGCCACAGCTTCTAC	AGGCAAATAGAATGCAATGCAAATC	476360	BZ938148
BMS357[2]	MS	50.0	412.66	57	TCCAAACAAGTCTTCTCTATTTACC	CCAAATAATTGCTGGTCAGG	65755	G18845
AW267148[3]	EST	45.6	432.35	57	ACTTTGTCTTCTGGAAATTAGC	ACTTCAACCTCGTGGGAATTAG	278204	AW267148
HUJ614[1,2]	GENE	45.6	441.81	63	CGCCAGGCATGGTGAAGTCG	CCCAGCACAGTACAGGCTGC	250838	M93653
BZ951725[3]	EST	37.8	471.01	57	TTAACACTAGGCTTCAGGCAATG	TAGGTCAAGTTGTTAGCCAGTAAC	476365	BZ951725
BZ948508[3]	EST	32.2	Placed	57	TATTCTTACACAGTATGCAGTATTC	TTGGTTGCTTATTGCTCAGG	476368	BZ948508

Table 2.1 continued

Marker	Type	RF (%)	Location (cR)	Tm (°C)	Forward Primer (5’-3’)	Reverse Primer (5’-3’)	UniSTS ID	Accession
CC562100[3]	EST	33.3	508.8	57	TGCTCACTCATGCTATCACTTCTCC	ACTGGCAAAGCTGGTCTCTTCTAAC	476371	CC562100
BM121[2]	MS	30.0	Placed	58	TGGCATTGTGAAAAGAAGTAAA	ACTAGCACTATCTGGCAAGCA	73368	G18420
BZ944687[3]	EST	27.8	550.27	63	CCTGCTGCTTGAAGTGCCACAG	ACTGACACCACTGCTCTGCTGAC	476373	BZ944687
BZ950494[3]	EST	24.4	581.77	58	TTGGCACTTGCACAACTGAATG	GAATGGTCATTGAGCACACAGAAAG	476375	BZ950494
AW289394[3]	EST	36.7	614.81	58	GGGTTGTTACATTCCGTGTCAG	CTGAAATGAAGTGCAGGGCTAC	278430	AW289394
TLR5	STS	36.6	627.62	58	CATCTGTTATAAGAAAGCCCAGA	TATTGAGAAACCAGTCAACATCC	519115	444870
AW461592[3]	EST	40.0	667.93	57	ACTTTCACGTGTCGGTTTCC	TTGCACATTTTAAAAGCACCC	278075	AW461592
BZ945895[3]	STS	34.4	692.050	57	AGATGCTTGCCTCAAACAAACTGTG	AGATGCTTGCTGTAACTCACTTTGG	476386	BZ945895
CSSM003[2]	MS	31.1	705.33	55	GTACCTTAAGGTCAAGGGCTTTCT	TGGGTCCAATTGAGAATCTTCATG	251063	U03786
AW289372[3]	GENE	31.1	721.84	60	GGCCTCAACCAAATACAAGC	GTACGGTTACTTGATGCGTG	279203	AW289372
BZ952478[3]	EST	30.0	735.49	65	CGGACAGCGGAGCGGTGAG	CTTCCTCTGACCAGCCGTCCAG	476395	BZ952478
IDVGA26[1,2]	MS	17.8	772.85	57	TGAGGACTCAACCCACATTTTG	AAAGAGTGCAACGGGAAAGTG	251442	X85045
BZ910068[3]	EST	20.0	844.43	54	AACCTCATGCTCGCTAACTCAATAC	TCTTACACATCACTCAGTTCCTTGC	476408	BZ910068
BM1706[2]	STS	28.9	877.32	58	ACAGGACGGTTTCTCCTTATG	CTTGCAGTTTCCCATACAAGG	7959	G18460
INRA048[2]	MS	24.4	894.95	58	CTGTCCCTCAGTAAACAAGTCG	AAGCTAAAGTAGCAGGGAAG	251130	251130
BMS462[2]	MS	24.4	920.28	60	TGCAGACGGGAGAAAAGC	CTCACTTCCTCCTCAGGTGC	71420	G18864
AW482289[3]	GENE	24.4	932.09	51	CCCACCAATGAATAATCTTATGCC	AAAGCTAACAACAGAGTCTTCGTAG	278825	AW482289

RF- Retention Frequency, EST- Expressed Sequence Tag, MS- Microsatellite, STS- Sequence Tagged Site

[1] FISH mapped markers

[2] Ihara *et al.* 2004

[3] Jann *et al.* 2006

Results and Discussion

Using the BBURH_{5000} panel, a RH map was constructed for river buffalo chromosome 5, a bi-armed chromosome orthologous to cattle chromosome 29 and 16 as shown by chromosome banding and fluorescent in-situ hybridization (FISH) mapping (Iannuzzi *et al.*, 2003; Amaral *et al.*, 2007).

Retention frequencies (the proportion of radiation hybrids that contain donor chromosome fragments) for individual markers ranged from 17.8% (IDVGA26) to 54.4% (BZ919809) as shown in Table 2.1 and graphically in Figure 2.1. Fifty markers predicted to be on chromosome 5 from their location on the cattle map were initially analyzed; however, three of these markers (TGLA45, TGLA35, and BM6121) were dropped during the early stage of making linkage groups because they did not achieve a sufficient two-point LOD score with any other marker. All other markers achieved a sufficient two-point LOD score and formed a single linkage group. Radiation hybrid mapping is affected by the density of the map. Marker density and proximity affects marker placement in relation to other markers since RH mapping depends on statistical association between chromosomal fragments and prospective markers. Therefore, if a segment of the chromosome is not densely or adequately populated with markers, then the software cannot form a statistical association between markers, which can result in a marker being “placed” or “framed”.

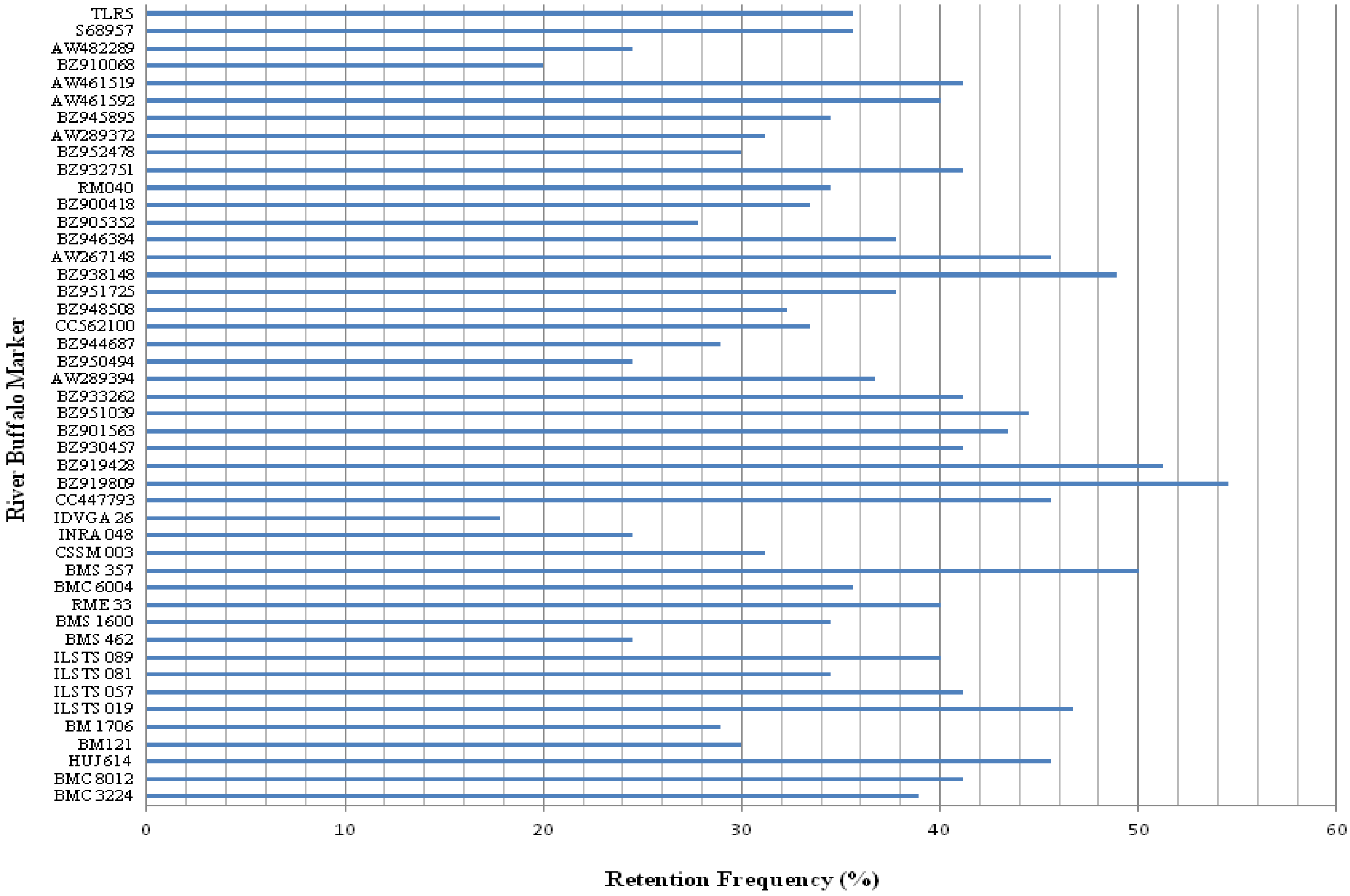


Figure 2.1 Retention frequencies for the 46 river buffalo markers used in this study.

Placed markers are in the area, but the exact location of "placed" markers cannot be confirmed due to the sparcity of other markers or the low pairwise LOD scores. Framed markers can be confidently placed on the map, however. Increasing the density of markers can change marker order since dense areas have markers that can be more strongly associated with each other due to proximity and association with chromosomal fragments that were initially generated on the RH panel. The high LOD score threshold prevents spurious associations between markers. River buffalo chromosome 5 is the only bi-armed chromosome that formed a single linkage group as shown in both the recently constructed whole-genome RH map (Amaral *et al.*, 2008) and the RH map constructed with fewer markers in this study (Figure 2.2).

Three markers that were mapped to the cytogenetic map (BMC8012, HUJ614, IDVGA26) corresponded to their respective counterparts on BBU5. This map was oriented consistently with the cytogenetic map for river buffalo and the latest cattle RH map (Iannuzzi *et al.*, 2003; Jann *et al.*, 2006). Two of the three markers mapped on the cytogenetic map flanked the centromere and confirmed our predicted orientation of the RH map based on the hypothesis of centromere fusion of the two homologous cattle chromosomes. Of the 46 markers, 39 were positioned on the MLE-consensus (a.k.a. framework) map, and the remaining 7 markers were placed in their most likely interval between two consecutive markers on the MLE-consensus map. The MLE-consensus map is estimated to be 932.1 cR in length.

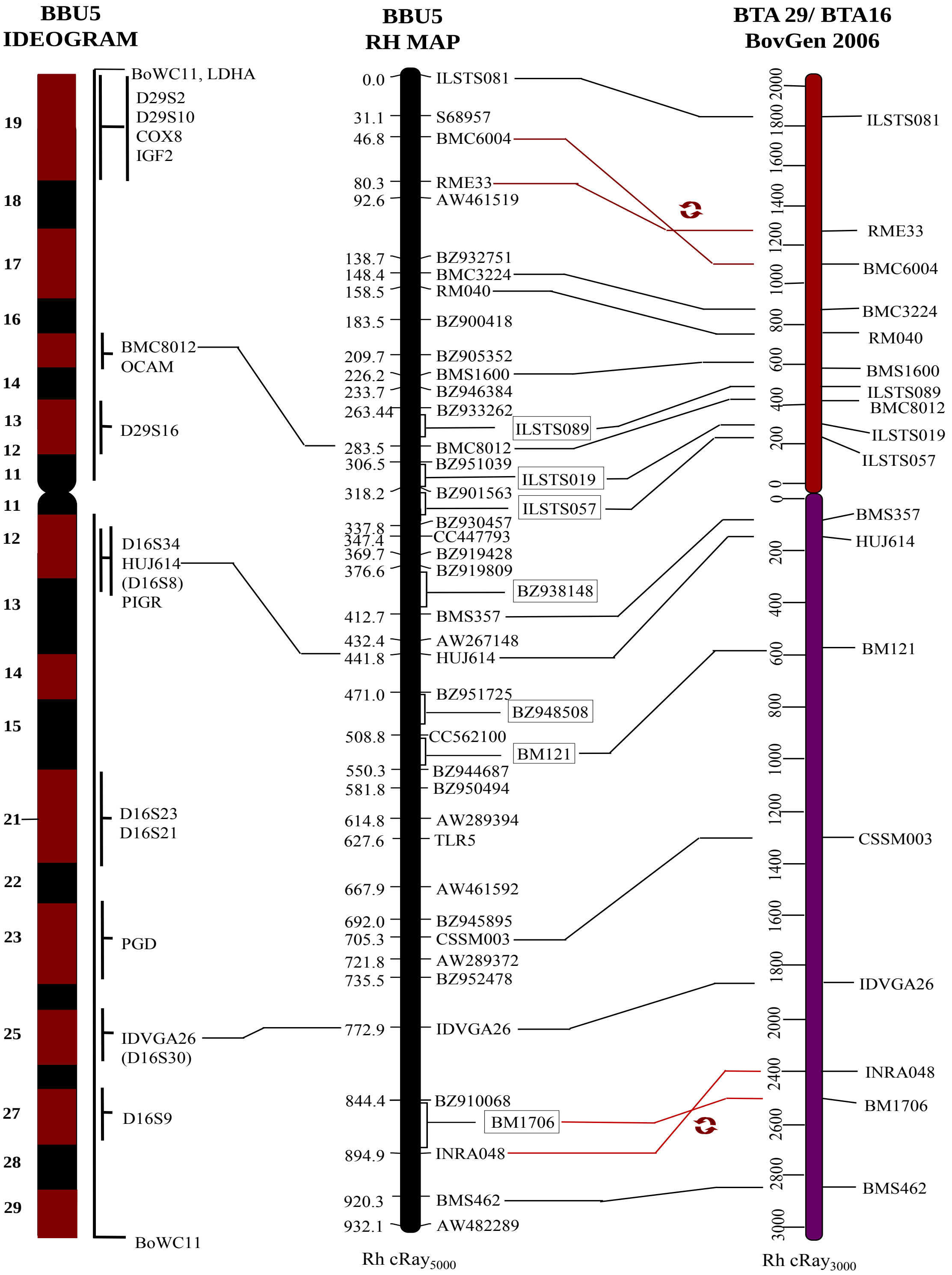


Figure 2.2 Comparison of the river buffalo chromosome 5 RH map. BBU5 RH map (center) with the buffalo cytogenetic map (left) and the bovine chromosomes 29 and 16 BovGen 2006 map (right). Framework markers are in black. Placed markers are boxed. Markers are connected to their counterparts by solid black lines. Inverted markers are denoted by a 🔄 symbol.

Two predicted inversions (BMC6004 and RME33, BM1706 and INRA048) were observed in marker orientation compared to the cattle BovGen 2006 map (Figure 2.2). Additionally, the generated RH map was compared to the 2004 MARC genetic linkage maps of BTA 29 and 16 (Ihara *et al.*, 2004). The linkage map also showed the same marker orientation as the BovGen map (data not shown). The recent river buffalo whole-genome (WG) RH map maintains the BMC6004 and RME33 inversion (Amaral *et al.*, 2008). The BM1706 and INRA048 inversion is not maintained. BM1706 is a placed marker so its location was subject to change with increased markers in the region and the WG RH map increases the marker density of that region.

Cattle chromosomes 29 and 16 are rich in quantitative trait loci (QTL) (http://bovineqtlv2.tamu.edu/index.html), suggesting that river buffalo chromosome 5 might be a candidate chromosome for corresponding buffalo QTL (Figure 2.3). The following cattle QTLs were confirmed by genetic analysis (whole genome scans that included half-sib families, backcrossing, and crossbred analysis) or by candidate gene studies.

Carcass quality (marbling score) and meat tenderness, carcass yield (hot carcass weight, retail product yield, and live weight), milk protein (protein yield) and milk yield, and weaning weight have been mapped on cattle chromosome 29 (Casas *et al.*, 2000; Smith *et al.*, 2000; MacNeil & Grosz, 2002; Casas *et al.*, 2003; Kim *et al.*, 2003; Viitala *et al.*, 2003). Hot carcass weight, live weight, meat tenderness, milk protein, retail product yield, and weaning weight were mapped in cattle to regions corresponding to the RME33/ BMC6004 inversion on the generated river buffalo RH map (Figure 2.2).

Similarly, carcass quality (marbling score), and carcass yield (fat depth, dressing percentage, hot carcass weight and live weight) were identified on cattle chromosome 16 (MacNeil & Grosz, 2002; Casas *et al.*, 2004). Fat depth was mapped to the region containing BM1706 (MacNeil & Grosz, 2002). BMS1706 is inverted with INRA048 on the generated RH map (Figure 2.2); however, as previously discussed, the inversion is not maintained on the WG RH map (Amaral *et al.*, 2008).

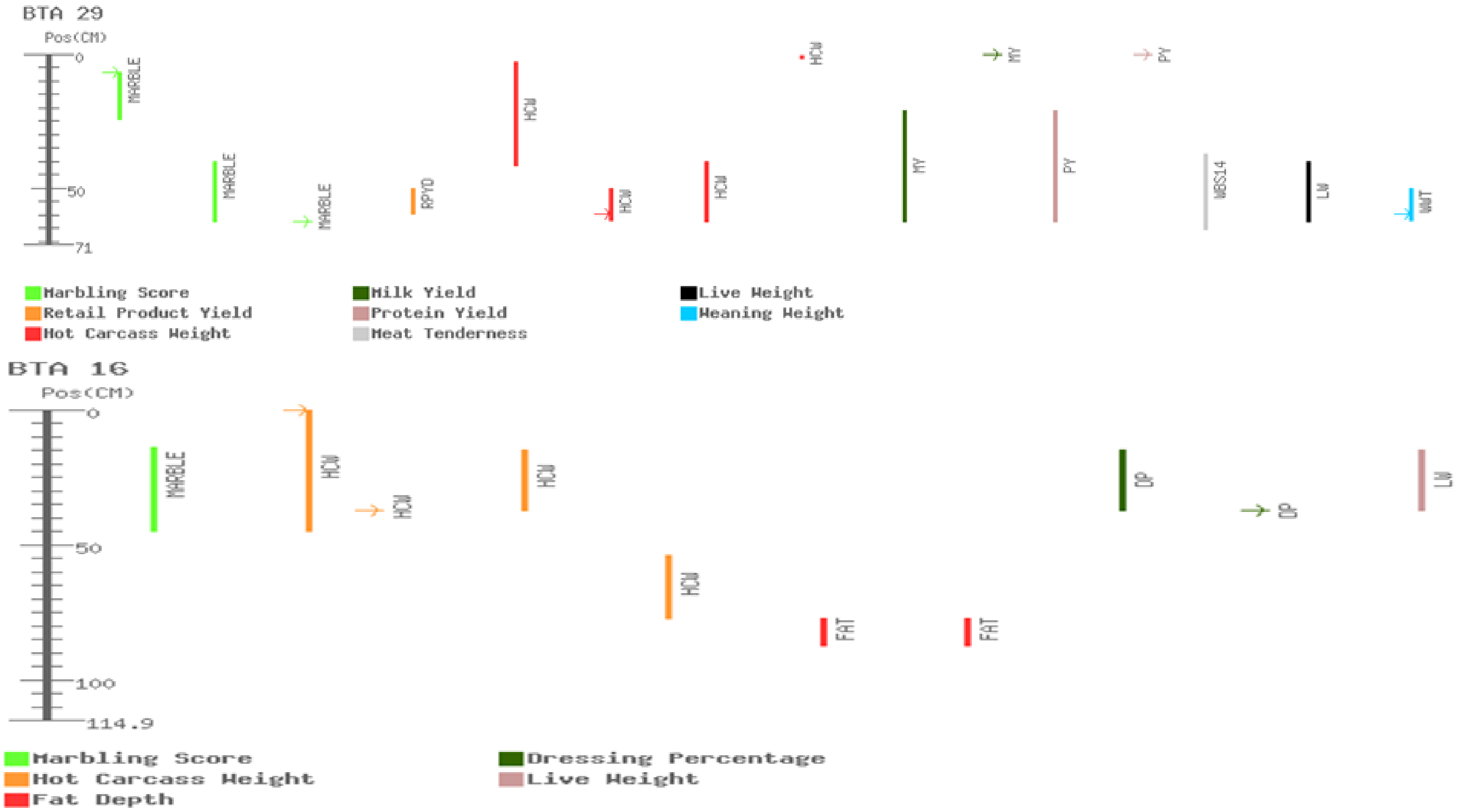


Figure 2.3 Cattle QTLs associated with BTA29 and BTA16. Figure generated using the Bovine QTL Database (http://bovineqtlv2.tamu.edu/index.html).

It is not guaranteed that a QTL in cattle will be a QTL in river buffalo but comparative studies are useful in illustrating differences that provide a starting point for investigators. Comparative studies that have identified a QTL in one species have been utilized to begin investigation in another: milk yield and composition QTL polymorphism comparisons of indicine cattle and riverine buffalo to taurine cattle (Tantia *et al.*, 2006), blood pressure QTLs in rat compared to the corresponding regions in human (Garrett *et al.*, 2001), and comparative mapping of porcine chromosome 7 for QTLs compared to multiple vertebrates (Demars *et al.*, 2006). The rearrangement suggested by the RH map presented here and observed in the WG RH map can be confirmed by sequencing the region, which would also serve to further elucidate the region for studies such as for polymorphisms and to identify other genes that may be in the region.

Chromosomal rearrangements, in this case an inversion, have the potential to separate a gene and the regulatory elements that are associated with it. This also serves to change gene order and introduce possible regulatory elements that have the potential to impact gene expression. In this case, possible QTLs in river buffalo have been rearranged, but other genes in that area that have not been identified yet could also be impacted.

The predicted inversion observed on the RH map generated in this study may be a reason for certain performance differences (discussed in Chapter I) between *Bos taurus* and *Bubalus bubalis*.

Because river buffalo are a major source of food and draught power in the world, and due to their close evolutionary relationship with cattle, mapping and comparing their genome to that of cattle provides important information for both species. The generated RH map shows two regions of possible rearrangements with corresponding cattle chromosomes. It is interesting that cattle QTL for two traits, milk protein and muscle fat, that are different from river buffalo are in regions marked by rearrangements. This region might impact QTL expression in river buffalo via a change in gene expression, the discovery of candidate genes, and/or due to sequence differences once candidate genes are revealed in comparison to *Bos taurus*. Other cattle QTL have been mapped to the two cattle chromosomes comprising BBU5, making it an important chromosome for future study in the river buffalo.

CHAPTER III

POLYMORPHISM AND HAPLOTYPE STRUCTURE IN RIVER BUFFALO (*BUBALUS BUBALIS*) TOLL-LIKE RECEPTOR 5 (TLR5) CODING SEQUENCE*

Introduction

The innate immune system of vertebrates evolved as the first line of host defense against pathogens, is evolutionarily conserved, and has the ability to prime acquired immunity (Akira *et al.*, 2001). The innate immune system, unlike its adaptive counterpart, does not learn from each invasion of pathogen. The recognition of broad categories of motifs enables the innate immune system to recognize a multitude of pathogens with no prior exposure necessary. In addition, pathogens cannot easily evade the innate immune system via mutation due to the fact that these broad motifs are basic to pathogens and such changes have the potential to negatively impact a pathogen's ability to invade, infect, and successfully colonize the host organism (Medzhitov, 2001; Andersen-Nissen *et al.*, 2005). Toll-like receptors (TLRs) are important components of the innate immune system. These receptors are homologous to the Toll family of receptors, which were first discovered in the fruit fly to provide host defense against fungal infection (Lemaitre *et al.*, 1996). Toll-like receptors are type I transmembrane proteins that recognize pathogen-associated molecular patterns (PAMPs) and are expressed differentially in cells involved in the innate immune system.

---

*Reprinted, in part, from *Animal Biotechnology.* Jones, B.C. & Womack, J.E. 2012. Polymorphism and haplotype structure in river buffalo (*Bubalus bubalis*) toll-like receptor 5 (TLR5) coding sequence. *Anim Biotechnol* 23(2):132-40. doi: 10.1080/10495398.2012.658466. Copyright 2012 by *Animal Biotechnology*.

Ten Toll-like receptors have been identified in most mammals. Toll-like receptors are predominately expressed in macrophages, neutrophils, and dendritic cells, but they are not exclusive to these cell types. TLRs are also differentially expressed across a variety of tissues (Zarember & Godowski, 2002; Vahanan *et al.*, 2008; Tirumurugaan *et al.*, 2010). Sequence variability in TLR genes has been explored extensively in cattle, with emphasis on finding genetic components of animal health and productivity (Seabury *et al.*, 2007; Fisher *et al.*, 2011).

In much of the world, however, water buffalo have more value and are produced with less expense than cattle. Water buffalo number approximately 194 million, with the majority located in Asian countries (FAO, 2012). They are able to utilize less digestible feeds better than cattle, are less susceptible to a variety of parasites and illnesses (often attributed to their wallowing behavior which coats them in a layer of mud), are better draught animals and have a higher percentage of total milk solids than cattle (Tripaldi *et al.*, 1997; FAO, 2000; Tripaldi *et al.*, 2003; Fagioli *et al.*, 2005; Michelizzi *et al.*, 2010). In this study, the sequence variability of TLR5 in river buffalo (*Bubalus bubalis bubalis)* was examined with the purpose of enhancing available genetic tools for the improvement of health and production in an animal of increasing worldwide economic importance.

This chapter will explore TLR5 single-nucleotide polymorphisms (SNPs), haplotypes, the theoretical impact of the SNPs detected, regulatory elements, and insertion/deletions in river buffalo (*Bubalus bubalis*). A comparative analysis of the protein domain architecture between river buffalo and other species and shared SNPs within the three domains (extracellular leucine-rich repeat, transmembrane, and intracellular Toll-like/Interleukin-1 receptor) of TLR5 will also be examined. Ancestral characters, ancient alleles and evolutionary concerns will be discussed in Chapter IV.

Materials and Methods

DNA Samples

The origins and identifications of the samples used in this study are shown in Table 3.1. The majority of the samples were from clinically normal river buffalo at Bufala di Vermont located in Woodstock, Vermont (http://www.bufaladivermont.com/).

Buffalo DNA was extracted from whole blood using standard methodology (Sambrook *et al.*, 1989; Sambrook & Russell, 2006). Fifty ml of whole blood was added to 10 ml of 4% sodium-EDTA anticoagulant. The sample was kept cool (but not frozen) until processing. Fifteen ml of the sample was collected into a 50 ml conical tube and 15 ml of 2X sucrose- Triton X-100 was added and left on ice for 20 min to lyse the red and white blood cells. The sample was then centrifuged at 500 x g for 20 min at 4˚C and the supernatant was decanted. The resultant pellet was gently resuspended in 10 ml of 2X sucrose-Triton X-100 and left on ice for 5 min. The sample was centrifuged at 500 x g for 20 min and the supernatant decanted. The pellet was gently resuspended in 5 ml 4% saline-EDTA (0.075M NaCl, 0.024M Na_2EDTA), 250 µl 20% sodium dodecyl sulfate (SDS), and 625 µl 20 mg/ml proteinase K and incubated overnight on a rotator at 8 rpm at 55°C. Five ml of phenol-chloroform-isoamyl alcohol (PCI) was then added; the test tubes were repeatedly inverted for at least 4 min and then centrifuged for 10 min at approximately 500 x g at room temperature. The supernatant (top layer aqueous phase) was removed and placed into a new 15 ml test tube. The supernatant was then extracted twice with chloroform-isoamyl alcohol (CI), with each cycle requiring at least 4 min of inverting the tube, centrifugation for 10 min at 500 x g, and the supernatant placed into a new 15 ml test tube. After the second CI extraction, 450 µl of 3M, pH 5.5 sodium acetate (NaOAc) and 14 ml of 95% ethanol (EtOH) were added and mixed by swirling the tube. The mixture was allowed to incubate at room temperature for 1 hr. The tubes were then centrifuged at 500 x g for 7-10 min and the alcohol removed by pouring it off or pipetting. Ten ml of ice cold 70% EtOH was added and the tube swirled to dislodge the DNA pellet. The tube was centrifuged at 500 x g for 7-10 min and the alcohol was removed (via pipetting and/or pouring off). The DNA pellet was removed to a clean 1.5 ml microtube, briefly centrifuged in a table top microcentrifuge; and, if any alcohol remained, it was removed. The DNA was dried completely and 0.3 ml – 1 ml of 1X Tris-EDTA (TE, 0.01M Tris, 0.001M EDTA) was added. The DNA was incubated overnight in a 37°C water bath to allow it to resuspend. The tube containing the DNA was then rotated for 1 hr and then the concentration of DNA was determined using the NanoDrop ND 1000 spectrophotometer (ThermoScientific).

Bison DNA was graciously provided by the CVM DNA Technologies Laboratory at Texas A&M University (Halbert & Derr, 2008). The DNA concentration was determined as above.

Table 3.1
Study population for genetic variation in TLR5. Identification (ID) numbers, species, origin, and GenBank accession numbers for the TLR5 coding region are included.

Sample ID	Species	Common Name	Origin	Accession
684	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615215
729	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615216
736	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615217
737	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615218
739	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615219
748	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615220
755	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615221
765	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615222
772	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615223
ET562	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615224
ET567	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615225
ET604	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615226
ET611	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615227
ET613	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615228
ET616	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615229

Table 3.1 continued

Sample ID	Species	Common Name	Origin	Accession
ET629	*Bubabulus bubalis bubalis*	River Buffalo	Bufala di Vermont	JN615230
JEW41	*Bubabulus bubalis bubalis*	River Buffalo	American Water Buffalo Association	JN615231
JEW43	*Bubabulus bubalis bubalis*	River Buffalo	American Water Buffalo Association	JN615232
JEW42	*Bubabulus bubalis carabanesis*	Swamp Buffalo	American Water Buffalo Association	JN615235
SCNM-1-777	*Syncerus caffer nanus*	African Forest Buffalo	San Diego Zoo	JN615233
SCNM-2-875	*Syncerus caffer nanus*	African Forest Buffalo	San Diego Zoo	JN615234
BB08-1	*Bison bison*	American Bison	Yellowstone National Park	JN615236

Primers and Polymerase Chain Reaction (PCR) Amplification

Previously described cattle TLR5 primers (Seabury et al., 2007) (Table 3.2) were used to obtain the initial river buffalo and bison TLR5 gene sequences. Two series of species-specific primers were designed from the river buffalo (JN615231) and bison (JN615236) TLR5 sequences (BBU5_1 through BBU5_9 and BBI5_01 through BBU5_09 respectively; Table 3.2). Annealing temperatures of 58°C using Primer3 online (Rozen & Skaletsky, 2000; Rozen, 2009) were used to amplify and sequence the TLR5 gene of the two species. River buffalo TLR5 primers (BBU5_1 through BBU5_9; Table 3.2) were used to amplify swamp buffalo and African forest buffalo TLR5. River buffalo primers shown in Table 3.2 facilitated the sequencing of the entire length of the swamp and African forest buffalo TLR5 amplicons. Species-specific bison primers (BBI5_01 through BBI5_09, Table 3.2) were used to amplify and sequence TLR5 in bison.

Table 3.2

Primers used for PCR amplification and sequencing. River buffalo, bison, and cattle primers for TLR5 are shown. River buffalo primers were used to generate sequence data for swamp buffalo and African forest buffalo.

	Forward (5’ to 3’)	Reverse (5’ to 3’)
River Buffalo TLR5[*]		
BBU5_1 (715bp)[‡]	CGGAGGATAAGACTGGAAATG	TGAAGAGGCTTTGTTGTATTGG
BBU5_2 (749bp)[‡]	CCACTGGACCACTAGGGAAG	TCCATCCTCACTTCCTACACAG
BBU5_3 (707bp)[‡]	CAAATGCTCAACACAGACAGAC	AGAAGGTCAAGGCAGTCTCC
BBU5_4 (715bp)[‡]	GGACCCAGAGGAACACAGG	GGGTTTGAACTCCTGCTCAC
BBU5_5 (736bp)[‡]	CTGTGGTCTCTCCGATGC	CCCAATGTGATTCTTCTGC
BBU5_6 (745bp)[‡]	CCTCGCCTACAACAAGATAAAC	ATCAGGATCAGGAGAGAGGAG
BBU5_7 (718bp)[‡]	AATTTCCTTCCACCAGGAG	TCTTTCTGCTGCTCCACAC
BBU5_8 (716bp)[‡]	ACTTTGAATGGGTGCAGAATG	CACAGGAGACTTGGGTTCG
BBU5_9 (716bp)[‡]	AGTTTCCACTTATCGCAAGC	TGACCTGTACTGAGCAATGG
Bison TLR5[†]		
BBI5_01 (733bp)[§]	TGGAAGGTAAAACTGACTTGC	TGAAAACATCCCTGGTTCAG
BBI5_02 (740bp)[§]	GCCTGCTTTTGATACTTTGG	ACTGTCTGTCTGGGTTGAGC
BBI5_03 (703bp)[§]	CCCCAAGCACCCAGTATC	CTCGGCATTCATTCATAAGG
BBI5_04 (720bp)[§]	TGCCTTGGGAAAGGAATG	ATCTGACTTCCACCCAGGTC
BBI5_05 (759bp)[§]	ACAGTCACAACCGCATCC	CTGGAGTGTCTCAAAGATTCG
BBI5_06 (728bp)[§]	GGGTTCTTCATTTGGCTTC	AGAGGAGTTGGAGATGAGAAAG
BBI5_07 (705bp)[§]	AAAACCATGCCCCTTCAG	TGAAGCACAAATAGGCATCG
BBI5_08 (765bp)[§]	AAGTTTTCCCTTTTCATCTTGG	ATGACCGAGCAACTGAACAC
BBI5_09 (849bp)[§]	CCAGGATGTTGACTGGTTTC	ATCCCTGAGACTGGGTATGAC
Cattle TLR5[¶]		
TLR5_01 (642 bp)	TTTGGGAAACGGAGGATAAG	GCACCTTTGAGGCTGTGA
TLR5_02 (661 bp)	GCCTGCTTTTGATACTTTGG	AGGTGTCCGCTATGTTCTCA
TLR5_03 (563 bp)	TCCCTTACCTTCCAGCAGA	AAGTTGGGGAAAACATTAGG
TLR5_04 (541 bp)	GGCAGATTAGAGGGGAAAGA	CCATCAAAGAAGCAGGAAGA
TLR5_05 (687 bp)	TCACTCTCCCTTCTTCTCCA	CAGACACTTGTTCCAGTCCA
TLR5_06 (700 bp)	CCTCCAAGGGAAAACACTCT	ATTGGCTGTAAGTGGGATGT
TLR5_07 (652 bp)	TTTTCTTCCAAGCATTCCTA	AGCCAGAGAGTTTGGGTACA
TLR5_08 (592 bp)	GAAACCAGCTCCTCTCTCCT	ATCTTTCTGCTGCTCCACAC
TLR5_09 (541 bp)	AGACTTTGAATGGGTGCAGA	TGGTAACTGGCGGAAATAAA
TLR5_10 (764 bp)	GGAGCAGTTTCCACTTATCG	ATTCTCATGCCGGTTTCTTT

[*] GenBank accession number of sequence used for primer design: JN615231. Used to sequence TLR5 coding region in river buffalo (*Bubalus bubalis bubalis*), swamp buffalo (*Bubalus bubalis carabenensis*), and African forest buffalo (*Syncerus caffer nanus*).

[†] GenBank accession number of sequence used for primer design: JN615236. Used to sequence TLR5 coding region in American bison (*Bison bison*).

[‡] Expected amplicon size based on JN615236 (JEW41)

[§] Expected amplicon size based on JN615236 (BB08-1)

[¶] Seabury *et al.* 2007

Each 25 µl PCR contained the following: 50-100 ng DNA, 0.2 mM each dNTP, 0.4 µM forward and reverse primer, 1.5 mM $MgCl_2$, 1X Gene Amp PCR Gold Buffer (Applied Biosystems, Foster City, Ca, USA), 0.2X MasterAmp PCR Enhancer (Epicentre, Madison, WI, USA), 1.66 units of AmpliTaq Gold DNA polymerase (Applied Biosystems), and enough DNAse/RNAse-free distilled water (Invitrogen, Grand Island, NY, USA) to reach the correct reaction volume. PCR amplicons were generated via the following step-down thermocycling program on the ABI GeneAmp PCR 9700 (Applied Biosystems): initial denaturation of 5 min at 95ºC; 30 s at 95ºC, 20 s ranging from 58ºC to 62ºC, and extension of 1 min at 72ºC for 5 cycles; then 30 s at 95ºC, 20 s ranging from 57ºC to 60ºC, and extension of 1 min at 72ºC for 45 cycles; with a final extension of 10 min at 72ºC, and a hold at 4ºC. PCR amplicons were then visualized by agarose gel electrophoresis. The PCR product was then purified using the QIAquick PCR Purification Kit (Qiagen, Inc., Valencia, CA, USA) according to manufacturer provided instructions. The DNA concentration was determined as described above.

Sequencing

The procedure for direct sequencing of all PCR products for river buffalo, swamp buffalo, African Forest buffalo, and bison was followed (Seabury *et al.*, 2007). After amplicons were amplified, visualized, and the PCR product was purified, a sequencing reaction protocol was followed. The sequencing reaction contained the following: 1-3 µl PCR product was used, depending on the concentration, to yield 6 ng/µl per 100 bp; 2.0 µl each of Big Dye (Applied Biosystems) and halfBig Dye (Genetix USA, Inc., Boston, MA, USA); 1.0 µl of forward or reverse primer (10 µM); 0.5X MasterAmp PCR Enhancer (Epicentre, Madison, WI, USA); and distilled water (Invitrogen, Grand Island, NY, USA) to a final total reaction volume of 10 µl. Thermocycling parameters were as follows: 5 min at 95ºC; 30 s at 95ºC, 20 s at 50ºC, and 4 min at 60ºC for 50 cycles; final extension of 5 min at 60ºC and hold at 4ºC.

The reaction product was then purified using G-50 Sephadex columns (Biomax, Odenton, MD, USA) as follows: The Sephadex columns were centrifuged using a table top microcentrifuge at 1000 x g for 4 min. To each sequencing reaction, 15 µl of distilled water (Invitrogen, Grand Island, NY, USA) was added, the 25 µl mixture was applied to the Sephadex columns, and centrifuged at 1000 x g for 3 min. Sequencing was performed by the DNA Technologies Core Laboratory at Texas A&M University using the ABI 3130 automated sequencer (Applied Biosystems). After the series of TLR5 amplicons was sequenced, Sequencher 5.0 (Gene Codes Corp., Ann Arbor, MI, USA) was used to assemble one contiguous (contig) strand for each isolate. Each single-nucleotide polymorphism (SNP) on the assembled contig was visually flagged. DNA was sequenced bi-directionally twice. Another round of PCR and sequencing was performed if the sequence data was ambiguous or of poor quality.

The cattle and goat TLR5 sequences were retrieved from GenBank and have the accession numbers EU006639 and FJ659852, respectively.

Cloning

Three river buffalo samples (ET567, ET616, and ET748) were cloned to independently verify the presence of heterozygous haplotypes. Primers BBU5_4F and BBU5_9R (Table 3.2) were used to amplify the coding region of TLR5. MasterAmp™ Extra-Long PCR kit is a high-fidelity PCR amplification kit that can sequence up to approximately 40 kb (Epicentre, Madison, WI, USA). Reactions were conducted according to maunfacturer's instructions. The kit includes 9 pre-mixes that contain dNTPs, buffer, and varying concentrations of $MgCl_2$. The primer was tested across all pre-mixes to determine the optimal salt ($MgCl_2$) concentration, and pre-mix 2 was selected. Amplification conditions were the same as described in the above section. The purified PCR product was mixed together with pCR-XLTOPO® vector and then transformed into One Shot® TOP10 *E.coli* chemically competent cells using the TOPO XL PCR Cloning Kit, which is a 5 min cloning of long PCR products (3-10 kb), according to manufacturer's instructions (Invitrogen, Grand Island, NY, USA).

After cloning, the resultant product was plated onto medium containing the antibiotic kanamycin (50 µg/ml). The colonies were allowed to grow overnight in a 37˚C incubator. The following morning, 10 colonies were picked and labeled and a PCR was performed using the same parameters and electrophoresed as described in the above section. This is to confirm that the colony contained the inserted the target sequence. Based on the results of the PCR, the corresponding colony was picked and grown in 5 ml of Luria broth medium with kanamycin for 12-16 hours while vigorously shaking on a shaking incubator at 37˚C.

The culture was processed to extract plasmid DNA using QIAprep Spin Miniprep Kit, which purifies up to 20 µg of molecular biology grade plasmid DNA, according to manufacturer's instructions (Qiagen, Inc., Valencia, CA, USA).

The resultant DNA was sequenced and analyzed as described in preceding sections.

Statistical Analysis

Fisher's Two-tailed Exact test was performed to compare the ratio of synonymous single-nucleotide polymorphisms (sSNPs) to non-synonymous single-nucleotide polymorphisms (nsSNPs) within the coding region using GraphPad Software, where $p<0.05$ was accepted as statistically significant (GraphPad Software, 2002).

Simple Modular Architecture Research Tool Analysis

A comparative analysis of protein domain structure of TLR5 of various bovids was performed utilizing the Simple Modular Architecture Research Tool (SMART) (Letunic *et al.*, 2009). Analyses used the normal mode and with the following parameters for SMART to find: PFAM (protein family) domains, signal peptides, and internal repeats.

Polymorphism Phenotyping Analysis

PolyPhen-2 (Polymorphism Phenotyping v2) software predicts the possible impact on the structure and functionality of a protein due to amino acid substitutions (Adzhubei *et al.*, 2010; European Molecular Biology Laboratory, 2011). The default settings were utilized to analyze the TLR5 sequences obtained in this study. The program makes a determination on the impact of phenotype and makes no comment on the genotype, i.e. there is no comment on whether the substitution is conservative, radical, or neutral and only comments if the predicted change, based on a human database, is benign, possibly damaging, or damaging.

PHASE v2.1.1

PHASE v2.1.1 was used to predict haplotypes for the nsSNPs (n=6) within the coding region of TLR 5 for this population of river buffalo (n=18) with the –X10 option (Stephens *et al.*, 2001; Stephens & Scheet, 2005; Adzhubei *et al.*, 2010; European Molecular Biology Laboratory, 2011). The input consisted of unphased diploid data. The best pairs for each sample were determined as well as frequencies of each determined haplotype within the population.

Regulatory Elements Prediction and Indel Scanning

Three non-long terminal repeats (LTR) retrotransposons were found using the CENSOR web server, which aligns sequences against a reference collection of repeats. Known repeats identified by CENSOR are classified and given in a report (Jurka *et al.*, 1996). CpGProD (CpG Island Promoter Detection) (Ponger & Mouchiroud, 2002) and PROSCAN (Prestridge, 1995) did not find any CpG islands or promoters, respectively.

The TLR5 sequences in river buffalo (*Bubalus bubalis*, JN615215) were manually scanned for insertions and deletions (indels).

Results and Discussion

Single Nucleotide Polymorphisms (SNPs) Detected

In this study, DNA sequence from 1760 bp upstream of the start codon to 711 bp downstream of the stop codon was generated for TLR5 (Figure 3.1). GenBank accession numbers for the coding regions of TLR5 obtained in this study are shown in Table 3.1. Analysis of all sequenced river buffalo TLR5 regions in this study yielded 16 novel SNPs, with 10 being transitions and 6 being transversions (Table 3.3). Of those observed SNPs, 6 were identified as non-synonymous, with 2 being transitions and 4 transversions. Overall, approximately 59% SNPs were identified as transitions (Table 3.3). The 2 SNPs located at genomic positions 947 and 948 were the second and third nucleotide of the same codon (Table 3.3). Fisher's Two-tailed Exact test revealed a mutational bias between transitions and transversions towards transitions within nsSNPs and sSNPs (p=0.0345).

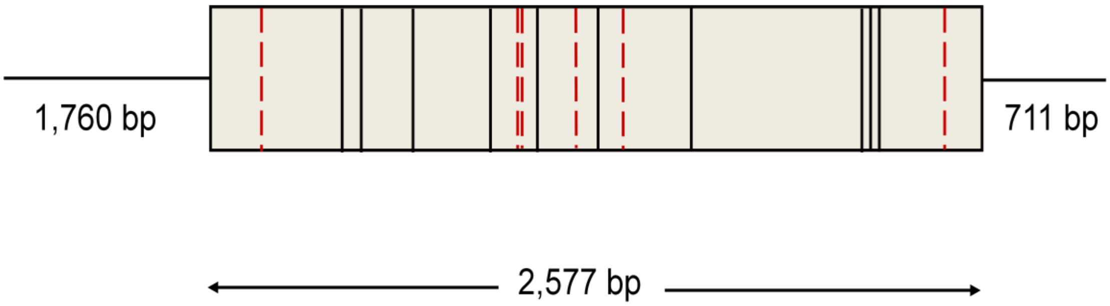


Figure 3.1 River buffalo TLR5 gene diagram. Dashed lines indicate non-synonymous single-nucleotide polymorphisms. Solid lines indicate synonymous single-nucleotide polymorphisms.

Table 3.3
Single-nucleotide polymorphisms. SNPs located in river buffalo TLR5 coding region. Allele, predicted SNP genomic position, predicted amino acid substitution, and SNP frequency are listed.

Alleles[*]	Genomic Position[†]	Predicted Amino Acid[‡]	Allele Frequency (%)
C/G (S)	**140**	**Thr/Ser**	**86.0 / 14.0**
C/T (Y)	396	Ser/Ser	94.0 / 6.0
A/G (R)	474	Gln/Gln	81.0 / 19.0
C/T (Y)	681	Val/Val	97.0 / 3.0
C/T (Y)	907	Leu/Leu	81.0 / 19.0
A/T (W)	**947**	**Glu/Val**	**81.0 / 19.0**
A/C (M)	**948**	**Glu/Asp**	**81.0 / 19.0**
T/C (W/M)	**947/948**	**Glu/Val**	**-**
G/A (R)	984	Ser/Ser	81.0 / 19.0
A/C (M)	**1133**	**Lys/Thr**	**86.0 / 14.0**
A/G (R)	1158	Leu/Leu	78.0 / 22.0
A/G (R)	**1286**	**Gln/Arg**	**89.0 / 11.0**
G/T (K)	1500	Gly/Gly	78.0 / 22.0
C/T (Y)	1944	Val/Val	78.0 / 22.0
G/A (R)	1977	Thr/Thr	86.0 / 14.0
G/A (R)	1992	Arg/Arg	86.0 / 14.0
C/G (S)	**2571**	**Ile/Met**	**83.0 / 17.0**

[*] Alleles in bold type indicate non-synonymous single-nucleotide polymorphisms
[†] Begins at the start codon of the exon. Accession # JN615231 (river buffalo JEW41)
[‡] Amino acid/Amino acid substitution

This is the first study to examine SNPs within the coding region of buffalo TLR5. The presence of nsSNPs and the fact that the animals used in this study from Bufala di Vermont were clinically normal suggests that there may be some flexibility within TLR5 despite the fact that it is a member of a gene family that is generally known to be well-conserved amongst species. This also implies that there is a measure of response to pathogens, i.e. organisms and pathogens adapt to each other. To the best of the author's knowledge, there haven't been studies that have linked specific TLR5 SNPs or haplotypes to an exacerbation or mitigation of a disease condition in river buffalo.

Haplotype Prediction

Twelve haplotypes were predicted for TLR5 in this population and four were observed in the initial PCR direct sequencing (Table 3.4). The most frequent haplotype within this population was CAAAAC. The majority of river buffalo (approximately 80%) had the potential to transmit the CAAAAC haplotype. The samples acquired from the American Water Buffalo Association, JEW43 and JEW41, exhibited different haplotypes. JEW43 showed the predominant haplotype, CAAAAC; while JEW41 had the potential to transmit the CAAAAC haplotype and also the GTCCGG haplotype, which was the second most common haplotype present in the population at approximately 13%. Putative heterozygotes were determined to be true heterozygotes as the alternative allele was found after cloning and sequencing those clones (Table 3.5).

Table 3.4

Haplotypes of river buffalo TLR5 estimated by PHASE v2.1.1.

Haplotype	Frequency
CAAAAC	0.796879
GTCCGG	0.13367
CTCAAC	0.025147
GTCAAG	0.019849
GTCAAC	0.006575
CTCAAG	0.003983
CAAAAG	0.003805
CTCCGG	0.002867
GAAAAG	0.00249
GAAAAC	0.00238
GTCCGC	0.0017
CTCCGC	0.000651

Table 3.5

River buffalo TLR5 sample clones. GenBank accession numbers and haplotypes are also shown.

Sample Identification	Accession Number	Haplotype
ET567A	JX456064	CAAAAC
ET567H	JX456065	GTCCGG
ET567I	JX456066	CAAAAC
ET567J	JX456067	CAAAAC
ET567X	JX456068	GTCCGG
ET616A	JX456069	CAAAAC
ET616B	JX456070	CTTAAC
ET616H	JX456071	CAAAAG
ET616I	JX456072	CAAAAC
ET616J	JX456073	CTCAAC
ET616X	JX456074	CTCAAG
748X	JX456075	GTCCAC
748K	JX456076	CTCAAC
748L	JX456077	CTCAAC
748M	JX456078	GTCCAG

It is necessary to broaden the scope of haplotype scanning in river buffalo. The study population was a transplanted herd that was recently established in Vermont and then relocated to Canada. Older herds that have developed and progressed in the tropical and sub-tropical environments they are best suited for would be more informative as the haplotype structure would reflect their environment. Specifically, the sample herd was created from individuals from Italian sources and through the American Water Buffalo Association. Therefore, it is reasonable to assume that the sample herd might possibly have achieved its own Hardy-Weinberg equilibrium that is not indicative of any other region where buffalo are adapted to the environments where they are bred for food, fiber or draught. Sub-tropical and tropical regions share many features; the environment in southern Iraq might encourage a different haplotype structure than the herd established in Italy or herds that are in Thailand or China. A study of TLR5 haplotypes in different herds from around the world could reveal allele or haplotype associations with different environments and classes of pathogens.

Polymorphism Phenotyping Analysis

The majority of amino acid substitutions observed was determined to be benign. Only one of the nsSNPs that were observed within the coding region of TLR5 in river buffalo was found to be possibly damaging, that being AA^{857} (Figure 3.2), which is located two positions upstream of the stop codon. The AA^{857} converted an isoleucine to a methionine. Both amino acids are non-polar and have hydrophobic side chains. This substitution could possibly be damaging due to its proximity to the Toll-like/ Interleukin-1 (TIR) domain, which interacts with the TIR domain of MyD88. However, the substitution might not be damaging because the SNP is not actually within the domain may not interrupt its functionality. While PolyPhen 2 has predicted that there may or may not be an impact on the functionality of the TLR5 gene in river buffalo due to a particular variation, it is still possible that the variation at that position does negatively impact health.

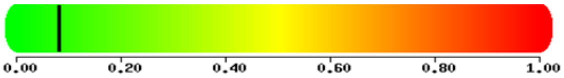
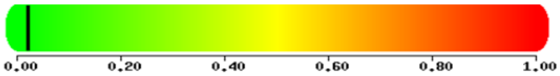
AA Position	AA Substitution	Results
47	Thr/Ser	This mutation is predicted to be **BENIGN** with a score of **0.081** (sensitivity: **0.92**; specificity: **0.81**) 
316	Glu/Val	This mutation is predicted to be **BENIGN** with a score of **0.000** (sensitivity: **1.00**; specificity: **0.00**) 
316	Glu/Asp	This mutation is predicted to be **BENIGN** with a score of **0.000** (sensitivity: **1.00**; specificity: **0.00**) 
378	Lys/Thr	This mutation is predicted to be **BENIGN** with a score of **0.046** (sensitivity: **0.94**; specificity: **0.79**) 
429	Gln/Arg	This mutation is predicted to be **BENIGN** with a score of **0.021** (sensitivity: **0.95**; specificity: **0.76**) 
857	Ile/Met	This mutation is predicted to be **POSSIBLY DAMAGING** with a score of **0.208** (sensitivity: **0.90**; specificity: **0.83**) 

Figure 3.2 PolyPhen-2 analysis of amino acid substitution effects. River buffalo TLR5 coding region was analyzed.

As discussed in Chapter I, there are studies that have linked SNPs (such as a premature stop codon in certain humans that confers resistance to lupus (Hawn *et al.*, 2005)) and expression levels of TLR5 production (regulation of TLR5 during various phases of bacterial growth (West *et al.*, 2009)), but not in water buffalo. While those studies can be informative, comparable studies in domesticated or wild ruminants have not been performed so direct conclusions cannot be inferred. Comparisons between the two species or multiple species or populations of river buffalo should be made to put the results into context. Cross species comparisons are important in an evolutionary sense, but they are also a way to indirectly measure the impact of environment on both the host organism and the pathogen.

Pathogens and their preferred host adapt to each other, but the environmental conditions can also serve to impact how they adapt together. For instance, a multi-year drought causes the host organism population to migrate and not return to its place of origin, but leaves a population behind that establishes a new equilibrium with the pathogen. Or, alternatively, the host organism still migrates but carries the pathogen with it and the new environment proves to be even better for the pathogen and/or the host organism than the environment of origin. In both scenarios, a new equilibrium must be established so the environment plays a role in how the two establish that equilibrium over time; but while that is happening, new alleles or haplotypes become more or less prevalent.

A basic violation of Hardy-Weinberg equilibrium would lead to different evolutionary hallmarks of both the host organism and pathogen due to environment as much as to basic evasion and adaptation tactics of the host and pathogen.

This makes case studies important. By case study, I mean to specifically use pedigrees and backcrossing to track the haplotypes or SNPs described here and possibly link them to susceptibility or resistance disease conditions, which should be made across river buffalo populations.

Comparative Analysis of Protein Domain Architecture

Leucine-rich repeats (LRRs) vary in length and the number of repeats (2-45). Three regions of leucine-rich repeats (Fig. 3.3) were observed in TLR5. River buffalo (*Bubalus bubalis bubalis*), swamp buffalo (*Bubalus bubalis carabanesis),* and African forest buffalo (*Syncerus caffer nanus)* all exhibited the same LRR patterns across all three regions of LRRs.

American bison (*Bison bison*) and cattle (*Bos taurus indicus*) also exhibited the same LRR patterns across all three LRR regions (Fig. 3.3), but shared an additional LRR next to the third LRR region. Goat (*Capra hircus*) was utilized as the outgroup and shared the same LRR patterning with the addition of an extra LRR region that was further upstream than the extra LRR region shared by American bison and cattle. Species that appear to be undergoing positive selection in the LRR region of TLR5 relative to river buffalo (pig, dog, chicken, ring-necked pheasant, human, and Philippine tarsier) have similar LRR regions, but there are variations within that group that depend on their divergence time from each other.

It is the same for species that appear to be undergoing neutral selection (chamois, white-tailed deer, goat, and greater kudu) and negative selection (African forest buffalo, cattle, and American bison). African-clawed frog was not analyzed for selective forces because its sequence was too divergent from river buffalo. Evolution and selective pressure are discussed in more depth in Chapter IV.

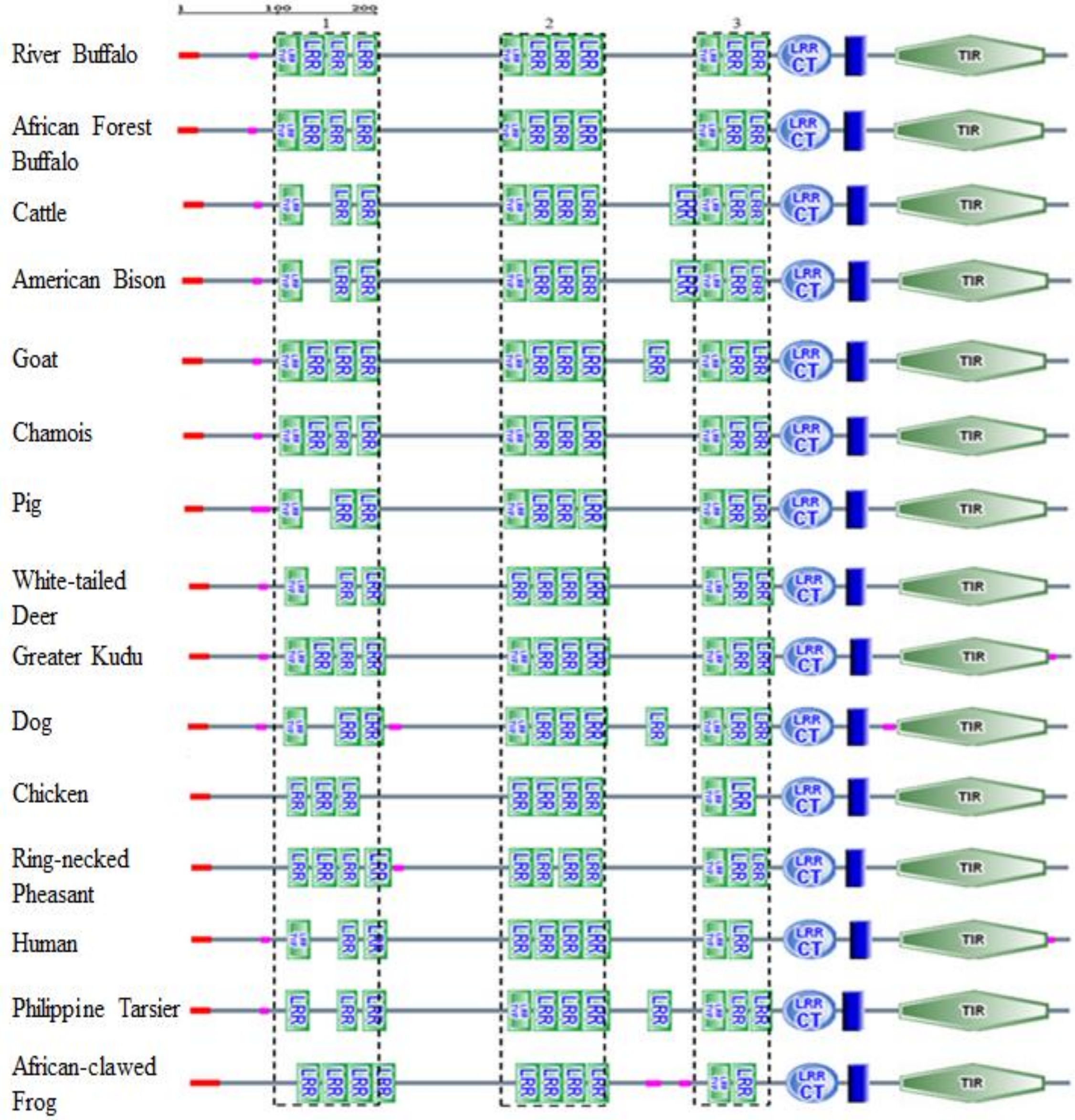


Figure 3.3 Comparative SMART analysis. The figure was generated using SMART. TLR5 predicted amino acid sequences for river buffalo (*Bubalus bubalis bubalis*; JN615218), African forest buffalo (*Syncerus caffer nanus*, JN615234), cattle (*Bos taurus taurus*, JQ805125), American bison (*Bison bison*, JN615236), goat (*Capra hircus*, HQ188378), chamois (*Rupicapra rupicapra*, JQ811845), pig (Sus *scrofa*, AB208697.2), white-tailed deer (*Odocoileus virginianus*, JQ811843), greater kudu (*Tragelaphus strepsiceros*, JQ811848), dog (*Canis lupus familiaris*, NM_001197176), chicken (*Gallus gallus*, HQ896214), ring-necked pheasant (*Phasianus colchicus*, JF767220), human (*Homo sapiens*, NM_003268), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1), African clawed frog (*Xenopus laevis,* NM_001094980). Predicted domains and proteins are as follows: signal peptides are represented by the longer, horizontal boxes at the beginning on the right, segments of low complexity are represented by small, horizontal boxes immediately following the signal peptide; conserved leucine-rich repeats (LRRs) are enclosed by dashed boxes; transmembrane segments are vertical lines; and the Toll - interleukin 1 – resistance is represented by TIR.

In addition to analyzing the protein domain structure and comparing it across multiple species, SNPs in these domains were analyzed across the coding region of TLR5 to determine which clades share SNP positions. River buffalo (*B. b. bubalis*) was used as the reference; therefore, the domain boundaries, as determined by SMART, for river buffalo were the reference to which all other species were compared (Table 3.6). From the tables (3.7-3.21), it can be seen that Clade 1 and 2 share a substantial number of SNP positions in all domains. The TIR domain had the largest number of clades that shared common SNP positions. Clade 1 shares the most SNP positions with all other clades. It is possible that the common ancestor between Clade 1 and other clades passed on those SNPs. LRRs vary and seem to have some flexibility; however, only 5 river buffalo SNPs were found to be non-synonymous, which still suggests a level of constraint that makes this family less likely to undergo rapid evolutionary changes. Primates (Clade 1) and avians (Clade 2) appear to be undergoing positive selection. Since these clades are undergoing various forms of selective pressure, it can be inferred that these pressures have encouraged changes in the LRR domain and thus these SNPs reflect those changes.

Table 3.6
River buffalo (*Bubalus bubalis*) TLR5 domain boundaries. Boundaries determined by SMART.

	Domain	Residue Range	Amino Acid Range
1st Region	LRR TYP	94-117	280-351
	LRR	118-143	352-429
	LRR	144-163	430-489
	LRR	169-192	505-576
2nd Region	LRR TYP	311-334	931-1002
	LRR	335-358	1003-1074
	LRR	359-382	1075-1146
	LRR	383-411	1147-1233
3rd Region	LRR	501-524	1501-1572
	LRR	525-548	1573-1644
	LRR	549-570	1645-1710
	C-Terminal LRR	579-630	1735-1890
	Transmembrane	644-666	1930-1998
	Toll-like/ Interleukin-1 Receptor	692-837	2074-2511

Table 3.7

Common divergent sites across all clades summation. LRR domain with river buffalo *(Bubalus bubalis)* used as the reference to determine domain boundaries.

	Clade 1*	Clade 2*	Clade 3*	Clade 4*	Clade 5*	Clade 6*	Clade 7*	Clade 8*	Clade 9*
Clade 1*	■	155	16	6	1	8	17	16	4
Clade 2*	155	■	12	4	1	5	12	10	7
Clade 3*	16	12	■	0	0	2	6	8	4
Clade 4*	6	4	0	■	0	1	0	2	0
Clade 5*	1	1	0	0	■	0	0	0	0
Clade 6*	8	5	2	1	0	■	1	2	0
Clade 7*	17	12	6	0	0	1	■	6	1
Clade 8*	16	10	8	2	0	2	6	■	0
Clade 9*	4	7	4	0	0	0	1	0	■

*Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726); **Clade 3**- banteng (*Bos javanicus*, JQ811841), domestic yak (*Bos grunniens*, JQ811841), American bison (*Bison bison*, JN615236), cattle (*Bos taurus taurus*: JQ805125, JQ805128, JQ805129, JQ805134, JQ805135, JQ805136, JQ805137; *Bos taurus indicus*: EU006636, EU006641); **Clade 4**- swamp buffalo (*Bubalus bubalis carabanesis*, JN615235), river buffalo (*Bubalus bubalis bubalis*; JN615218, JN615220, JN615224, JN615225, JN615229); **Clade 5**- African forest buffalo (*Syncerus caffer nanus*, JN615234 and JN615233); **Clade 6**- lesser kudu (*Tragelaphus imberbis*, JQ811849), greater kudu (*Tragelaphus strepsiceros*, JQ811848); **Clade 7**- goat (*Capra hircus*, HQ188378), sheep (*Ovis aries*, NM_001135926), chamois (*Rupicapra rupicapra*, JQ811845); **Clade 8**- Gemsbok oryx (*Oryx gazelle*, JQ811846), scimitar-horned oryx (*Oryx dammah*, JQ811850), Arabian oryx (*Oryx leucoryx*, JQ811847); **Clade 9**- mule deer (*Odocoileus hemionus*, JQ811842), white-tailed deer (*Odocoileus virginianus*, JQ811843).

Table 3.8

Common divergent sites across multiple clades, residues 94-117. LRR TYP domain with river buffalo *(Bubalus bubalis)* used as the reference to determine domain boundaries.

	Clade 1*	Clade 2*	Clade 3*
Clade 1*	■	5	1
Clade 2*	5	■	0
Clade 3*	1	0	■

*Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726); **Clade 3**- banteng (*Bos javanicus*, JQ811841), domestic yak (*Bos grunniens*, JQ811841), American bison (*Bison bison*, JN615236), cattle (*Bos taurus taurus*: JQ805125, JQ805128, JQ805129, JQ805134, JQ805135, JQ805136, JQ805137; *Bos taurus indicus*: EU006636, EU006641).

Table 3.9

Common divergent sites across multiple clades, residues 118-143. LRR domain with river buffalo *(Bubalus bubalis)* used as the reference to determine domain boundaries.

	Clade 1*	Clade 2*	Clade 3*	Clade 4*	Clade 8*
Clade 1*	■	4	1	1	1
Clade 2*	4	■	0	1	1
Clade 3*	1	0	■	0	0
Clade 4*	1	1	0	■	1
Clade 8*	1	1	0	1	■

*Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726); **Clade 3**- banteng (*Bos javanicus*, JQ811841), domestic yak (*Bos grunniens*, JQ811841), American bison (*Bison bison*, JN615236), cattle (*Bos taurus taurus*: JQ805125, JQ805128, JQ805129, JQ805134, JQ805135, JQ805136, JQ805137; *Bos taurus indicus*: EU006636, EU006641); **Clade 4**- swamp buffalo (*Bubalus bubalis carabanesis*, JN615235), river buffalo (*Bubalus bubalis bubalis*; JN615218, JN615220, JN615224, JN615225, JN615229); **Clade 8**- Gemsbok oryx (*Oryx gazelle*, JQ811846), scimitar-horned oryx (*Oryx dammah*, JQ811850), Arabian oryx (*Oryx leucoryx*, JQ811847).

Table 3.10

Common divergent sites across multiple clades, residues 144-163. LRR domain with river buffalo *(Bubalus bubalis)* used as the reference to determine domain boundaries.

	Clade 1*	Clade 2*	Clade 3*	Clade 4*
Clade 1*	■	2	0	1
Clade 2*	2	■	1	0
Clade 3*	0	1	■	0
Clade 4*	1	0	0	■

*Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726); **Clade 3**- banteng (*Bos javanicus*, JQ811841), domestic yak (*Bos grunniens*, JQ811841), American bison (*Bison bison*, JN615236), cattle (*Bos taurus taurus*: JQ805125, JQ805128, JQ805129, JQ805134, JQ805135, JQ805136, JQ805137; *Bos taurus indicus*: EU006636, EU006641); **Clade 4**- swamp buffalo (*Bubalus bubalis carabanesis*, JN615235), river buffalo (*Bubalus bubalis bubalis*; JN615218, JN615220, JN615224, JN615225, JN615229).

Table 3.11

Common divergent sites across multiple clades, residues 169-192. LRR domain with river buffalo *(Bubalus bubalis)* used as the reference to determine domain boundaries.

	Clade 1*	Clade 2*	Clade 3*
Clade 1*	■	5	1
Clade 2*	5	■	0
Clade 3*	1	0	■

*Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726); **Clade 3**- banteng (*Bos javanicus*, JQ811841), domestic yak (*Bos grunniens*, JQ811841), American bison (*Bison bison*, JN615236), cattle (*Bos taurus taurus*: JQ805125, JQ805128, JQ805129, JQ805134, JQ805135, JQ805136, JQ805137; *Bos taurus indicus*: EU006636, EU006641).

Table 3.12

Common divergent sites across multiple clades, residues 311-334. LRR TYP domain with river buffalo *(Bubalus bubalis)* used as the reference to determine domain boundaries.

	Clade 1*	Clade 2*	Clade 4*	Clade 6*	Clade 8*
Clade 1*	■	4	1	1	1
Clade 2*	4	■	2	0	1
Clade 4*	1	2	■	1	0
Clade 6*	1	0	1	■	0
Clade 8*	1	1	0	0	■

*Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726); **Clade 4**- swamp buffalo (*Bubalus bubalis carabanesis*, JN615235), river buffalo (*Bubalus bubalis bubalis*; JN615218, JN615220, JN615224, JN615225, JN615229); **6**- lesser kudu (*Tragelaphus imberbis*, JQ811849), greater kudu (*Tragelaphus strepsiceros*, JQ811848); **Clade 8**- Gemsbok oryx (*Oryx gazelle*, JQ811846), scimitar-horned oryx (*Oryx dammah*, JQ811850), Arabian oryx (*Oryx leucoryx*, JQ811847).

Table 3.13

Common divergent sites across multiple clades, residues 359-382. LRR domain with river buffalo *(Bubalus bubalis)* used as the reference to determine domain boundaries.

	Clade 1*	Clade 2*	Clade 3*	Clade 9*
Clade 1*	■	3	0	0
Clade 2*	3	■	1	0
Clade 3*	0	1	■	1
Clade 9*	0	0	1	■

*Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726); **Clade 3**- banteng (*Bos javanicus*, JQ811841), domestic yak (*Bos grunniens*, JQ811841), American bison (*Bison bison*, JN615236), cattle (*Bos taurus taurus*: JQ805125, JQ805128, JQ805129, JQ805134, JQ805135, JQ805136, JQ805137; *Bos taurus indicus*: EU006636, EU006641); **Clade 9**- mule deer (*Odocoileus hemionus*, JQ811842), white-tailed deer (*Odocoileus virginianus*, JQ811843).

Table 3.14

Common divergent sites across multiple clades, residues 383-411. LRR domain with river buffalo *(Bubalus bubalis)* used as the reference to determine domain boundaries.

	Clade 1*	Clade 2*	Clade 6*	Clade 7*
Clade 1*	■	1	1	1
Clade 2*	1	■	0	0
Clade 6*	1	0	■	0
Clade 7*	1	0	0	■

*Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726; **Clade 6**- lesser kudu (*Tragelaphus imberbis*, JQ811849), greater kudu (*Tragelaphus strepsiceros*, JQ811848); **Clade 7**- goat (*Capra hircus*, HQ188378), sheep (*Ovis aries*, NM_001135926), chamois (*Rupicapra rupicapra*, JQ811845).

Table 3.15

Common divergent sites across multiple clades, residues 501-524. LRR domain with river buffalo *(Bubalus bubalis)* used as the reference to determine domain boundaries.

	Clade 1*	Clade 2*	Clade 3*	Clade 4*	Clade 6*	Clade 7*
Clade 1*	■	5	1	0	1	1
Clade 2*	5	■	1	1	0	0
Clade 3*	1	1	■	0	0	0
Clade 4*	0	1	0	■	0	0
Clade 6*	1	0	0	0	■	0
Clade 7*	1	0	0	0	0	■

*Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726); **Clade 3**- banteng (*Bos javanicus*, JQ811841), domestic yak (*Bos grunniens*, JQ811841), American bison (*Bison bison*, JN615236), cattle (*Bos taurus taurus*: JQ805125, JQ805128, JQ805129, JQ805134, JQ805135, JQ805136, JQ805137; *Bos taurus indicus*: EU006636, EU006641); **Clade 4**- swamp buffalo (*Bubalus bubalis carabanesis*, JN615235), river buffalo (*Bubalus bubalis bubalis*; JN615218, JN615220, JN615224, JN615225, JN615229); **Clade 6**- lesser kudu (*Tragelaphus imberbis*, JQ811849), greater kudu (*Tragelaphus strepsiceros*, JQ811848); **Clade 7**- goat (*Capra hircus*, HQ188378), sheep (*Ovis aries*, NM_001135926), chamois (*Rupicapra rupicapra*, JQ811845).

Table 3.16

Common divergent sites across multiple clades, residues 549-570. LRR domain with river buffalo *(Bubalus bubalis)* used as the reference to determine domain boundaries.

	Clade 1[*]	Clade 2[*]	Clade 8[*]
Clade 1[*]	■	2	1
Clade 2[*]	2	■	0
Clade 8[*]	1	0	■

[*] Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726); **Clade 8**- Gemsbok oryx (*Oryx gazelle*, JQ811846), scimitar-horned oryx (*Oryx dammah*, JQ811850), Arabian oryx (*Oryx leucoryx*, JQ811847).

Table 3.17

Common divergent sites across multiple clades, residues 579-630. C-terminal LRR domain with river buffalo *(Bubalus bubalis)* used as the reference to determine domain boundaries.

	Clade 1[*]	Clade 2[*]	Clade 3[*]	Clade 6[*]	Clade 8[*]
Clade 1[*]	■	14	1	1	4
Clade 2[*]	14	■	1	1	2
Clade 3[*]	1	1	■	0	2
Clade 6[*]	1	1	0	■	0
Clade 8[*]	4	2	2	0	■

[*] Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726); **Clade 3**- banteng (*Bos javanicus*, JQ811841), domestic yak (*Bos grunniens*, JQ811841), American bison (*Bison bison*, JN615236), cattle (*Bos taurus taurus*: JQ805125, JQ805128, JQ805129, JQ805134, JQ805135, JQ805136, JQ805137; *Bos taurus indicus*: EU006636, EU006641); **Clade 6**- lesser kudu (*Tragelaphus imberbis*, JQ811849), greater kudu (*Tragelaphus strepsiceros*, JQ811848); **Clade 8**- Gemsbok oryx (*Oryx gazelle*, JQ811846), scimitar-horned oryx (*Oryx dammah*, JQ811850), Arabian oryx (*Oryx leucoryx*, JQ811847).

Table 3.18

Common divergent sites across multiple clades, residues 644-666. Transmembrane Domain with river buffalo *(Bubalus bubalis)* used as the reference to determine domain boundaries.

	Clade 1*	Clade 2*	Clade 3*	Clade 4*	Clade 7*	Clade 8*
Clade 1*		10	5	2	2	2
Clade 2*	10		3	0	2	1
Clade 3*	5	3		0	2	2
Clade 4*	2	0	0		0	1
Clade 7*	2	2	2	0		1
Clade 8*	2	1	2	1	1	

*Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726); **Clade 3**- banteng (*Bos javanicus*, JQ811841), domestic yak (*Bos grunniens*, JQ811841), American bison (*Bison bison*, JN615236), cattle (*Bos taurus taurus*: JQ805125, JQ805128, JQ805129, JQ805134, JQ805135, JQ805136, JQ805137; *Bos taurus indicus*: EU006636, EU006641); **Clade 4**- swamp buffalo (*Bubalus bubalis carabanesis*, JN615235), river buffalo (*Bubalus bubalis bubalis*; JN615218, JN615220, JN615224, JN615225, JN615229); **Clade 7**- goat (*Capra hircus*, HQ188378), sheep (*Ovis aries*, NM_001135926), chamois (*Rupicapra rupicapra*, JQ811845); **Clade 8**- Gemsbok oryx (*Oryx gazelle*, JQ811846), scimitar-horned oryx (*Oryx dammah*, JQ811850), Arabian oryx (*Oryx leucoryx*, JQ811847).

Table 3.19

Common divergent sites across multiple clades, residues 692-837. Toll-like/Interleukin-1 Receptor Domain with river buffalo *(Bubalus bubalis)* used as the reference to determine domain boundaries.

	Clade 1*	Clade 2*	Clade 3*	Clade 5*	Clade 6*	Clade 7*	Clade 8*	Clade 9*
Clade 1*		16	4	1	2	4	3	1
Clade 2*	16		2	1	1	1	1	0
Clade 3*	4	2		0	2	3	3	0
Clade 5*	1	1	0		0	0	0	0
Clade 6*	2	1	2	0		1	2	0
Clade 7*	4	1	3	0	1		1	0
Clade 8*	3	1	3	0	2	1		0
Clade 9*	1	0	0	0	0	0	0	

*Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726); **Clade 3**- banteng (*Bos javanicus*, JQ811841), domestic yak (*Bos grunniens*, JQ811841), American bison (*Bison bison*, JN615236), cattle (*Bos taurus taurus*: JQ805125, JQ805128, JQ805129, JQ805134, JQ805135, JQ805136, JQ805137; *Bos taurus indicus*: EU006636, EU006641); **Clade 4**- swamp buffalo (*Bubalus bubalis carabanesis*, JN615235), river buffalo (*Bubalus bubalis bubalis*; JN615218, JN615220, JN615224, JN615225, JN615229); **Clade 5**- African forest buffalo (*Syncerus caffer nanus*, JN615234 and JN615233); **Clade 6**- lesser kudu (*Tragelaphus imberbis*, JQ811849), greater kudu (*Tragelaphus strepsiceros*, JQ811848); **Clade 7**- goat (*Capra hircus*, HQ188378), sheep (*Ovis aries*, NM_001135926), chamois (*Rupicapra rupicapra*, JQ811845); **Clade 8**- Gemsbok oryx (*Oryx gazelle*, JQ811846), scimitar-horned oryx (*Oryx dammah*, JQ811850), Arabian oryx (*Oryx leucoryx*, JQ811847); **Clade 9**- mule deer (*Odocoileus hemionus*, JQ811842), white-tailed deer (*Odocoileus virginianus*, JQ811843).

Table 3.20

Common divergent sites across all clades and domains summation. River buffalo *(Bubalus bubalis)* is used as the reference to determine domain boundaries.

	Clade 1*	Clade 2*	Clade 3*	Clade 4*	Clade 5*	Clade 6*	Clade 7*	Clade 8*	Clade 9*
Clade 1*		80	14	5	1	6	8	12	1
Clade 2*	80		9	4	1	2	3	6	0
Clade 3*	14	9		0	0	2	5	7	1
Clade 4*	5	4	0		0	1	0	2	0
Clade 5*	1	1	0	0		0	0	0	0
Clade 6*	6	2	2	1	0		1	2	0
Clade 7*	8	3	5	0	0	1		2	0
Clade 8*	12	6	7	2	0	2	2		0
Clade 9*	1	0	1	0	0	0	0	0	

*Clade composition with scientific name and GenBank accession number in parenthesis: **Clade 1**-marmoset (*Callithrix jacchus*, ACFV01163303.1), sooty mangabey (*Cercocebus torquatus atys*, EU204938), crab-eating macaque (*Macaca fascicularis*, AB445650), Rhesus macaque (*Macaca mulatta*, NM_001130429.1), gorilla (*Gorilla gorilla*, AB445648), human (*Homo sapiens*, NM_003268), pygmy chimpanzee (*Pan paniscus*, AB445647), chimpanzee (*Pan troglodytes*, NM_001130462), Bornean orangutan (*Pongo pygmaeus*, AB445649), Philippine tarsier (*Tarsius syrichta*, ABRT010212218.1); **Clade 2**- chicken (*Gallus gallus*, HQ896214), Ceylon junglefowl (*Gallus lafayetii*, FJ915547), turkey (*Meleagris gallopavo*, HQ436463), ring-necked pheasant (*Phasianus colchicus*, JF767220), helmeted guineafowl (*Numida meleagris*, JF767221), zebra finch (*Taeniopygia guttata*, XM_002188726); **Clade 3**- banteng (*Bos javanicus*, JQ811841), domestic yak (*Bos grunniens*, JQ811841), American bison (*Bison bison*, JN615236), cattle (*Bos taurus taurus*: JQ805125, JQ805128, JQ805129, JQ805134, JQ805135, JQ805136, JQ805137; *Bos taurus indicus*: EU006636, EU006641); **Clade 4**- swamp buffalo (*Bubalus bubalis carabanesis*, JN615235), river buffalo (*Bubalus bubalis bubalis*; JN615218, JN615220, JN615224, JN615225, JN615229); **Clade 5**- African forest buffalo (*Syncerus caffer nanus*, JN615234 and JN615233); **Clade 6**- lesser kudu (*Tragelaphus imberbis*, JQ811849), greater kudu (*Tragelaphus strepsiceros*, JQ811848); **Clade 7**- goat (*Capra hircus*, HQ188378), sheep (*Ovis aries*, NM_001135926), chamois (*Rupicapra rupicapra*, JQ811845); **Clade 8**- Gemsbok oryx (*Oryx gazelle*, JQ811846), scimitar-horned oryx (*Oryx dammah*, JQ811850), Arabian oryx (*Oryx leucoryx*, JQ811847); **Clade 9**- mule deer (*Odocoileus hemionus*, JQ811842), white-tailed deer (*Odocoileus virginianus*, JQ811843).

Regulatory Elements and Indel Scanning

As previously discussed, 1760 bp upstream of the start codon and 711 bp downstream of stop codon which form the 5'- and 3'- untranslated regions (UTR) were sequenced (Figure 3.1). There are numerous insertion/deletions (indels) in comparison to cattle sequences throughout both the 5'- and 3'-UTRs (Figure 3.4). These indels, particularly in the 5'-UTR, would make it difficult for human- or cattle-based regulatory element databases to correctly align and find regulatory elements as candidate sequences might be disrupted by indels.

Interspersed elements are repetitive elements with the ability to move and copy themselves into other parts of the genome and comprise 40-50% of a mammalian genome (Adelson *et al.*, 2009). There are two classes of mobile elements: class I (retrotransposons) and class II (DNA transposons). Retrotransposons copy and paste themselves in the genome by transcribing their mRNA, which is then reverse transcribed and the resultant DNA is inserted into the new location. This results in an increased copy number of that element and can increase the size of a genome (Ray, 2007). Transposons cut themselves from their original location and paste into a new location (Grabundzija *et al.*, 2010). Despite the possible alignment issues stated above, CENSOR (Jurka *et al.*, 1996) was able to find two transposable elements, which are classed as non-long terminal repeat retrotransposon short-interspersed nuclear elements (SINEs) by CENSOR (Figure 3.5, Figure 3.6, Table 3.21). Artiodactyla was chosen as the DNA source and all defaults were maintained for CENSOR.

5’-UTR

```
Cattle          AACAGAGTAGACTTGGAAGGTAAAACTGAC-----TTGCTAACAT-GGGGGTGACATTTC 54
River Buffalo   AACAGAGTAGACTTGGGAGGTAAAACTGACATGACTTGCTAACATTGGGGGTGACATTTC 60
                **************** *************     ********** **************

Cattle          TTCAAATGTGAAACGGCAATGGTTGTTTTTCATCTGATGGTGTACACGAGT-TACCATGC 293
River Buffalo   TTCAAATGTGAAATGGCAATGGTTATTTTTCATCTCATGGTATACATGAGTATACCATGC 300
                ************* ********** ********** ***** **** **** ********

Cattle          CCCCCCCAACTCTTTTCTTTTAATTTAATG----TATTGATTTTTGGCTGCCTTGGATCT 349
River Buffalo   CCCCC--AACTCTTTTCTTTTAATTTAATGAATTTATTTATTTTTGGCTGCCTTGGATCT 358
                *****  ***********************    **** *********************

Cattle          TTGGGTCAACTCAGGAGTTGATGT-------------------------GTGTCACAGCC 564
River Buffalo   TTGGGTCAACTCAGGAGTTGATGTCTCCTTCTGATCAGCTGTAAATTGTGTGTCAGAGCC 598
                ************************                         ****** ****

Cattle          TTCTTTCTTTCTTTTTTTTTATTTTATTTTTAAACTTTACATAATTGTATTAGTTTTGCC 804
River Buffalo   TTCTTT------------------------------------------------------ 784
                ******

Cattle          AAATATCAAAATGAATCCGCCACAGGTATACACGTGCTCCCCATCCTGAACCCTCCTCCC 864
River Buffalo   -------------------------------------------------ACTCTCCCCC- 794
                                                                 ** **** **

Cattle          TCCTCCCTCCCCACACCATCCCTCTGGGTCGTCCCAGTGCACCAGCCCCAAGCACCCAGT 924
River Buffalo   ------------------TCACTCTG------CCC------------------------- 805
                                  ** *****      ***

Cattle          ATCGTGCATCGAACCTGGACTGGCATCTCGTTTCATACGTGATATTTTACATGTTTCTGA 984
River Buffalo   -------------------------------------------------------TCTGA 810
                                                                       *****

Cattle          TGAGGGGCCCGTGTGCACCCTCTGTACCCTCACAGCTCCCAGCACAGCACTGAGAACATA 1164
River Buffalo   T-AGGGGCCCTCGTGCACCCTCTGTACCCTCACAGCTCCYAGCACAGCACTGAGAACATA 989
                * ********  *************************** ********************

Cattle          -GCGGACACCTTCATTCGGCGCCTTTTGCCGCTCTGTACAAGCAAATGCTCAACCCAGAC 1223
River Buffalo   AGCGGACACCTTCATTCGGCGCCTTTTGCCGCYCTGTACAAGCAAATGCTCAACACAGAC 1049
                 ******************************* ********************* *****

Cattle          CACATGGTCACCACAAGTGCCAGGCATGCAGTTGGTGCTTAGTGCATCCTTATTAAACTG 1343
River Buffalo   CACATGGTCAC-ACAAGTGCCAGGCATGCTGTTGGTGCTTAGTGCATCCTTATTAAACTG 1168
                *********** ***************** ******************************

Cattle          GAATTCACAACCTTATGAATGAATGCTGAGTTATCACAAAGATTAAATAT----TTTCTG 1639
River Buffalo   GAATTCACAACCTTATGAATGAATGCTGAGTTATCACAAAGATTAAATAAAGTATTTCTG 1468
                *************************************************     ******

Cattle          ACACAGGGTCTAAGAAGCAACCACATCACAAAGGGGTCCCCCAGGCCCTAA-CACCCTCA 1818
River Buffalo   ACACAGGGTCTAAGAAGCAACTACATCACAAAGGGGTCCCCCAGGCCCTAAGCATCCTCA 1648
                ********************* ***************************** ** *****
```

3’-UTR

```
Cattle          AGA--GGGGCTGGTCAGTGGTTCTGAGG-CTCTGTGCCTAGCACAACA---CTAAATAGA 5112
River Buffalo   AGAAGGGGGCTGGTCAGTGATTCTGAGGGCTCTGTGCCTAGCACAACAACACTAAATAGA 4948
                ***  ************** ******** *******************   *********
```

Figure 3.4 Indels located within the 5'- and 3'-UTR. River buffalo (*Bubalus bubalis*, GenBank Accession No. JN615215) was used as the reference to cattle (*Bos taurus*, GenBank Accession No. JQ805125). Red bolded sequence is a deletion, while blue bolded is insertion.

CHR-2B, region 419-575

```
419 GGTTCAGTAGTTGTGGCACAKGGGCTTAGTTGCCCCACGGCATGTGGGATCTTCCCAGACCAGGGATGAA 488
    ||:||||||||||||||:|| ||||||||||||:||||||||||||||||||||||:|||||||||| :|
129 GGCTCAGTAGTTGTGGCGCACGGGCTTAGTTGCTCCACGGCATGTGGGATCTTCCCGGACCAGGGATTGA 60

489 ACCCATGTCTCCTGCCCTGGCAGGCAGATTCTTAACCACTGGACCACTAGGGAAGTC 545
    ||||:||||:||||| :||||||||||||||||||||||||||||||:|||||||||
 59 ACCCGTGTCCCCTGCATTGGCAGGCAGATTCTTAACCACTGGACCACCAGGGAAGTC 3
```

Bov-tA1

```
4421 TGTTCAGTTGCTT-GGTCATGTCCTACTCTTTGCGACCCCATGGACTGTAGCCCACCAGGCGCCTCTGTT 4489
     ||:|||+||:|||-:||||||||| ||||||||||||||:||||||||||||||:|||||+ |||||||:
 216 TGCTCARTTACTTCAGTCATGTCCGACTCTTTGCGACCCTATGGACTGTAGCCCGCCAGGYTCCTCTGTC 147

4490 CATGGGATTTCCTAGGCAAGAATACTGGAGTGGTTTGCCATTTCCTCCTCCAGGGGATCTTCGTGACCCA 4559
     |||||||||::|:|||||||||||||||||||| ||||||| +||||||||||||||||||| :||||||
 146 CATGGGATTCTCCAGGCAAGAATACTGGAGTGGGTTGCCATGYCCTCCTCCAGGGGATCTTCCCGACCCA 77

4560 GGGATCGAACCCAAGTCTCCTGTGTCTCTTGTATTAGCAGGCAGAGTCTTTACCACT-GAGTCACCTAGG 4628
     ||||||||||||: |||||:|::|||||:||:|||:||||||:|: |||||||||||-| |:|||||:||
  76 GGGATCGAACCCGCGTCTCTTACGTCTCCTGCATTGGCAGGCGGGTTCTTTACCACTAGCGCCACCTGGG 7

4629 AAGCCC 4634
     ||||||
   6 AAGCCC 1
```

Figure 3.5 Retrotransposons found by CENSOR. Cetartiodactyl was the DNA source that was chosen as the reference for repeat elements. River buffalo (*Bubalus bubalis*, GenBank Accession No. JN615215) was the sequence used to generate the CENSOR repeat report.

River Buffalo: 419-545

```
GACTTCCCTAGTGGTCCAGTGGTTAAGAATCTGCCTGCCAGGGCAGGAGACATGGGTTTCATCCCTGGTC
TGGGAAGATCCCACATGCCGTGGGGCAACTAAGCCCMTGTGCCACAACTACTGAACC
```

River Buffalo: 4421-4634

```
GGGCTTCCTAGGTGACTCAGTGGTAAAGACTCTGCCTGCTAATACAAGAGACACAGGAGACTTGGGTTCG
ATCCCTGGGTCACGAAGATCCCCTGGAGGAGGAAATGGCAAACCACTCCAGTATTCTTGCCTAGGAAATC
CCATGAACAGAGGCGCCTGGTGGGCTACAGTCCATGGGGTCGCAAAGAGTAGGACATGACCAAGCAACTG
AACA
```

Figure 3.6 Masked regions sequence. Cetartiodactyl was the DNA source that was chosen as the reference for repeat elements. River buffalo (*Bubalus bubalis*, GenBank Accession No. JN615215) was the sequence used to generate the CENSOR repeat report.

Table 3.21

Repeat element summary generated by CENSOR.

Repeat Class	Fragments	Length
Transposable Element	2	341
Non-LTR Retrotransposon	2	341
SINE	2	341
SINE2/tRNA	1	214
Total	**2**	**341**

[*] Cetartiodactyl was the DNA source that was chosen as the reference for repeat elements. River buffalo (*Bubalus bubalis*, GenBank Accession No. JN615215) was the sequence used to generate the CENSOR repeat report.

A previous study with Iranian river buffalo has looked at repeat elements by sequencing random amplified polymorphic DNA (RAPD) fragments (Shokrollahi *et al.*, 2010)**.** CHR-2B was previously discovered in Iranian river buffalo and is generally found in the genome of ruminants. CHR-2B is a member of the CHR-2 SINE family, which has been associated with a common ancestor of cetaceans, hippopotamuses, and ruminants, forming the basis for the acronym CHR (Shimamura *et al.*, 1999). The other SINE discovered by CENSOR is a member of the Bov-tA family, which has been shown to have developed from recombination between CHR-2 and Bov-A (Shimamura *et al.*, 1999). Unlike the results for Iranian river buffalo (Shokrollahi *et al*. 2010), CENSOR found Bov-tA1 for the river buffalo in this study, and not Bov-tA2. Bov-tA is composed of a Bov-A that is 115 bp and a tRNA pseudogene that is 73 bp (Nijman *et al.*, 2002).

Impact of these regulatory elements and indels on gene expression between species cannot be resolved without determining gene expression of each individual species and comparing the data with the sequence, in essence, an association study between levels of gene expression and the indel to link the observed phenotype with the genotype. Sequencing the region containing TLR5 would be necessary to capture the full UTR regions of river buffalo and would yield the full sequence for bioinformatic scanning or regulatory elements and the full exploration of the sequence for gene expression studies.

It is becoming increasingly important to predict the possible impact of variability in genes of interest on both the functionality of the gene and the organism’s ability to detect and overcome illness. Despite the results from SMART analysis that suggest differences in the number and position of LRR regions between members of family bovidae in TLR5, specifically between *Bos taurus, Bison bison,* and *Bubalus bubalis*, the impact to animal health is not necessarily solely due to structural differences in this particular region of the gene, but also to differences in gene expression. These observed differences in gene structure could be impacted by regulatory components upstream of the start codon, and might also play a role in how these animals have adapted to their varying environments; however, it is necessary to generate both UTRs and actually conduct gene expression analysis to link the presence of indels to expression. The regulatory elements that have been predicted are consistent with ruminant SINE families. In addition, the immune system, as a whole, is complex. Because of this complexity and interactions between different parts of the immune system, the potential exists for compensatory changes in other families in the immune system. Therefore, investigating single components and elucidating what the roles they might play within the system can serve to reduce this complexity.

River buffalo are important to global agriculture, and the exploration of their genome for variation is only beginning. Case studies can examine the impact of regional differences and biota diversity on the haplotypes described here and even potentially reveal more with a larger and more varied population.

Therefore, it is not a leap to focus on the ruminant gastro-intestinal tract to develop tools that can potentially be exploited to assess diversity in breeding populations or in selection for enhanced health and productivity.

Previous studies in mice have investigated the impact of TLR5 on commensal bacterial loads (Vijay-Kumar *et al.*, 2007). True ruminants have four compartments of their digestive tract that allows them to acquire nutrients from plant substances. As such, to varying degrees, these compartments will be exposed to bacteria so an investigation that looks at native commensal bacterial loads, specifically flagellated bacteria, and how TLR5 regulates the load and if it is differentially expressed in the four compartments would serve to add to the profile of TLR5 in context of disease and maintenance. Furthermore, linking commensal load maintenance and TLR5 gene expression to a haplotype or SNP has the potential to impact animal breeding.

CHAPTER IV

A PHYLOGENETIC EXAMINATION OF TOLL-LIKE RECEPTOR 5 (TLR5) IN A VARIETY OF SPECIES

Introduction

The ability of the vertebrate immune system to recognize broad motifs which are not shared by the host organism enables them to successfully respond to invasions by pathogens without prior exposure. The innate immune system depends on pattern recognition receptors (PRRs) for its ability to recognize broad motifs of pathogens (Akira *et al.*, 2001). These broad motifs or pathogen-associated molecular patterns (PAMPs) are functionally important and are evolutionarily conserved within pathogens, thus making it difficult for organisms to mutate these features and still be able to successfully invade and colonize the preferred host organism (Medzhitov, 2001).

An important PRR family within the innate immune system of vertebrates is the Toll-like receptor (TLR) family. The TLR family, first discovered in *Drosophila melanogaster* for its contribution to dorsoventral polarity, provides fruit flies defense against fungal infection (Steward & Nusslein-Volhard, 1986; Lemaitre *et al.*, 1996). Toll-like receptors are type I transmembrane proteins, which differentially expressed across tissues and cells within the innate immune system in mammals and localize on the surface of cells or within the cell on specialized organelles (Kawai & Akira, 2006; Vahanan *et al.*, 2008). Toll-like receptors form either hetero- or homodimers and signal through MyD88 to begin a cytokine storm (Takeuchi *et al.*, 2000). To date, there have been ten TLRs discovered in most vertebrates, including water buffalo (Akira *et al.*, 2001).

There are two competing hypotheses on the evolution of TLR genes. This family recognizes PAMPs, which are difficult for pathogens to mutate and still maintain the ability to invade and colonize the host (Medzhitov, 2001). Therefore, the first hypothesis is that this system should be evolutionarily conserved and should not change as robustly over time as other genes. Thus, Toll-like receptors are generally referred to as an example of an evolutionarily conserved gene family (Wlasiuk *et al.*, 2009). Despite the inability of pathogens to easily mutate PAMPs to evade TLR stimulation, there are classes of pathogens that can successfully invade and colonize their preferred host (Andersen-Nissen *et al.*, 2005). The ability of certain pathogens to successfully mutate their flagellin recognition site to evade TLR5 detection or to downgrade their flagellin implies a co-evolutionary response of host and pathogen and forms the basis of the second hypothesis that TLRs do evolve and change over time in response to unique evasion tactics of pathogens. Studies in *Drosophila* indicate that PRRs evolve quickly between species, though it is has not been demonstrated that vertebrate and invertebrate responses are similar (Sackton *et al.*, 2007). Previous studies in primates (including humans) and avians have identified changes in Toll-like receptor 5 (TLR5) that are generally associated with the leucine-rich repeat (LRR) domains, which are extracellular and are involved with recognizing bacterial flagellin (Hawn *et al.*, 2005; Wlasiuk *et al.*, 2009; Ruan *et al.*, 2012).

This study focuses on the evolutionary relationship of the TLR5 gene within the artiodactyl order. Phylogenetic trees were drafted for the coding region of TLR5 across multiple orders and also specifically for the order artiodactyl. In addition, the McDonald-Kreitman Poisson Random Field test was applied across representatives from select orders to examine the selective pressures that have occurred over time between species separated at the order level.

Materials and Methods

DNA Samples

Samples used in this study are shown in Table 4.1. Cattle DNA samples BTA1 through BTA13 were provided by the J.E. Womack Laboratory (Texas A&M University) (Seabury *et al.*, 2007). The remaining DNA samples from *Giraffa*, *Oryx*, *Odocoileus*, *Rupicapra*, and *Tragelaphus* were provided by the J.E. Womack Laboratory cell collection.

Primers and Polymerase Chain Reaction (PCR) Amplification

Previously described *Bos taurus* TLR5 primers (Seabury *et al.*, 2007) (Table 3.2) were used to amplify the TLR5 gene from the DNA samples. PCR amplicons were generated via the following step-down thermocycling program: 5 min at 95ºC; 30 s at 95ºC, 20 s ranging from 58ºC to 62ºC, 1 min at 72ºC for 5 cycles; then 30 s at 95ºC, 20 s ranging from 57ºC to 60ºC for 45 cycles. Each 25 µl PCR contained the following: 50-100 ng DNA, 0.2 mM each dNTP, 0.4 µM forward and reverse primer, 1.5 mM $MgCl_2$, 1X Gene Amp PCR Gold Buffer (Applied Biosystems, Foster City, Ca, USA), 0.2X MasterAmp PCR Enhancer (Epicentre, Madison, WI, USA), and 1.66 units of AmpliTaq

Gold DNA polymerase (Applied Biosystems). PCR amplicons were then visualized by agarose gel electrophoresis. The PCR product was then purified using the QIAquick PCR Purification Kit (Qiagen, Inc., Valencia, CA, USA) according to manufacturer provided instructions.

Sequencing

Toll-like receptor 5 sequence data for river buffalo, swamp buffalo, African forest buffalo, and bison were previously determined (Chapter III). Cattle (*Bos taurus*), banteng (*Bos javanicus*), Masai giraffe (*Giraffa camelopardalis*), mule deer (*Odocoileus hemionus*), white-tailed deer (*Odocoileus virginianus*), scimitar-horned oryx (*Oryx dammah*), Gemsbok oryx (*Oryx gazella*), Arabian oryx (*Oryx leucoryx*), chamois (*Rupicapra rupicapra*), lesser kudu (*Tragelaphus imberbis*), and greater kudu (*Tragelaphus strepsiceros*) TLR5 sequences were obtained using the previously described *Bos taurus* primers (Seabury *et al.*, 2007) (Table 3.2). Sequencing reactions were performed by the DNA Core Laboratory at Texas A&M University.

Toll-like receptor 5 DNA sequence data were assembled individually for each isolate as described in Chapter III. Thirty-eight additional TLR5 sequences were retrieved from GenBank (Table 4.1).

Table 4.1
Evolutionary study species. Identification (ID) numbers, species, and GenBank accession numbers for TLR5 are included.

Sample IDs	Species	Common Name	Accession Number
BBU1[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615215
BBU2[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615216
BBU3[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615217
BBU4[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615218
BBU5[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615219
BBU6[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615220
BBU7[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615221
BBU8[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615222
BBU9[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615223
BBU10[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615224
BBU11[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615225
BBU12[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615226
BBU13[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615227
BBU14[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615228
BBU15[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615229
BBU16[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615230
BBU17[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615231
BBU18[*]	*Bubalus bubalis bubalis*	River Buffalo	JN615232
BCA[*]	*Bubalus bubalis carabanesis*	Swamp Buffalo	JN615235
SCA1[*]	*Syncerus caffer*	African Forest Buffalo	JN615234
SCA2[*]	*Syncerus caffer*	African Forest Buffalo	JN615233
BBI[*]	*Bison bison*	American Bison	JN615236
BTA1[†]	*Bos taurus*	Cattle	JQ805125
BTA2[†]	*Bos taurus*	Cattle	JQ805126
BTA3[†]	*Bos taurus*	Cattle	JQ805127
BTA4[†]	*Bos taurus*	Cattle	JQ805128
BTA5[†]	*Bos taurus*	Cattle	JQ805129
BTA6[†]	*Bos taurus*	Cattle	JQ805130
BTA7[†]	*Bos taurus*	Cattle	JQ805131
BTA8[†]	*Bos taurus*	Cattle	JQ805135
BTA9[†]	*Bos taurus*	Cattle	JQ805132
BTA10[†]	*Bos taurus*	Cattle	JQ805133
BTA11[†]	*Bos taurus*	Cattle	JQ805134
BTA12[†]	*Bos taurus*	Cattle	JQ805136
BTA13[†]	*Bos taurus*	Cattle	JQ805137
BTA14	*Bos indicus*	Cattle	GQ248711
BTA15	*Bos taurus*	Cattle	EU006639
BTA16	*Bos taurus*	Cattle	EU006640
BTA17	*Bos indicus*	Cattle	EU006636
BTA18	*Bos indicus*	Cattle	EU006641
BGR	*Bos grunniens*	Yak	GU647093
AME	*Ailuropoda Melanoleuca*	Giant Panda	XM_002922391
CHI	*Capra hircus*	Goat	HQ188378
CJA	*Callithrix jacchus*	Common Marmoset	ACFV01163303.1
CLU	*Canis lupus familiaris*	Dog	NM_001197176
CTO	*Cercocebus torquatus atys*	Sooty Mangabey	EU204938
DRE	*Danio rerio*	Zebrafish	NM_001130595

Table 4.1 continued

Sample IDs	Species	Common Name	Accession Number
ETE	*Echinops telfairi*	Lesser Hedgehog Tenrec	AAIY01425931.1
GCA[†]	*Giraffa camelopardalis*	Masai Giraffe	JQ811844
GGA	*Gallus gallus*	Chicken	HQ896214
GGO	*Gorilla gorilla*	Gorilla	AB445648
GLA	*Gallus lafayetii*	Sri Lankan jungelfowl	FJ915547
HSA	*Homo sapiens*	Human	NM_003268
MDO	*Monodelphis domestica*	Gray Short-tailed Opossum	XM_001376152
MFA	*Macaca fascicularis*	Crab-eating Macaque	AB445650
MGA	*Meleagris gallopavo*	Turkey	HQ436463
MMU	*Mus musculus*	House mouse	NM_016928
MMUL	*Macaca mulatta*	Rhesus Monkey	NM_001130429.1
MPU	*Mustela putorius*	Ferret	AEYP01103745.1
NME	*Numida meleagris*	Helmeted Guineafowl	JF767221
OAN	*Ornithorhynchus anatinus*	Platypus	XM_001512183
OAR	*Ovis aries*	Sheep	NM_001135926
ODA[†]	*Oryx dammah*	Scimitar-horned Oryx	JQ811850
OGA[†]	*Oryx gazella*	Gemsbok Oryx	JQ811846
OHE[†]	*Odocoileus hemionus*	White-tailed Deer	JQ811842
OLE[†]	*Oryx leucoryx*	Arabian Oryx	JQ811847
OMY	*Oncorhynchus mykiss*	Rainbow Trout	AB062504
OPR	*Ochotona princeps*	American Pika	AAYZ01013936.1
OVI[†]	*Odocoileus virginianus*	Mule Deer	JQ811843
PAL	*Pteropus alecto*	Black Flying Fox	GU045604
PCO	*Phasianus colchicus*	Ring-necked Pheasant	JF767220
PPA	*Pan paniscus*	Pygmy Chimpanzee	AB445647
PPY	*Pongo pygmaeus*	Bornean Orangutan	AB445649
PTR	*Pan troglodytes*	Chimpanzee	NM_001130462
RRU[†]	*Rupicapra rupicapra*	Chamois	JQ811845
SSC	*Sus scrofa*	Pig	AB208697.2
SHA	*Sarcophilus harrisii*	Tasmanian Devil	AFEY01269194.1
TGU	*Taeniopygia guttata*	Zebra Finch	XM_002188726
TIM[†]	*Tragelaphus imberbis*	Lesser Kudu	JQ811849
TST[†]	*Tragelaphus strepsiceros*	Greater Kudu	JQ811848
TSY	*Tarsius syrichta*	Philippine Tarsier	ABRT010212218.1
XLA	*Xenopus laevis*	African Clawed Frog	NM_001094980

[*] TLR5 sequence data obtained in Chapter III.

[†] TLR5 sequence data obtained in this study.

Phylogenetic Analysis

Sequences used in the phylogenetic analyses were edited with BioEdit (ver. 7.0.5.3) (Hall, 1999; Hall, 2005) and aligned with ClustalX (ver. 2.0.12) (Larkin *et al.*, 2007). The protein-coding genes were aligned based on translated amino acid sequences. The nucleotide substitution model, GTR+Γ+I, was selected by MrModeltest (ver. 2.3) (Nylander, 2004) based on the corrected Akaike Information Criterion (AICc).
The phylogenetic tree that shows multiple orders was inferred by MrBayes (ver. 3.1.2) (Ronquist & Huelsenbeck, 2003) utilizing Bayesian phylogenetic analysis under Metropolis-coupled Markov Chain Monte Carlo (MCMC) algorithm (Huelsenbeck & Ronquist, 2001; Ronquist & Huelsenbeck, 2003). Every 1,000th tree was sampled after two analyses were performed for 12 million generations. Each analysis consisted of four incrementally heated chains. After the posterior distribution of tree was summarized by removing 2,001 sample trees as burn-in, 10,000 sample trees remained.

Nodal support was estimated under a Neighbor-Joining method by PAUP* 4.0b10 (Swofford, 1993). The previously outlined procedure (Huelsenbeck & Crandall, 1997) was followed for substitution model selection. All model parameters were estimated by the likelihood procedure as implemented in PAUP* through an iterative process. The likelihood scores were compared by using likelihood ratio test as implemented in Modeltest 3.7 (Huelsenbeck & Crandall, 1997). The model of GTR+Γ+I was selected as the best-fit model for the data sets. The frequencies of each nucleotide base were 0.2669 for A, 0.2626 for C, 0.2167 for G, and 0.2538 for T. When assumed GT substitution rate [R(GT)] was 1, then the relative substitution rate of R(AC) was

1.3605, R(AG) was 4.8247, R(AT) was 0.6122, R(CG) was 1.2353, and R(CT) was 3.8617. The proportion of invariable sites was 0.1324, and the gamma shape was 1.7364. Support values were based on the full heuristic search on 10,000 bootstrap replications. Starting trees were obtained by stepwise addition with one tree held at each step.

For the phylogenetic tree that emphasized the artiodactyl order, nodal support was estimated under a Maximum Parsimony method by PAUP* 4.0b10 (Swofford, 1993). The likelihood scores were compared by using likelihood ratio test as implemented in Model test 3.7 (Posada & Buckley, 2004). The model of GTR+Γ+I was selected as the best-fit model for the data sets. The frequencies of each nucleotide base were 0.2606 for A, 0.2518 for C, 0.2067 for G. When assumed GT substitution rate [R(GT)] was 1, then the relative substitution rate of R(AC) was 1.4604, R(AG) was 7.0795, R(AT) was 0.7200, R(CG) was 1.5526, and R(CT) was 4.8039. The proportion of invariable sites was 0.8246, and the gamma shape was 0.3437. Support values were based on the full heuristic search on 1,000 bootstrap replications. Starting trees were obtained by stepwise addition with one tree held at each step. Phylogenetic trees were visualized and formatted with TreeGraph 2 software package (Stover & Muller, 2010).

Selective Constraint of Evolution

The program MKPRF (Swofford, 1993) was used to estimate the selection coefficient γ (=$2N_es$) of TLR5 coding region gene that diverged in different clades. The program samples from the posterior distribution of parameters in the MKPRF models using a Markov Chain Monte Carlo algorithm (Bustamante et al., 2002; Barrier et al., 2003; for Poisson random field theory, see Sawyer & Hartl, 1992).

Results and Discussion

The McDonald-Kreitman Poisson Random Field (MKPRF) test was utilized to examine the divergence over time between multiple orders. River buffalo (*B. b. bubalis*) was the reference species in this study. The MKPRF test is normally performed in one species to examine the fixed changes between closely related species. This study essentially compared divergent sites between species. Therefore, it is a more appropriate analysis is to say that the overall divergent sites between closely and distantly related species appears to conform to the appearance of positive, neutral, or negative selection in relation to river buffalo. That is, species that appear to be undergoing positive selection are retaining certain alleles while negatively selected species appear to be removing certain alleles. In this study, humans were determined to be undergoing positive selection in relation to river buffalo, but a more accurate statement would be that humans are retaining certain alleles that may or may not be beneficial or sweeping the population.

The direction of selection in comparison with the divergence time from river buffalo is shown in Figure 4.1. Unlike other methodologies, notably PAML, utilizing the MKPRF in this way allowed for the determination of the direction of the selection of the entire coding region of TLR5. Previous studies used the software PAML to examine site specific selection. In other words, each site was compared independently of other sites. Therefore, it is possible for sites in the LRR region to be positively selected and the entire coding region to be undergoing negative selection.

Phylogenetic trees were inferred for the coding sequence of TLR5 to show the evolutionary relationships between representative species across multiple orders (Figure 4.2). Primates (including humans) and avians have previously been determined to be undergoing strong positive selection. Another tree that focused exclusively on the artiodactyls order was also constructed to show the evolutionary relationship between members of the order that are more closely related (Figure 4.3).

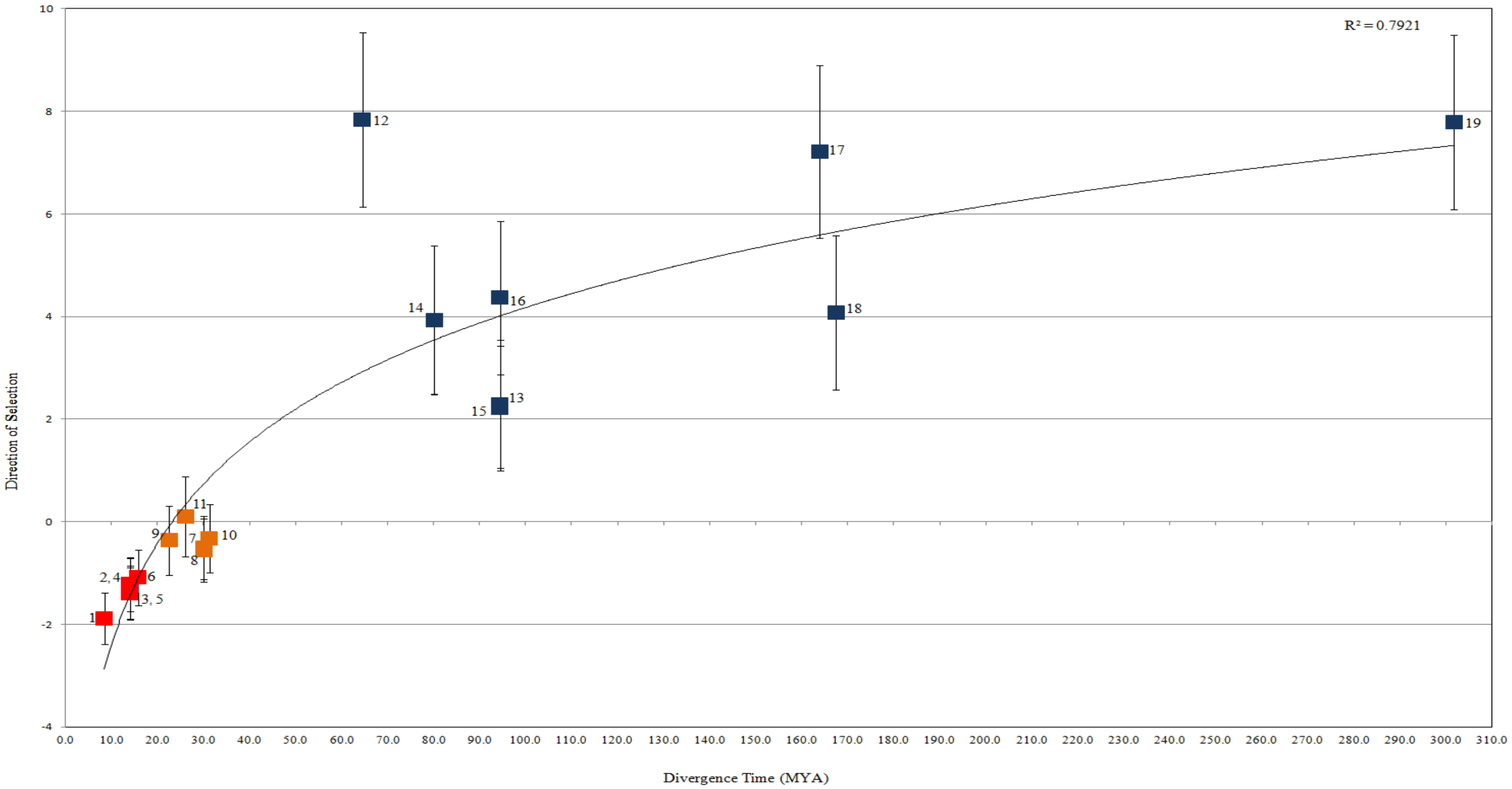


Figure 4.1 The McDonald-Kreitman Poisson Random Field (MKPRF) test. MKPRF was plotted with the divergence time for the TLR5 coding sequence. Error bars represent the standard deviation unique to each species. For clarity, species included have been assigned the following numbers on the figure with the Latin name, selection value, and divergence time in parenthesis: 1-African forest buffalo (*Syncerus caffer*, -1.89, 8.5 MYA), 2-American bison (*Bison bison*, -1.40, 14 MYA), 3-domestic yak (*Bos grunniens*, -1.23, 14 MYA), 4-cattle (*Bos taurus*, -1.38, 14 MYA), 5-banteng (*Bos javanicus*, -1.22, 14 MYA), 6-greater kudu (*Tragelaphus strepsiceros*, -1.09, 15.8 MYA), 7-sheep (*Ovis aries*, -0.51, 30.1 MYA), 8- chamois (*Rupicapra rupicapra*, -0.55, 30.1 MYA), 9-Arabian oryx (*Oryx leucoryx*, -0.37, 22.6 MYA), 10-Masai giraffe (*Giraffa camelopardalis*,-0.33, 31.3 MYA), 11-white-tailed deer (*Odocoileus virginianus*, 0.10, 26.1 MYA), 12-domestic pig (*Sus scrofa*, 7.83, 64.5 MYA), 13-human (*Homo sapiens*, 2.29, 94.4 MYA), 14-dog (*Canis lupus familiaris*, 3.93, 80.2 MYA), 15-mouse (*Mus Musculus*, 2.21, 94.4 MYA), 16-common marmoset (*Callithrix jacchus*, 4.37, 94.4 MYA), 17-Tasmanian devil (*Sarcophilus harrisii*, 7.21, 163.9 MYA), 18-platypus (*Ornithorhynchus anatinus*, 4.08, 167.4 MYA), 19-chicken (*Gallus gallus*, 7.79, 301.7 MYA). The trendline exhibits Poisson distribution. R^2=0.7921.

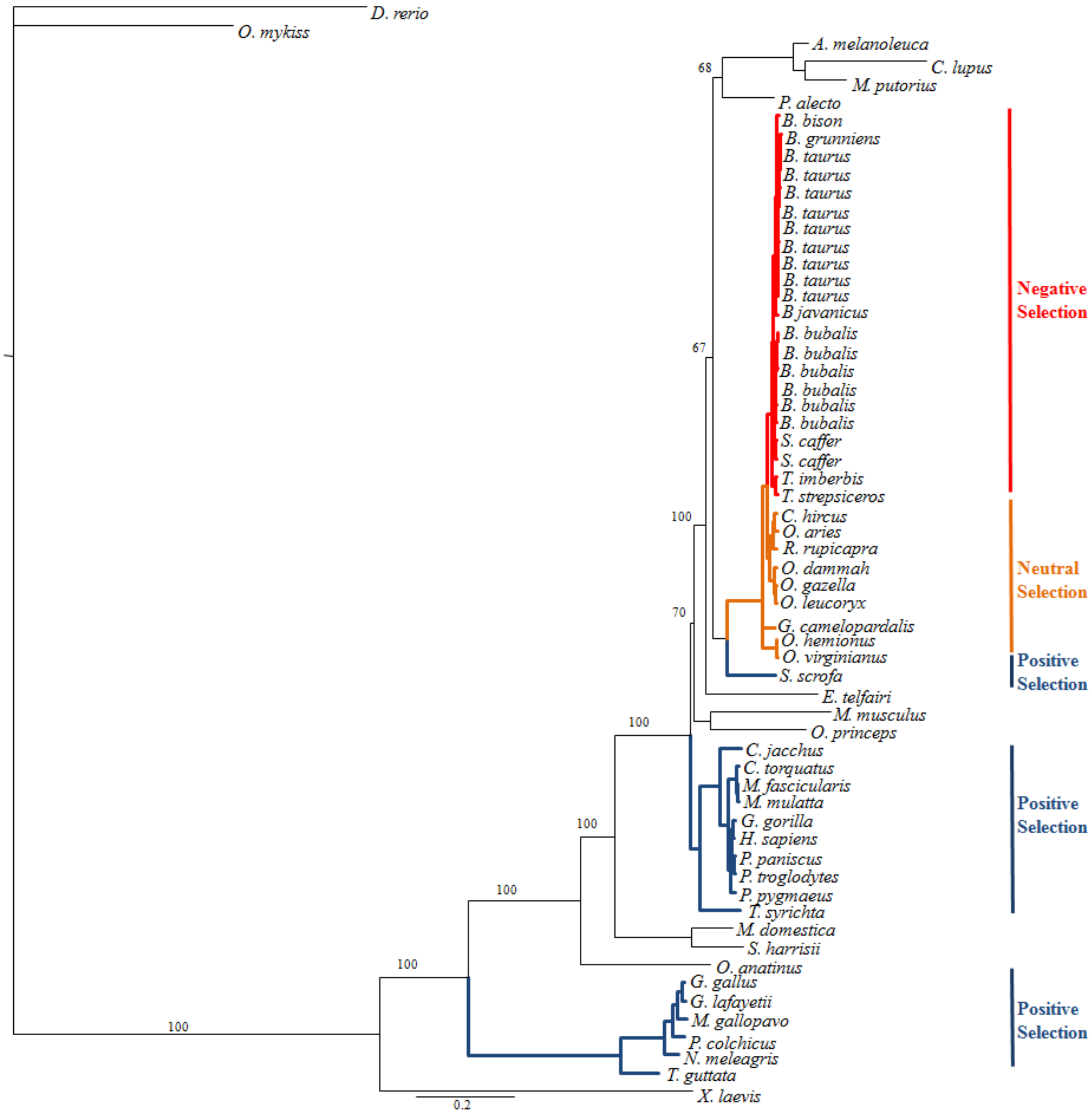


Figure 4.2 Phylogenetic tree inferred across multiple orders. The tree is based on TLR5. Bootstrap values for the coding region of TLR5 with a scale bar to indicate branch distance (in units of nucleotide substitution per site) and an outgroup are included. The tree was inferred using Mr Bayes and nodal support was estimated under a Neighbor-Joining method by PAUP*. The bootstrap value was determined on 10,000 replications. Negative, neutral, and positive selection are noted at the side.

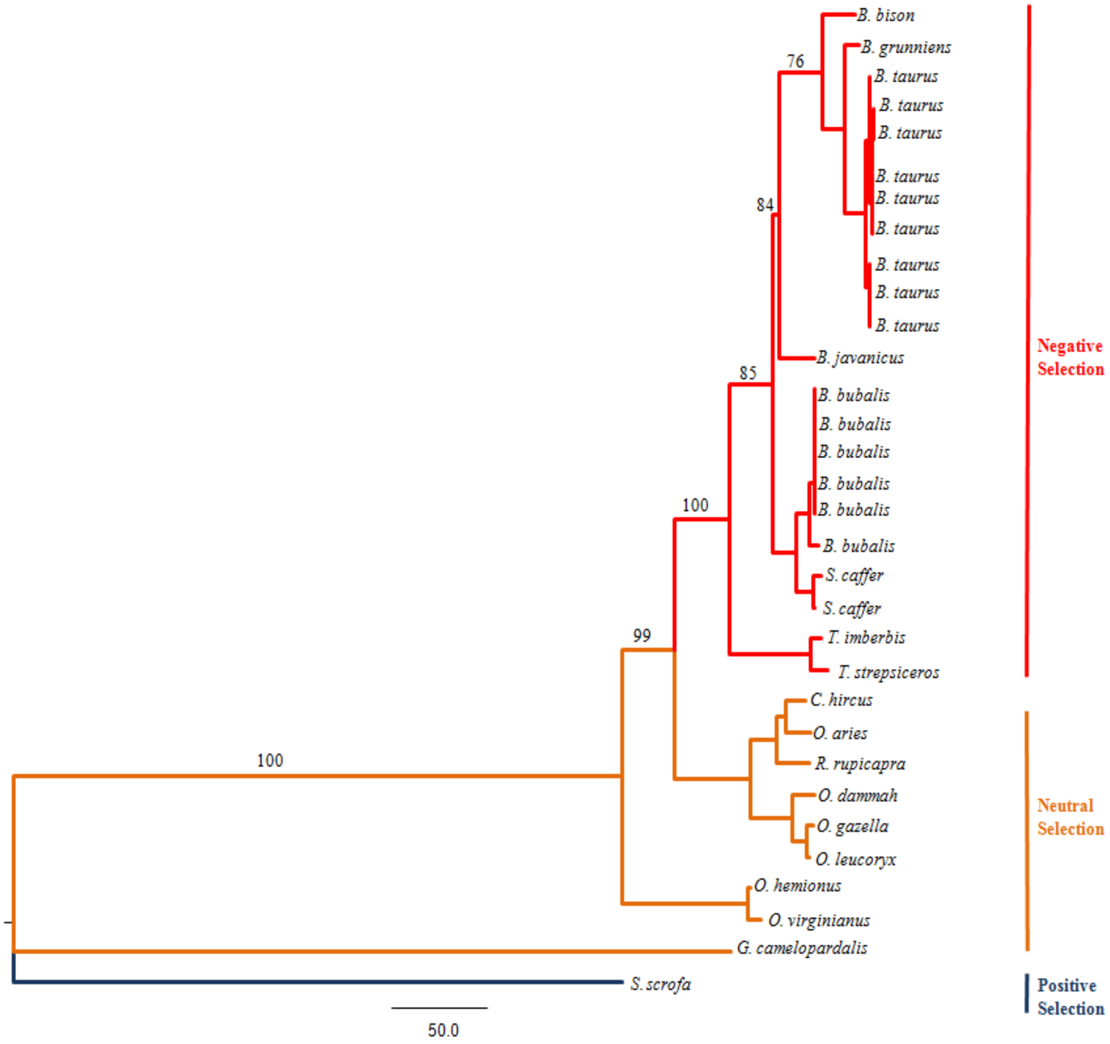


Figure 4.3 Phylogenetic tree inferred for artiodactyls. The tree is based on the TLR5 coding region. Bootstrap values for the coding region of TLR5 with a scale bar to indicate distance branch distance (in units of nucleotide substitution per site) and an outgroup are included. The tree is inferred under Maximum Parsimony by PAUP*. Every 1,000th tree was sampled for the bootstrap value. Negative, neutral, and positive selection are noted at the side.

Figure 4.4 is a modified phylogenetic tree (Figure 4.2) that shortens the branch length to the fish species (zebra fish and rainbow trout) and shows six characters that were previously determined to be river buffalo TLR5 haplotypes (Chapter III). Specifically, Figure 4.4 is Figure 4.2 but with the specific characters examined listed alongside the species. Ancestral characters that were found to be SNPs in the river buffalo are not necessarily SNPs in other species; however, by comparing these sites in other species, allele origin can be possibly assessed to examine where the allele might have originated. Characters that are the same color represent identical characters (Figure 4.4). Characters in black are not observed in other species. These seem to be orphan characters that may or may not have originated in that species. Most of the shared characters will be derived through a common ancestor and not through interspecies breeding. *Bos taurus* is fully capable of producing hybrids with other *Bos* species and the American bison. This represents the species that would most likely perpetuate these characters at these specific sites through species interbreeding.

American bison, domestic yak, cattle, banteng, goat, sheep, chamois, scimitar-horned oryx, Gemsbok oryx, Arabian oryx, Masai giraffe, mule deer, and white-tailed deer share the same 6 characters, CTCAAC, however, these characters appear to have originated with cervid species (Figure 4.4). One river buffalo was found to share the same characters of one of their haplotypes with the aforementioned group as did one of the African forest buffaloes. No viable hybrids have been found between river buffalo and cattle, although it is possible to create them in vitro (Kochhar *et al.*, 2002), or between river buffalo and African forest buffalo. This would be unlikely to occur since these species do not share any bi-armed chromosomes.

The characters CAAAAC are represented in the majority of river buffalo, an African forest buffalo, lesser kudu, and the greater kudu. The characters GTCCGG are not represented outside of river buffalo in this study. One river buffalo was previously determined to be heterozygous at these sites (Chapter III). The aforementioned river buffalo sequence was phase resolved and revealed that the river buffalo had the potential to transmit CAAAAC or CTCAAC. CTCAAC are characters that are represented in *Bos* and *Bison*. This suggests that these characters are present in the study river buffalo population.

The characters CTT--- seem to have originated with monotremes and are well represented in primates. The characters ---AAC seem to have originated in avians. All of the primates, the lesser hedgehog Tenrec, and the black flying fox have CTTAAC, which is a combination of the two oldest characters. The most common characters that have survived are ---AAC, which are well represented in primates, avians, and artiodactyls as well as the black flying fox (*Pteropus alecto*), the domestic ferret (*Mustela putorius*), and the dog (*Canis lupus*) in this study.

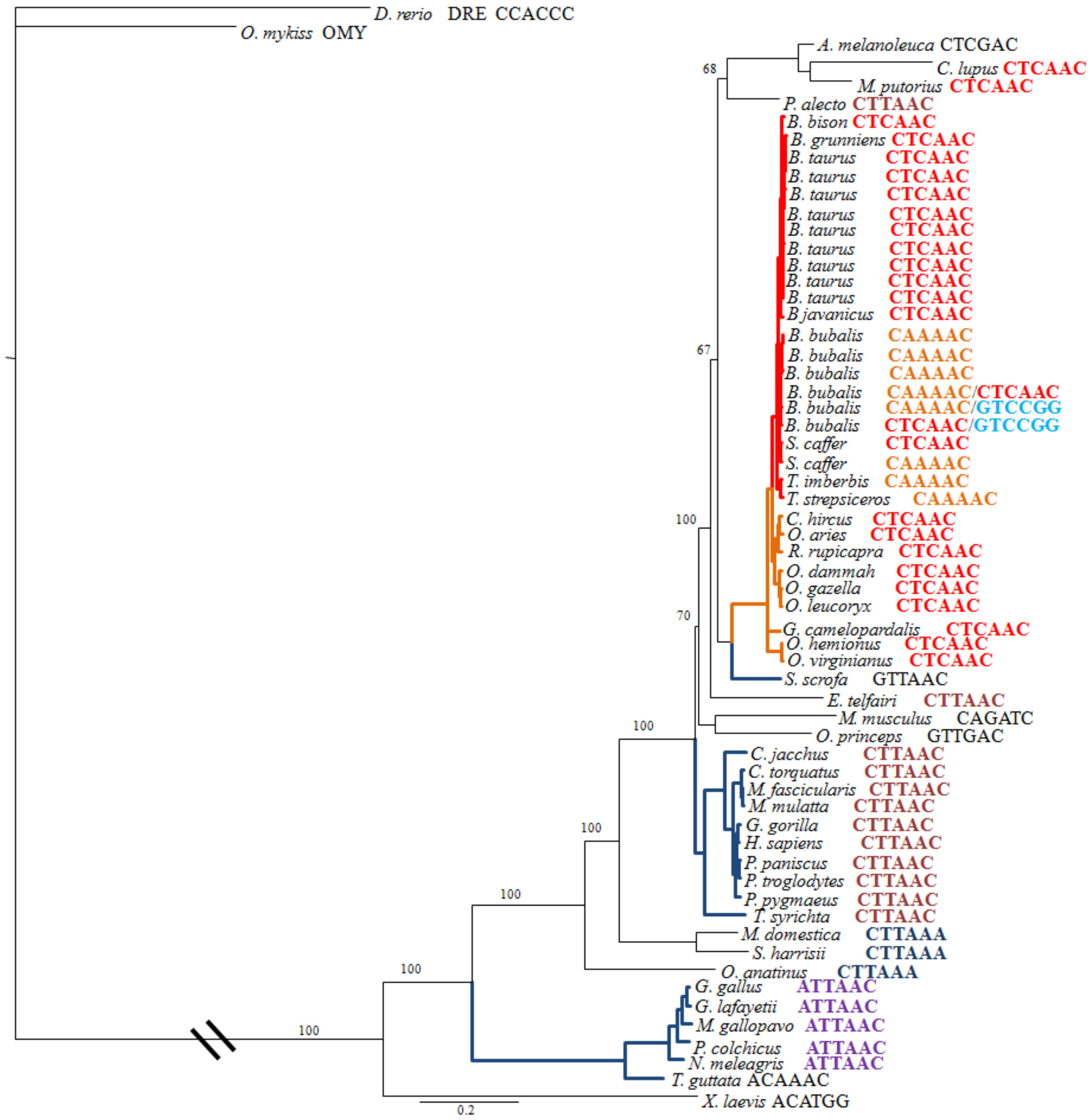


Figure 4.4 Modified Figure 4.2 to show TLR5 site characters. Bootstrap value for the coding region of TLR5 with a scale bar to indicate distance and an outgroup are included. The tree was inferred using Mr. Bayes and nodal support was estimated under a Neighbor-Joining method by PAUP. Every 10,000th tree was sampled for the bootstrap value. Haplotypes that are the same are represented by the same font color. Black, non-bolded haplotypes do not have another haplotype in common with other species. The double hash mark represents the break point in the the phylogenetic tree.

African forest buffalo (*Syncerus caffer*), American bison (*Bison bison*), domestic yak (*Bos grunniens*), cattle (*Bos taurus*), banteng (*Bos javanicus*), and greater kudu (*Tragelaphus strepsiceros)* appear to exhibit weak negative selection relative to river buffalo. Sheep (*Ovis aries*), chamois (*Rupicapra rupicapra*), Arabian oryx (*Oryx leucoryx*), Masai giraffe (*Giraffa camelopardalis*), and white-tailed deer (*Odocoileus virginianus*) fit the neutral model of selection. Pig (*Sus scrofa*), human (*Homo sapiens*), dog (*Canis lupus familaris*), mouse (*Mus musculus*), the common marmoset (*Callithrix jacchus*), Tasmanian devil (*Sarcophilus harrisii*), platypus (*Ornithorhynchus anatinus*), and chicken (*Gallus gallus*) appear to be undergoing strong positive selection.

It is useful to examine the natural history of the species studied when considering these results. The American bison suffered a severe population contraction during the early history of the United States due to the combination of hunting and foreign diseases that came with the expansion of cattle (Halbert *et al.*, 2012). This contraction caused a bottleneck and reduced genetic variability. In addition, certain populations of American bison in the United States exhibit cattle introgression (Halbert & Derr, 2007). The bison sample utilized in this study originated from Yellowstone National Park, which has not exhibited cattle introgression (Halbert & Derr, 2007; Halbert *et al.*, 2012).

This contraction of the population would have removed alleles, many of which might have been beneficial to overall robustness of the herd, and could produce results that reflect negative selection when alleles become fixed, prove to be deleterious, and are subsequently not passed on to offspring. Introgression of cattle genes into bison herds would increase variability, but it may introduce traits that have been specifically selected for by producers, which would limit the nature of the variability and could also produce results that would be similar to the strength and direction of cattle selection.

Cattle, domestic yak, and banteng are heavily influenced by human breeding programs that have selected for specific economically important traits. This specific selection of other traits may effectively reduce the population size and the pool of available alleles. In general, when breeding programs are used to select for a trait, other traits may be selected against. This kind of selective pressure exterted onto domesticated livestock by humans may have the same effect as the population contraction of the American bison. Selection for specific traits necessarily implies the reduction in population variability. For example, the effective population size of dairy cattle is low since the same sires are used extensively to maintain high milk production, thus the genetic variability of this breed is reduced (Flori *et al.*, 2009).

The exceptions to the possible link between domestication and the direction and strength of selection presented here is that both African forest buffalo and the greater kudu are not livestock species that have been heavily bred to achieve specific outcomes but they also exhibit weak negative selection. Sheep are domesticated but exhibit neutral selection within the margin of error. Pig, dog, and chicken have also been heavily influenced by human intervention but they exhibit strong positive selection. This possible positive selection could represent the populations recovering variability as the aforementioned species diverged from river buffalo long ago and humans have influenced these species over a longer period of time.

The divergence time is relatively close to the selection value for all species used as an outgroup for MKPRF analysis, except for the domestic pig (Figure 4.1). A phylogenetic tree was constructed for multiple orders (Figure 4.2) and another for artiodactyls (Figure 4.3). Study designations can be found in Table 4.1. Comparing the MKPRF test results with the phylogenetic tree that spans multiple orders and the phylogenetic tree that emphasizes artiodactyls reveals that negative, neutral, and positive selection are consistent within clades. Pig, which had the largest gap between its selection value (Figure 4.1) and divergence time, was used as the outgroup (Figure 4.3).

The species that diverged later from river buffalo, less than 20 million years ago (MYA), and are more closely related to river buffalo, were found to undergo weak negative selection. Species with a slightly later divergence time, 20-31 MYA, were found to undergo neutral selection. Species that diverged from river buffalo more than 64 MYA show strong positive selection.

Pig appears to be an outlier in that it diverged later, but exhibits a much stronger positive selection in relation to its divergence time from river buffalo.

Studies have shown that both avians and primates (including humans) exhibit positive selection in the LRR domain (Wlasiuk *et al.*, 2009; Ruan *et al.*, 2012). Data presented here for representative species of both avians and primates also show positive selection when utilized as outgroups for the MKPRF test in relation to river buffalo.

It is reasonable to infer a continuum for other orders in relation to their divergence time from river buffalo, which is to say that the relationship between the strength and direction of selection and divergence time will maintain a Poisson distribution, i.e. there is a relatively rapid substitution rate at the beginning and the time required, or rate, to reinstate the original nucleotide becomes slower with a wider distribution.

CHAPTER V

CONCLUSION

Results presented here were derived from three studies, comparative mapping, SNP analysis, and an evolutionary study, all focused on the TLR5 gene in river buffalo.

River buffalo chromosome 5 is the smallest of the bi-armed chromosomes. Cytogenetic studies have determined that BBU5 is a fusion of BTA 16 and BTA 29 (El Nahas *et al.*, 2001; Iannuzzi *et al.*, 2003). The radiation hybrid map was generated using methods described in Chapter II. Forty-six markers were used to generate the RH map, which is estimated to be 932.1 cR in total length. Retention frequencies (RF) of individual markers ranged from 17.8% (IDVGA26) to 54.4% (BZ919809). Even though IDVGA26 has a relatively low RF, it was incorporated into the single linkage group for the BBU5 chromosome map. The average RF for the markers used in this study was 36.6%, which compares favorably to the RF across the whole-genome radiation hybrid map (Amaral *et al.*, 2008).

Comparative mapping revealed two possible rearrangements relative to the cattle genome. These two regions have been previously shown to contain cattle QTLs which are related to milk protein and muscle fat (Casas *et al.*, 2000; MacNeil & Grosz, 2002; Casas *et al.*, 2003; Kim *et al.*, 2003; Viitala *et al.*, 2003; Casas *et al.*, 2004). River buffalo differ from cattle in both milk protein content and in reduced muscle fat, making further comparative study of this chromosome a potentially worthwhile endeavor. While it can be argued that the presence of QTLs in one species does not predict QTLs in another species, comparative analysis serves to narrow the focus. Regardless of whether buffalo QTLs exist in this region or whether the inversions observed between river buffalo and cattle on the RH map proves to be real, this region should be a prime target of investigation for important QTLs in buffalo. Next-generation sequencing (non-Sanger methods) will provide sequence of large regions of targeted chromosomes. It seems that the next steps might be the study of a BAC library or high resolution in situ hybridization to resolve the issue of the inversion observed on the RH map between river buffalo and cattle and inclusion of markers from this region in association studies for QTLs.

Variation in the TLR5 coding region was examined in a population of 18 river buffalo. Those results were then compared to other closely related species. The analysis revealed 16 total SNPs within the TLR5 coding region. Ten SNPs were determined to be sSNPs and 6 were nsSNPs. Fisher's Two-tailed Exact test determined that there was a mutational bias between transitions and transversions within nsSNPs and sSNPs. In addition, 4 total haplotypes were determined for this population. The most prevalent haplotype discovered was CAAAAC, which was present on about 80% of the genotyped haplotypes present in the population. The second most common haplotype was GTCCGG, which was present at a frequency of about 13%.

Utilizing the SMART software, the predicted TLR5 protein domain structure in river buffalo was compared to other species, both closely related and not. River buffalo, swamp buffalo, and African forest buffalo exhibited common LRR patterning. American bison and cattle exhibited LRR patterning common to each other but different from the buffalo group. The LLR domain is directly responsible for recognizing bacteria. This comparison of the protein domain architecture is useful in determining whether functional differences in TLR5 between species could be due in part to sequence variation within the TLR5 coding region. It can be reasonably inferred that differences in the predicted protein domain structure implies the possibility of differential immunity between species.

An analysis of the possible impact of the SNPs discovered in river buffalo was also performed. Polyphen-2 Analysis predicted that only one SNP, which was located near the TIR domain, might have an impact on the function of the protein. This observation is important because the TIR domain is responsible for signaling through MyD88 to begin the cytokine storm so this polymorphism could impact how well TLR5 functions. Case studies would help to properly understand and place these discovered haplotypes into context of the variation found within the coding region of TLR5. Linking the SNP to a haplotype could help determine if that SNP is beneficial or harmful in river buffalo. It is possible that thepredicted amino acid substitution near the TIR domain could result in either more efficient or less efficient signaling through MyD88.

It is apparent that the scope of SNP characterization in river buffalo should be widened. Data here were generated with a few individuals in a population that was a new transplant and did not have time to adapt to the new environment. Populations in different environs that mirror its natural habitat would be a better measure of evolutionary adaptation and variation in TLR5. That is, these animals have not had the long evolutionary history of their current environment, but their microbiota has changed to reflect their new environment. Despite this, it doesn't represent the evolutionary history of the current environment's pathogens in relation to TLR5, but gut pathology has changed to allow these animals to survive. So they no longer reflect the microbiota of their native environment, nor does TLR5 adaptation reflect the current environment.

In addition, human studies have characterized the microbiota within the gut (Gupta *et al.*, 2011) and the same can be done with river buffalo. Their four compartments provide four different environments in the same animal for commensal bacteria to develop with the purpose of extracting nutrients from food sources. An association of the expression level of TLR5 within these tissues with SNPs and environment could provide a good profile and genetic tool for breeding and management purposes. Being able to link the haplotype or SNP profile with the microbiota profile of the gut in river buffalo (and other species) has the potential to allow managers to select for specific haplotypes within the animal population to increase herd health.

SNP characterization and evolution across all TLRs have been reported (Fisher *et al.*, 2011). A key finding from the study is the flexibility that surface TLRs, such as TLR5, have in terms of variation in their sequence. Surface TLRs recognize bacterial PAMPs. Most bacteria will express more than one PAMP. Therefore, if one TLR has weak engagement or the bacterial agent in question has adapted evasion tactics to evade that particular TLR, another can also engage and recognize the bacterial pathogen. In addition to that, how a TLR engages a bacterial agent can be tissue dependent. A good example of this phenomenon is pneumonic *Burkholderia thailandensis*. *B. thailandensis* is avirulent in humans and a close relative of *Burkholderia pseudomallei*, which causes meliodosis (West *et al.*, 2009). TLRs 4, 2, and 5, and MyD88 (an adaptor molecule) are involved in disease clearance. The key finding of the study is that TLR4 and MyD88 are required for tumor necrosis factor α induction. However, TLR4 was found to not be needed for bacterial containment in late infection, while MyD88 controls infection and host survival (West *et al.*, 2009). TLR5 and 2 are not needed for low-dose infection, but TLR2 does offer a slight survival advantage. Since TLR5 recognizes bacterial flagellin, it does engage *B. thailandensis*, but it is time dependent. TLR5 is more stimulated when the pathogen is in log-phase (West *et al.*, 2009). This system suggests that redundancy is necessary. TLR5 and 2 may not be required at key points but they function in containment and clearance nonetheless.

The last part of this study focused on TLR5 and river buffalo in the context of evolution. Toll-like receptors are generally believed to be evolutionarily conserved and would not change robustly over time. Toll-like receptors recognize PAMPs, which are not subject to change since any changes might negatively impact the ability of pathogens to successfully infect and colonize the preferred host organism (Andersen-Nissen *et al.*, 2005). However, there are flagellated bacteria that have successfully found ways to evade detection by TLR5, which implies a degree of co-evolution (Andersen-Nissen *et al.*, 2005). Studies in primates have shown the presence of positive selection in the LRR domain and that certain populations of humans possess a premature stop codon and suggest that there might be redundant functionality elsewhere that allows for the detection of flagellated bacteria (Hawn *et al.*, 2005; Wlasiuk *et al.*, 2009; Ruan *et al.*, 2012).

In this study, two phylogenetic trees were constructed of the TLR5 coding region, one across multiple orders and the other including only artiodactyls. The strength and direction of selection was plotted in conjunction with the divergence of each species from river buffalo. Generally the MKPRF test is employed to detect fixed differences within species, however, in this study it was deployed to detect fixed differences with multiple outgroups in relation to river buffalo. Results of positive selection within avians and primates was also seen when the MKPRF was deployed in this way. The species that diverged from river buffalo less than 20 MYA showed weak negative selection, the 20-31 MYA divergence range showed neutral selection, and those species that diverged from river buffalo over 65 MYA showed strong positive selection. Analysis appears to support the idea that TLR5 might not be so evolutionarily constrained and can tolerate a fair amount of sequence variation.

The research presented here is only a beginning. It represents a foundation that can be built upon to potentially enhance animal health in both river buffalo and cattle, to add more understanding of how variation in the TLR5 gene coding region might change its functionality and to enhance the economic and social profile of river buffalo.

REFERENCES

Adelson, D.L., Raison, J.M. & Edgar, R.C. 2009. Characterization and distribution of retrotransposons and simple sequence repeats in the bovine genome. *Proc Natl Acad Sci U S A* **106:** 12855-12860.

Adzhubei, I.A., Schmidt, S., Peshkin, L., Ramensky, V.E., Gerasimova, A., Bork, P., Kondrashov, A.S. & Sunyaev, S.R. 2010. A method and server for predicting damaging missense mutations. *Nat Methods* **7:** 248-249.

Agarwala, R., Applegate, D.L., Maglott, D., Schuler, G.D. & Schaffer, A.A. 2000. A fast and scalable radiation hybrid map construction and integration strategy. *Genome Res* **10:** 350-364.

Akira, S., Takeda, K. & Kaisho, T. 2001. Toll-like receptors: critical proteins linking innate and acquired immunity. *Nat Immunol* **2:** 675-680.

Alexopoulou, L., Holt, A.C., Medzhitov, R. & Flavell, R.A. 2001. Recognition of double-stranded RNA and activation of NF-kappaB by Toll-like receptor 3. *Nature* **413:** 732-738.

Amaral, M.E., Owens, K.E., Elliott, J.S., Fickey, C., Schaffer, A.A., Agarwala, R. & Womack, J.E. 2007. Construction of a river buffalo (*Bubalus bubalis*) whole-genome radiation hybrid panel and preliminary RH mapping of chromosomes 3 and 10. *Anim Genet* **38:** 311-314.

Amaral, M.E., Grant, J.R., Riggs, P.K., Stafuzza, N.B., Filho, E.A., Goldammer, T., Weikard, R., Brunner, R.M., Kochan, K.J., Greco, A.J., Jeong, J., Cai, Z., Lin, G., Prasad, A., Kumar, S., Saradhi, G.P., Mathew, B., Kumar, M.A., Miziara, M.N., Mariani, P., Caetano, A.R., Galvao, S.R., Tantia, M.S., Vijh, R.K., Mishra, B., Kumar, S.T., Pelai, V.A., Santana, A.M., Fornitano, L.C., Jones, B.C., Tonhati, H., Moore, S., Stothard, P. & Womack, J.E. 2008. A first generation whole genome RH map of the river buffalo with comparison to domestic cattle. *BMC Genomics* **9:** 631.

Andersen-Nissen, E., Smith, K.D., Strobe, K.L., Barrett, S.L., Cookson, B.T., Logan, S.M. & Aderem, A. 2005. Evasion of Toll-like receptor 5 by flagellated bacteria. *Proc Natl Acad Sci U S A* **102:** 9247-9252.

Andersen-Nissen, E., Hawn, T.R., Smith, K.D., Nachman, A., Lampano, A.E., Uematsu, S., Akira, S. & Aderem, A. 2007. Cutting edge: Tlr5-/- mice are more susceptible to *Escherichia coli* urinary tract infection. *J Immunol* **178:** 4717-4720.

Anderson, K.V. 2000. Toll signaling pathways in the innate immune response. *Curr Opin Immunol* **12:** 13-19.

Applegate, D., Bixby, R., Chvátal, V. & Cook, W. 2006. *The Traveling Salesman Problem: A Computational Study*. Princeton University Press, Princeton.

Barile, V. 2005. Reproductive Efficiency in Female Buffaloes. *REU Technical Series*, Food and Agriculture Organization of the United Nations. Rome, Italy. **67:** 77-108.

Barquet, N. & Domingo, P. 1997. Smallpox: the triumph over the most terrible of the ministers of death. *Ann Intern Med* **127:** 635-642.

Bonnert, T.P., Garka, K.E., Parnet, P., Sonoda, G., Testa, J.R. & Sims, J.E. 1997. The cloning and characterization of human MyD88: a member of an IL-1 receptor related family. *FEBS Lett* **402:** 81-84.

Borghese, A. 2005a. Buffalo Meat and Meat Industry. *REU Technical Series* Food and Agricultural Organization of the United Nations. Rome, Italy. **67:** 197-217.

Borghese, A. 2005b. Buffalo Cheese and Milk Industry. *REU Technical Series*, Food and Agriculture Organization of the United Nations. Rome, Italy. **67:** 185-195.

Borghese, A. & Mazzi, M. 2005. Buffalo Population and Strategies in the World. *REU Technical Series*, Food and Agricultural Organization of the United Nations. Rome, Italy. **67:** 1-50.

Casas, E., Shackelford, S.D., Keele, J.W., Stone, R.T., Kappes, S.M. & Koohmaraie, M. 2000. Quantitative trait loci affecting growth and carcass composition of cattle segregating alternate forms of myostatin. *J Anim Sci* **78:** 560-569.

Casas, E., Shackelford, S.D., Keele, J.W., Koohmaraie, M., Smith, T.P. & Stone, R.T. 2003. Detection of quantitative trait loci for growth and carcass composition in cattle. *J Anim Sci* **81:** 2976-2983.

Casas, E., Keele, J.W., Shackelford, S.D., Koohmaraie, M. & Stone, R.T. 2004. Identification of quantitative trait loci for growth and carcass composition in cattle. *Anim Genet* **35:** 2-6.

Cavalier-Smith, T. 1987. The simultaneous symbiotic origin of mitochondria, chloroplasts, and microbodies. *Ann N Y Acad Sci* **503:** 55-71.

Cell Signaling Technologies 2012. NF-kB Signaling. Retrieved May 31, 2012, from http://www.cellsignal.com/pathways/nk-kappab-signaling.jsp.

Cossart, P. & Sansonetti, P.J. 2004. Bacterial invasion: the paradigms of enteroinvasive pathogens. *Science* **304:** 242-248.

Costerton, J.W., Stewart, P.S. & Greenberg, E.P. 1999. Bacterial biofilms: a common cause of persistent infections. *Science* **284:** 1318-1322.

Cox, D.R., Burmeister, M., Price, E.R., Kim, S. & Myers, R.M. 1990. Radiation hybrid mapping: a somatic cell genetic method for constructing high-resolution maps of mammalian chromosomes. *Science* **250:** 245-250.

Dalton, J.C., Nadir, S., Bame, J.H., Noftsinger, M., Nebel, R.L. & Saacke, R.G. 2001. Effect of time of insemination on number of accessory sperm, fertilization rate, and embryo quality in nonlactating dairy cattle. *J Dairy Sci* **84:** 2413-2418.

Demars, J., Riquet, J., Feve, K., Gautier, M., Morisson, M., Demeure, O., Renard, C., Chardon, P. & Milan, D. 2006. High resolution physical map of porcine chromosome 7 QTL region and comparative mapping of this region among vertebrate genomes. *BMC Genomics* **7:** 13.

El Nahas, S.M., Oraby, H.A., de Hondt, H.A., Medhat, A.M., Zahran, M.M., Mahfouz, E.R. & Karim, A.M. 1996. Synteny mapping in river buffalo. *Mamm Genome* **7:** 831-834.

El Nahas, S.M., de Hondt, H.A. & Womack, J.E. 2001. Current status of the river buffalo (*Bubalus bubalis L.*) gene map. *J Hered* **92:** 221-225.

European Molecular Biology Laboratory 2011. SMART. Retrieved July 25, 2011, from http://smart.embl-heidelberg.de.

Fagioli, A., Roncoroni, C., Lai, O. & Borghese, A. 2005. Buffalo Pathologies. *REU Technical Series*, Food and Agriculture Organization of the United Nations. Rome, Italy. **67:** 249-296.

Food and Agriculture Organization of the United Nations (FAO). 2000. Water Buffalo: an asset undervalued. F. R. O. f. A. a. t. Pacific, Bangkok, Thailand**:** 1-6.

Food and Agriculture Organization of the United Nations (FAO). 2012. FAOSTAT Database. Retrieved November 10, 2011, from faostat.fao.org/site/573/DesktopDefault.aspx?PageID=573#ancor.

Fisher, C.A., Bhattarai, E.K., Osterstock, J.B., Dowd, S.E., Seabury, P.M., Vikram, M., Whitlock, R.H., Schukken, Y.H., Schnabel, R.D., Taylor, J.F., Womack, J.E. & Seabury, C.M. 2011. Evolution of the bovine TLR gene family and member associations with *Mycobacterium avium* subspecies *paratuberculosis* infection. *PLoS One* **6:** e27744.

Flori, L., Fritz, S., Jaffrezic, F., Boussaha, M., Gut, I., Heath, S., Foulley, J.L. & Gautier, M. 2009. The genome response to artificial selection: a case study in dairy cattle. *PLoS One* **4:** e6595.

Foote, R.H. 1982. Cryopreservation of spermatozoa and artificial insemination: past, present and future. *J Androl* **3:** 85-100.

Fritz, J.H. & Girardin, S.E. 2005. How Toll-like receptors and Nod-like receptors contribute to innate immunity in mammals. *J Endotoxin Res* **11:** 390-394.

Garrett, M.R., Zhang, X.T., Dukhanina, O.I., Deng, A.Y. & Rapp, J.P. 2001. Two linked blood pressure quantitative trait loci on chromosome 10 defined by Dahl rat congenic strains. *Hypertension* **38:** 779-785.

Gewirtz, A.T., Vijay-Kumar, M., Brant, S.R., Duerr, R.H., Nicolae, D.L. & Cho, J.H. 2006. Dominant-negative TLR5 polymorphism reduces adaptive immune response to flagellin and negatively associates with Crohn's disease. *Am J Physiol Gastrointest Liver Physiol* **290:** G1157-1163.

Grabundzija, I., Irgang, M., Mates, L., Belay, E., Matrai, J., Gogol-Doring, A., Kawakami, K., Chen, W., Ruiz, P., Chuah, M.K., VandenDriessche, T., Izsvak, Z. & Ivics, Z. 2010. Comparative analysis of transposable element vector systems in human cells. *Mol Ther* **18:** 1200-1209.

GraphPad Software 2002. GraphPad QuickCalcs. Retrieved August 29, 2011, from http://www.graphpad.com/quickcalcs/contingency1.cfm

Gupta, S.S., Mohammed, M.H., Ghosh, T.S., Kanungo, S., Nair, G.B. & Mande, S.S. 2011. Metagenome of the gut of a malnourished child. *Gut Pathog* **3:** 7.

Halbert, N.D. & Derr, J.N. 2007. A comprehensive evaluation of cattle introgression into US federal bison herds. *J Hered* **98:** 1-12.

Halbert, N.D. & Derr, J.N. 2008. Patterns of genetic variation in US federal bison herds. *Mol Ecol* **17:** 4963-4977.

Halbert, N.D., Gogan, P.J., Hedrick, P.W., Wahl, J.M. & Derr, J.N. 2012. Genetic population substructure in bison at Yellowstone National Park. *J Hered* **103:** 360-370.

Hall, T.A. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series* **41:** 95-98.

Hall, T.A. 2005. *BioEdit: Biological sequence alignment editor for Win95/98/NT/2K/XP. 7.0.5 ed.*

Hansson, G.K. & Edfeldt, K. 2005. Toll to be paid at the gateway to the vessel wall. *Arterioscler Thromb Vasc Biol* **25:** 1085-1087.

Hasler, J.F. 1998. The current status of oocyte recovery, in vitro embryo production, and embryo transfer in domestic animals, with an emphasis on the bovine. *J Anim Sci* **76:** 52-74.

Hawn, T.R., Wu, H., Grossman, J.M., Hahn, B.H., Tsao, B.P. & Aderem, A. 2005. A stop codon polymorphism of Toll-like receptor 5 is associated with resistance to systemic lupus erythematosus. *Proc Natl Acad Sci U S A* **102:** 10593-10597.

Hayashi, F., Smith, K.D., Ozinsky, A., Hawn, T.R., Yi, E.C., Goodlett, D.R., Eng, J.K., Akira, S., Underhill, D.M. & Aderem, A. 2001. The innate immune response to bacterial flagellin is mediated by Toll-like receptor 5. *Nature* **410:** 1099-1103.

Heil, F., Hemmi, H., Hochrein, H., Ampenberger, F., Kirschning, C., Akira, S., Lipford, G., Wagner, H. & Bauer, S. 2004. Species-specific recognition of single-stranded RNA via toll-like receptor 7 and 8. *Science* **303:** 1526-1529.

Hemmi, H., Takeuchi, O., Kawai, T., Kaisho, T., Sato, S., Sanjo, H., Matsumoto, M., Hoshino, K., Wagner, H., Takeda, K. & Akira, S. 2000. A Toll-like receptor recognizes bacterial DNA. *Nature* **408:** 740-745.

Hemmi, H., Kaisho, T., Takeuchi, O., Sato, S., Sanjo, H., Hoshino, K., Horiuchi, T., Tomizawa, H., Takeda, K. & Akira, S. 2002. Small anti-viral compounds activate immune cells via the TLR7 MyD88-dependent signaling pathway. *Nat Immunol* **3:** 196-200.

Huelsenbeck, J.P. & Crandall, K.A. 1997. Phylogeny estimation and hypothesis testing using maximum likelihood. *Annual Review of Ecology and Systematics* **28:** 437-466.

Huelsenbeck, J.P. & Ronquist, F. 2001. MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics* **17:** 754-755.

Hugot, J.P., Chamaillard, M., Zouali, H., Lesage, S., Cezard, J.P., Belaiche, J., Almer, S., Tysk, C., O'Morain, C.A., Gassull, M., Binder, V., Finkel, Y., Cortot, A., Modigliani, R., Laurent-Puig, P., Gower-Rousseau, C., Macry, J., Colombel, J.F., Sahbatou, M. & Thomas, G. 2001. Association of NOD2 leucine-rich repeat variants with susceptibility to Crohn's disease. *Nature* **411:** 599-603.

Iannuzzi, L., Di Meo, G.P., Perucatti, A., Schibler, L., Incarnato, D., Gallagher, D., Eggen, A., Ferretti, L., Cribiu, E.P. & Womack, J. 2003. The river buffalo (*Bubalus bubalis*, 2n = 50) cytogenetic map: assignment of 64 loci by fluorescence in situ hybridization and R-banding. *Cytogenet Genome Res* **102:** 65-75.

Iannuzzi, L. 2007. The water buffalo: evolutionary, clinical and molecular cytogenetics. *Ital J Anim Sci* **6 (suppl. 2):** 227-236.

Ihara, N., Takasuga, A., Mizoshita, K., Takeda, H., Sugimoto, M., Mizoguchi, Y., Hirano, T., Itoh, T., Watanabe, T., Reed, K.M., Snelling, W.M., Kappes, S.M., Beattie, C.W., Bennett, G.L. & Sugimoto, Y. 2004. A comprehensive genetic map of the cattle genome based on 3802 microsatellites. *Genome Res* **14:** 1987-1998.

IUCN 2011. IUCN Red List of Threatened Species. Retrieved November 10, 2011, from www.iucnredlist.org.

Iwasaki, A. & Medzhitov, R. 2004. Toll-like receptor control of the adaptive immune responses. *Nat Immunol* **5:** 987-995.

Jann, O.C., Aerts, J., Jones, M., Hastings, N., Law, A., McKay, S., Marques, E., Prasad, A., Yu, J., Moore, S.S., Floriot, S., Mahe, M.F., Eggen, A., Silveri, L., Negrini, R., Milanesi, E., Ajmone-Marsan, P., Valentini, A., Marchitelli, C., Savarese, M.C., Janitz, M., Herwig, R., Hennig, S., Gorni, C., Connor, E.E., Sonstegard, T.S., Smith, T., Drogemuller, C. & Williams, J.L. 2006. A second generation radiation hybrid map to aid the assembly of the bovine genome sequence. *BMC Genomics* **7:** 283.

Jurka, J., Klonowski, P., Dagman, V. & Pelton, P. 1996. CENSOR--a program for identification and elimination of repetitive elements from DNA sequences. *Comput Chem* **20:** 119-121.

Kathariou, S., Kanenaka, R., Allen, R.D., Fok, A.K. & Mizumoto, C. 1995. Repression of motility and flagellin production at 37 degrees C is stronger in *Listeria monocytogenes* than in the nonpathogenic species *Listeria* innocua. *Can J Microbiol* **41:** 572-577.

Kawai, T. & Akira, S. 2006. TLR signaling. *Cell Death Differ* **13:** 816-825.

Kim, J.J., Farnir, F., Savell, J. & Taylor, J.F. 2003. Detection of quantitative trait loci for growth and beef carcass fatness traits in a cross between *Bos taurus* (Angus) and *Bos indicus* (Brahman) cattle. *J Anim Sci* **81:** 1933-1942.

Kobayashi, K.S., Chamaillard, M., Ogura, Y., Henegariu, O., Inohara, N., Nunez, G. & Flavell, R.A. 2005. Nod2-dependent regulation of innate and adaptive immunity in the intestinal tract. *Science* **307:** 731-734.

Kochhar, H.P., Rao, K.B., Luciano, A.M., Totey, S.M., Gandolfi, F., Basrur, P.K. & King, W.A. 2002. In vitro production of cattle-water buffalo (*Bos taurus--Bubalus bubalis*) hybrid embryos. *Zygote* **10:** 155-162.

Kurokawa, K., Ryu, K.H., Ichikawa, R., Masuda, A., Kim, M.S., Lee, H., Chae, J.H., Shimizu, T., Saitoh, T., Kuwano, K., Akira, S., Dohmae, N., Nakayama, H. & Lee, B.L. 2012. Novel bacterial lipoprotein structures conserved in low-GC content gram-positive bacteria are recognized by Toll-like receptor 2. *J Biol Chem* **287:** 13170-13181.

Larkin, M.A., Blackshields, G., Brown, N.P., Chenna, R., McGettigan, P.A., McWilliam, H., Valentin, F., Wallace, I.M., Wilm, A., Lopez, R., Thompson, J.D., Gibson, T.J. & Higgins, D.G. 2007. Clustal W and Clustal X version 2.0. *Bioinformatics* **23:** 2947-2948.

Lemaitre, B., Nicolas, E., Michaut, L., Reichhart, J.M. & Hoffmann, J.A. 1996. The dorsoventral regulatory gene cassette spatzle/Toll/cactus controls the potent antifungal response in *Drosophila* adults. *Cell* **86:** 973-983.

Letunic, I., Doerks, T. & Bork, P. 2009. SMART 6: recent updates and new developments. *Nucleic Acids Res* **37:** D229-232.

Lodes, M.J., Cong, Y., Elson, C.O., Mohamath, R., Landers, C.J., Targan, S.R., Fort, M. & Hershberg, R.M. 2004. Bacterial flagellin is a dominant antigen in Crohn's disease. *J Clin Invest* **113:** 1296-1306.

MacEachern, S., McEwan, J. & Goddard, M. 2009. Phylogenetic reconstruction and the identification of ancient polymorphism in the Bovini tribe (Bovidae, Bovinae). *BMC Genomics* **10:** 177.

MacNeil, M.D. & Grosz, M.D. 2002. Genome-wide scans for QTL affecting carcass traits in Hereford x composite double backcross populations. *J Anim Sci* **80:** 2316-2324.

Medzhitov, R., Preston-Hurlburt, P. & Janeway, C.A., Jr. 1997. A human homologue of the *Drosophila* Toll protein signals activation of adaptive immunity. *Nature* **388:** 394-397.

Medzhitov, R. 2001. Toll-like receptors and innate immunity. *Nat Rev Immunol* **1:** 135-145.

Mendoza, J.L., Lana, R. & Diaz-Rubio, M. 2009. *Mycobacterium avium* subspecies *paratuberculosis* and its relationship with Crohn's disease. *World J Gastroenterol* **15:** 417-422.

Miao, E.A., Andersen-Nissen, E., Warren, S.E. & Aderem, A. 2007. TLR5 and Ipaf: dual sensors of bacterial flagellin in the innate immune system. *Semin Immunopathol* **29:** 275-288.

Michelizzi, V.N., Dodson, M.V., Pan, Z., Amaral, M.E., Michal, J.J., McLean, D.J., Womack, J.E. & Jiang, Z. 2010. Water buffalo genome science comes of age. *Int J Biol Sci* **6:** 333-349.

Miziara, M.N., Goldammer, T., Stafuzza, N.B., Ianella, P., Agarwala, R., Schaffer, A.A., Elliott, J.S., Riggs, P.K., Womack, J.E. & Amaral, M.E. 2007. A radiation hybrid map of river buffalo (*Bubalus bubalis*) chromosome 1 (BBU1). *Cytogenet Genome Res* **119:** 100-104.

Morris, A.E., Liggitt, H.D., Hawn, T.R. & Skerrett, S.J. 2009. Role of Toll-like receptor 5 in the innate immune response to acute *P. aeruginosa* pneumonia. *Am J Physiol Lung Cell Mol Physiol* **297:** L1112-1119.

Nijman, I.J., van Tessel, P. & Lenstra, J.A. 2002. SINE retrotransposition during the evolution of the Pecoran ruminants. *J Mol Evol* **54:** 9-16.

Nylander, J.A.A. 2004. MrModeltest v2. Program distributed by the author. Evolutionary Biology Center, Uppsala University, Uppsala, Sweden.

O'Mahony, D.S., Pham, U., Iyer, R., Hawn, T.R. & Liles, W.C. 2008. Differential constitutive and cytokine-modulated expression of human Toll-like receptors in primary neutrophils, monocytes, and macrophages. *Int J Med Sci* **5:** 1-8.

Pierce, E.S. 2009. Where are all the *Mycobacterium avium* subspecies *paratuberculosis* in patients with Crohn's disease? *PLoS Pathog* **5:** e1000234.

Pierce, E.S. 2010. Ulcerative colitis and Crohn's disease: is *Mycobacterium avium* subspecies *paratuberculosis* the common villain? *Gut Pathog* **2:** 21.

Polge, C., Smith, A.U. & Parkes, A.S. 1949. Revival of spermatozoa after vitrification and dehydration at low temperatures. *Nature* **164:** 666.

Poltorak, A., He, X., Smirnova, I., Liu, M.Y., Van Huffel, C., Du, X., Birdwell, D., Alejos, E., Silva, M., Galanos, C., Freudenberg, M., Ricciardi-Castagnoli, P., Layton, B. & Beutler, B. 1998. Defective LPS signaling in C3H/HeJ and C57BL/10ScCr mice: mutations in Tlr4 gene. *Science* **282:** 2085-2088.

Ponger, L. & Mouchiroud, D. 2002. CpGProD: identifying CpG islands associated with transcription start sites in large genomic mammalian sequences. *Bioinformatics* **18:** 631-633.

Posada, D. & Buckley, T.R. 2004. Model selection and model averaging in phylogenetics: advantages of akaike information criterion and bayesian approaches over likelihood ratio tests. *Syst Biol* **53:** 793-808.

Prestridge, D.S. 1995. Predicting Pol II promoter sequences using transcription factor binding sites. *J Mol Biol* **249:** 923-932.

Prigent-Combaret, C., Vidal, O., Dorel, C. & Lejeune, P. 1999. Abiotic surface sensing and biofilm-dependent regulation of gene expression in *Escherichia coli*. *J Bacteriol* **181:** 5993-6002.

Ray, D.A. 2007. SINEs of progress: Mobile element applications to molecular ecology. *Mol Ecol* **16:** 19-33.

Rhee, S.H., Im, E. & Pothoulakis, C. 2008. Toll-like receptor 5 engagement modulates tumor development and growth in a mouse xenograft model of human colon cancer. *Gastroenterology* **135:** 518-528.

Ronquist, F. & Huelsenbeck, J.P. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* **19:** 1572-1574.

Rozen, S. & Skaletsky, H. 2000. Primer3 on the WWW for general users and for biologist programmers. *Methods Mol Biol* **132:** 365-386.

Rozen, S. 2009. Primer3 (v.0.4.0). Retrieved February 2, 2009, from http://frodo.wi.mit.edu/.

Ruan, W., Wu, Y. & Zheng, S.J. 2012. Different genetic patterns in avian Toll-like receptor (TLR)5 genes. *Mol Biol Rep* **39:** 3419-3426.

Sackton, T.B., Lazzaro, B.P., Schlenke, T.A., Evans, J.D., Hultmark, D. & Clark, A.G. 2007. Dynamic evolution of the innate immune system in Drosophila. *Nat Genet* **39:** 1461-1468.

Sahoo, M., Ceballos-Olvera, I., del Barrio, L. & Re, F. 2011. Role of the inflammasome, IL-1beta, and IL-18 in bacterial infections. *ScientificWorldJournal* **11:** 2037-2050.

Sambrook, J., Fritsch, E.F. & Mantiatis, T. 1989. *Analysis and Cloning of Eukaryotic Genomic DNA*. Cold Spring Laboratory Press, Cold Spring Harbour, NY.

Sambrook, J. & Russell, D.W. 2006. *The Condensed Protocols*. Cold Spring Laboratory Press, Cold Spring Harbour, NY.

Scanu, A.M., Bull, T.J., Cannas, S., Sanderson, J.D., Sechi, L.A., Dettori, G., Zanetti, S. & Hermon-Taylor, J. 2007. *Mycobacterium avium* subspecies *paratuberculosis* infection in cases of irritable bowel syndrome and comparison with Crohn's disease and Johne's disease: common neural and immune pathogenicities. *J Clin Microbiol* **45:** 3883-3890.

Schaffer, A.A., Rice, E.S., Cook, W. & Agarwala, R. 2007. rh_tsp_map 3.0: end-to-end radiation hybrid mapping with improved speed and quality control. *Bioinformatics* **23:** 1156-1158.

Seabury, C.M., Cargill, E.J. & Womack, J.E. 2007. Sequence variability and protein domain architectures for bovine Toll-like receptors 1, 5, and 10. *Genomics* **90:** 502-515.

Shimamura, M., Abe, H., Nikaido, M., Ohshima, K. & Okada, N. 1999. Genealogy of families of SINEs in cetaceans and artiodactyls: the presence of a huge superfamily of tRNA(Glu)-derived families of SINEs. *Mol Biol Evol* **16:** 1046-1060.

Shokrollahi, B., Amirinia, C. & Djadid, N.D. 2010. Identification of retrotransposon-like sequences in Iranian river buffalo. *African Journal of Biotechnology* **9:** 1999-2009.

Sitaraman, S.V., Klapproth, J.M., Moore, D.A., 3rd, Landers, C., Targan, S., Williams, I.R. & Gewirtz, A.T. 2005. Elevated flagellin-specific immunoglobulins in Crohn's disease. *Am J Physiol Gastrointest Liver Physiol* **288:** G403-406.

Smith, T.P., Casas, E., Rexroad, C.E., 3rd, Kappes, S.M. & Keele, J.W. 2000. Bovine CAPN1 maps to a region of BTA29 containing a quantitative trait locus for meat tenderness. *J Anim Sci* **78:** 2589-2594.

Stafuzza, N.B., Ianella, P., Miziara, M.N., Agarwala, R., Schaffer, A.A., Riggs, P.K., Womack, J.E. & Amaral, M.E. 2007. Preliminary radiation hybrid map for river buffalo chromosome 6 and comparison to bovine chromosome 3. *Anim Genet* **38:** 406-409.

Stephens, M., Smith, N.J. & Donnelly, P. 2001. A new statistical method for haplotype reconstruction from population data. *Am J Hum Genet* **68:** 978-989.

Stephens, M. & Scheet, P. 2005. Accounting for decay of linkage disequilibrium in haplotype inference and missing-data imputation. *Am J Hum Genet* **76:** 449-462.

Steward, R. & Nusslein-Volhard, C. 1986. The genetics of the dorsal-Bicaudal-D region of *Drosophila melanogaster*. *Genetics* **113:** 665-678.

Stover, B.C. & Muller, K.F. 2010. TreeGraph 2: combining and visualizing evidence from different phylogenetic analyses. *BMC Bioinformatics* **11:** 7.

Strober, W., Fuss, I. & Mannon, P. 2007. The fundamental basis of inflammatory bowel disease. *J Clin Invest* **117:** 514-521.

Swofford, D.L. 1993. PAUP - a computer-program for phylogenetic inference using maximum parsimony. *J Gen Physiol* **102:** A9-A9.

Takeuchi, O., Takeda, K., Hoshino, K., Adachi, O., Ogawa, T. & Akira, S. 2000. Cellular responses to bacterial cell wall components are mediated through MyD88-dependent signaling cascades. *Int Immunol* **12:** 113-117.

Tantia, M.S., Vijh, R.K., Mishra, B.P., Mishra, B., Kumar, S.T. & Sodhi, M. 2006. DGAT1 and ABCG2 polymorphism in Indian cattle (*Bos indicus*) and buffalo (*Bubalus bubalis*) breeds. *BMC Vet Res* **2:** 32.

Tirumurugaan, K.G., Dhanasekaran, S., Raj, G.D., Raja, A., Kumanan, K. & Ramaswamy, V. 2010. Differential expression of toll-like receptor mRNA in selected tissues of goat (*Capra hircus*). *Vet Immunol Immunopathol* **133:** 296-301.

Tripaldi, C., Catillo, G., Martillotti, F. & Angelucci, M. 1997. Influence of some characteristics of diet on the milk quality of water buffalo. *Buffalo J* **1:** 1-13.

Tripaldi, C., Terramoccia, S., Bartocci, S., Angelucci, M. & Danese, V. 2003. Effect of the somatic cell count on yield, composition and coagulating properties of Mediterranean buffalo milk. *Asian-Australasian J Animal Sci* **16:** 738-742.

USDA 2012. Animal Health Publications. Retrieved February 12, 2012, from http://www.aphis.usda.gov/publications/animal_health/content/printable_version/fs_fmd_con_07.pdf.

Vahanan, B.M., Raj, G.D., Pawar, R.M., Gopinath, V.P., Raja, A. & Thangavelu, A. 2008. Expression profile of toll like receptors in a range of water buffalo tissues (*Bubalus bubalis*). *Vet Immunol Immunopathol* **126:** 149-155.

Viitala, S.M., Schulman, N.F., de Koning, D.J., Elo, K., Kinos, R., Virta, A., Virta, J., Maki-Tanila, A. & Vilkki, J.H. 2003. Quantitative trait loci affecting milk production traits in Finnish Ayrshire dairy cattle. *J Dairy Sci* **86:** 1828-1836.

Vijay-Kumar, M., Sanders, C.J., Taylor, R.T., Kumar, A., Aitken, J.D., Sitaraman, S.V., Neish, A.S., Uematsu, S., Akira, S., Williams, I.R. & Gewirtz, A.T. 2007. Deletion of TLR5 results in spontaneous colitis in mice. *J Clin Invest* **117:** 3909-3921.

Vijay-Kumar, M., Aitken, J.D., Sanders, C.J., Frias, A., Sloane, V.M., Xu, J., Neish, A.S., Rojas, M. & Gewirtz, A.T. 2008. Flagellin treatment protects against chemicals, bacteria, viruses, and radiation. *J Immunol* **180:** 8280-8285.

Watts, J.C., Balachandran, A. & Westaway, D. 2006. The expanding universe of prion diseases. *PLoS Pathog* **2:** e26.

West, T.E., Hawn, T.R. & Skerrett, S.J. 2009. Toll-like receptor signaling in airborne *Burkholderia thailandensis* infection. *Infect Immun* **77:** 5612-5622.

Whiteley, M., Bangera, M.G., Bumgarner, R.E., Parsek, M.R., Teitzel, G.M., Lory, S. & Greenberg, E.P. 2001. Gene expression in *Pseudomonas aeruginosa* biofilms. *Nature* **413:** 860-864.

Wlasiuk, G., Khan, S., Switzer, W.M. & Nachman, M.W. 2009. A history of recurrent positive selection at the toll-like receptor 5 in primates. *Mol Biol Evol* **26:** 937-949.

Womack, J.E. 2005. Advances in livestock genomics: opening the barn door. *Genome Res* **15:** 1699-1705.

Yonekura, K., Maki-Yonekura, S. & Namba, K. 2003. Complete atomic model of the bacterial flagellar filament by electron cryomicroscopy. *Nature* **424:** 643-650.

Zarember, K.A. & Godowski, P.J. 2002. Tissue expression of human Toll-like receptors and differential regulation of Toll-like receptor mRNAs in leukocytes in response to microbes, their products, and cytokines. *J Immunol* **168:** 554-561.

Zimin, A.V., Delcher, A.L., Florea, L., Kelley, D.R., Schatz, M.C., Puiu, D., Hanrahan, F., Pertea, G., Van Tassell, C.P., Sonstegard, T.S., Marcais, G., Roberts, M., Subramanian, P., Yorke, J.A. & Salzberg, S.L. 2009. A whole-genome assembly of the domestic cow, *Bos taurus*. *Genome Biol* **10:** R42.

APPENDIX A

RIVER BUFFALO SEQUENCE WITH PRIMER POSITIONS

The following sequence is river buffalo, JEW41, and shows the placement of each primer pair first mentioned in Chapter III, Table 3.2. Primers were designed using Primer3 (Rozen & Skaletsky, 2000; Rozen, 2009) and are numbered, bolded, and different colored font. Primer pairs are the same colors and the sequence is highlighted. The symbol, >, denotes forward primer and < denotes the reverse primer.

```
  1 CGGAGGATAAGACTGGAAATGAGAGAGATCAGTGAGAACTCTCAAGAGATGGGAGCTTGA
    >>>>>>>>>>>>>>>>>>>>>1

 61 ACAGAGTAGACTTGGGAGGTAAAACTGACATGACTTGCTAACATTGGGGGTGACATTTCA

121 GAGAACAAAGGTGACTCAGCTGTTGTTACCCTGAGCCCATGGGTGGGAATGGCAGAGAAA

181 TTAAGAGCCTCGATAAACATTCTCACCAAGTTCTTTCCTATGATTCTCAAGTGCCTGGTT

241 TGGGGGTTATTTTTAATAGTAGGTTATATTTAATTACTACCAACTGGAAATTGTTTAATT

301 TCAAATGTGAAATGGCAATGGTTATTTTTCATCTCATGGTATACATGAGTATACCATGCC

361 CCCCAACTCTTTTCTTTTAATTTAATGAATTTATTTATTTTTGGCTGCCTTGGATCTTTG

421 TTGCTGCATGTGGGTTCAGTAGTTGTGGCACAGGGGCTTAGTTGCCCCACGGCATGTGGG

481 ATCTTCCCAGACCAGGGATGAAACCCATGTCTCCTGCCCTGGCAGGCAGATTCTTAACCA
                                                             >>>

541 CTGGACCACTAGGGAAGTCTTGCTGGCTTACTGTTAACGTGGCCTGCTTTTGATACTTTG
    >>>>>>>>>>>>>>>>>2

601 GGTCAACTCAGGAGTTGATGTCTCCTTCTGATCAGCTGTAAATTGTGTGTMAGAGCCTCA

661 RAGGTGCTGTGGAAACCCTACCACAAATCACCCCCAATACAACAAAGCCTCTTCAGAGCC
                                    1<<<<<<<<<<<<<<<<<<<<<<
                                      GGTTATGTTGTTTCGGAGAAGT
721 TGCAGGTGATCCAGGGCCAGCGCCTCCTCTGGTGCCATGGCCTCTTCATGCTGTCTACCC

781 AGATATGGAAACTGAACCAGGGATGTTTTCATAAACCAGAGCCCTCTTCTTGTTTCTTTC
```

```
 841 TTTACTCTCCCCCTCACTCTGCCCTCTGAACCATGTAGCTCCTTCCTTACCTTCCAGCAG

 901 AGGCCTTCTGATACTACACGTAGCTCAAGTTGAGTACTTGGCAGGCACCAGCTGGAGGTG

 961 CCATGCYGGTGGGTAGAGGTGAAGCTCTCTAGGGGCCCTCGTGCACCCTCTGTACCCTCA

1021 CAGCTCCYAGCACAGCACTGAGAACATAAGCGGACACCTTCATTCGGCGCCTTTTGCCRC

1081 TCTGTACAAGCAAATGCTCAACACAGACAGACAGTGAATTTACCTGTTGGACTAGGTAAG
               >>>>>>>>>>>>>>>>>>>>>>3

1141 GGGTYTGGTTTTTGTTTAKTTGTATGCTCACATGGTCACACAAGTGCCAGGCATGCWGTT

1201 GGTGCTTAGTGCATCCTTATTAAACTGAAAAATGGTGTACCCAATTTTTACATGATGAGC

1261 TATACTGTGTAGGAAGTGAGGATGGATAAATAGAGATGACTTAGTATCTTTGGCAGATTA
        2<<<<<<<<<<<<<<<<<<<<<<
         GACACATCCTTCACTCCTACCT
1321 GAGGGGAAAGAAAAATCAGTGGATTTATTTTCTAGTCCTCAGCAGAGGCTGCCTTGGGAT

1381 AGGAATGGGGTCCCTGGCTGGGGTGAAGTTCAAATATATCTCTTCCTAATGTTTTCCCCA

1441 ACTTCCATCAGCAAATCTTGAATGAATGAATTCACAAYCTTATGAATGAATGCTGAGTTA

1501 TCACAAAGATTAAATAAAGTATTTCTGAAGTAYTTACAACCATGCTTGCTATGTAAAAAA

1561 AAANGCAACATAATAGATAAAAAGAGAGAAAAGCTCTGTCTGCACCACACAGTATCTGCC

1621 AATAGGCATGGCCATGGACCCAGAGGAACACAGGGTCTAAGAAGCAACYACATCACAAAG
                    >>>>>>>>>>>>>>>>>>4

1681 GGGTCCCCCAGGCCCTAAGCATCCTCAAGGCTGTTGCTCAGTGCCTTGAGCTTAGATGTC

1741 TGTGTCTTCACTCTCCCTTCTTCTCCATAGGATCATGGGAGACTGCCTTGACCTTCTCTT
                                         3<<<<<<<<<<<<<<<<<<<<
                                          CCTCTGACGGAACTGGAAGA
1801 AGGAGTTGTACTCCTGACCAGTCCTGCACTTGGAATTTCTTCCTGCTTCTTCGATGGTTG

1861 GAGAGCCATCTATCTTTCCTGCAACCTCACCCAAGTGCCCCAGGTCCCCAACAGCACCAA

1921 GAGCCTCCTGCTCAGCTTCAACTATATCAGGACAGTCACAACCGCATCCTTCCCCTTCCT

1981 GGAGCAGTTGCAGCTGCTGGAGCTGGGAACTCAGTTTACCCCCTTGACCATTTACAGAGA
```

```
2041 AGCCTTCCGAAACCTGCCCAATCTCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTT

2101 CTTGCATCCAGATGCTTTTCAGGGACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTG
                                                              >>>

2161 TGGTCTCTCCGATGCTGTATTAAAAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCA
     >>>>>>>>>>>>>>>5

2221 CTTGGACCTATCCAAAAATAAAATTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACT

2281 GAATTCCTTGAAGTCCATTGATTTTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGA
                                                      4<<<<<<<<<<
                                                       CACTCGTCCT
2341 GTTCAAACCCCTCCAAGGGAAAACACTCTCCTTCTTAAGCCTTGCTGATAACCACCTGTA
     <<<<<<<<<<
     CAAGTTTGGG
2401 CAGCAGGGTCTCAGTGGACTGGAAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGA

2461 AACCCTAGATGTTTCTGGCAATGGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGC

2521 CATCAATGGGAGCCAGATTTTCTCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATT

2581 TGGCTTCTCCAACCTGAAGGATCCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTC

2641 GATGATACAGCTGGACATTTCACATGGGTATATCTTCTCCYTGAACTTCCGAGTCTTTGA

2701 GACACTCCAGGAGCTGAAGGWMCTAAACCTCGCCTACAACAAGATAAACAGTATTTCRAG
                                >>>>>>>>>>>>>>>>>>>>>>6

2761 GAATGCGTTTTATGGACTCGACAACCTCCAAGTTCTCAATATATCATATAACCTTCTTGG

2821 GGAATTATATAATTATGATTTCGATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAA
                                                          5<<<<<<
                                                           CGTCTT
2881 GAATCACATTGGGATCATTCAGGACAMAACATTCAAATTCCTGGGGAAATTRAATACCTT
     <<<<<<<<<<<<<
     CTTAGTGTAACCC
2941 GGACCTCCGGGATAATGCTCTTAAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTT

3001 CTTAAGTGGCAATAAGCTGATGACTTTGCCAAATATCCCACTTACAGCCAATTTCATCCM

3061 ATTATCAGAGAATAGGCTAGAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCA

3121 TCTCCAGATTCTCATTTTAAATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCC

3181 TTCAGAGAATTCCAGCCTAGAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTG
```

```
3241 GGAAACTGGGTCATGTTGGGATATTTTTAAGGGKCTTTCTCATCTCCAACTCCTCTATCT

3301 AAATAAAAACTACCTGAATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAG
                     >>>>>>>>>>>>>>>>>>>7

3361 GGGACTCAGCCTCAAAGACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAA

3421 CTTAGAGATCCTGGATATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGC
                                   6<<<<<<<<<<<<<<<<<<<<<
                                    GAGGAGAGAGGACTAGGACTA
3481 ATCACTGAGTGCCATAGACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGC

3541 TTTTATCCATTGGCTCAATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTA

3601 CTGCATGTACCCAAACTCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTG

3661 TGAAGAAGAAGAAGTTTTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTYAC

3721 CTTGACTGTGTTCCTCGTGATCACCCTCACRGTTACTAAGTTCAGRGGGTTTTGGTTCAT

3781 CTGTTATAAGAAAGCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGA

3841 TATGTACAAATACGATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAA
                                              >>>>>>>>>>>>>>>>>>>

3901 TGCTTTGCTCAAACACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTT
     >>8

3961 TGAAGAAAGAGACTTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTG
                                                           7<<<<<
                                                            CACAC
4021 GAGCAGCAGAAAGACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCT
     <<<<<<<<<<<<<<
     CTCGTCGTCTTTCT
4081 CGAAGCCTTCAGTTATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCAT

4141 GGTGGTGGTGGGGTCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTT

4201 CGTCCAGAAACGGCAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCT

4261 CAATAAACTCTCTCAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTACTAT
```

```
4321 TCAGCTGCAAAATGTAACCACCATSTCCTAGGCAAAGGAGCAGTTTCCACTTATCGCAAG
                                              >>>>>>>>>>>>>>>>>>>

4381 CCACAGATAACTCTGTACCTTTTATTTCCACCAGTTACCATTTGCATACCTTTGTGTTCA
     >9

4441 GTTGCTTGGTCATGTCCTACTCTTTGCGACCCCATGGACTGTAGCCCACCAGGCGCCTCT

4501 GTTCATGGGATTTCCTAGGCAAGAATACTGGAGTGGTTTGCCATTTCCTCCTCCAGGGGA

4561 TCTTCGTGACCCAGGGATCGAACCCAAGTCTCCTGTGTCTCTTGTATTAGCAGGCAGAGT
                      8<<<<<<<<<<<<<<<<<<<
                       GCTTGGGTTCAGAGGACAC
4621 CTTTACCACTGAGYCACCTAGGAAGCCCTTAAGTTGCCATTTGGGGGTCCTTTATGGAGT

4681 TGTTGTTTTCCTACAATGAAAAGAACATAAATCTCCTTGATTTTCATAGCAACACAATGT

4741 TTTGTCTTGCCAACGTCCAAATGGAAAGTAATAGATCTAGAAAATTGCAACKGCCCCCAG

4801 CAGTTCTTACTCTGCATTGATTTCCTTTCAGAACCAGTAACACTGATCTCTCCCATTGCA

4861 TCGACTACAGGATATATCCTCTGCATGGCAAGGGCACCTTGGGAGAAGTTACAGATGGCT

4921 GACACCCTTTCTCTAGCATTCGTTTCCAGAAGGGGGCTGGTCAGTGATTCTGAGGGCTCT

4981 GTGCCTAGCACAACAACACTAAATAGAAAACAAACAGAAAAAGAGGCATGGTTCCTACTA

5041 TTACCCTGAGAACAATGCCATTGCTCAGTACAGGTCATGCCCAGTCTC
                     9<<<<<<<<<<<<<<<<<<<<
                      GGTAACGAGTCATGTCCAGT
```

APPENDIX B

SPECIES ALIGNMENT

The aligned sequences as generated by Clustal W (Larkin *et al.*, 2007). Refer to Chapter IV, Table 4.1 for study species IDs and designations.

```
PPA             ATGGGAGACCACC---TGGACCTTCTCCTAGGAGTGGTGCTCATGGCCGGTCCTGTGTTT 57
PTR             ATGGGAGACCACC---TGGACCTTCTCCTAGGAGTGGTGCTCATGGCCGGTCCTGTGTTT 57
HSA             ATGGGAGACCACC---TGGACCTTCTCCTAGGAGTGGTGCTCATGGCCGGTCCTGTGTTT 57
GGO             ATGGGAGACCACC---TGGACCTTCTCCTAGGAGTGGTACTCATGGCCGGTCCTGTGTTT 57
PPY             ATGGGAGACCACC---TAGACCTTCTCCTAGGAGTGGTGCTCATGGCCAGTCCTGTGTTT 57
MFA             ATGGGAGACCACC---TGGACCTTCTCCTAGGAGTGGTGCTTGTGGCCAGTCCTGTGTTT 57
MMUL            ATGGGAGACCACC---TGGACCTTCTCCTAGGAGTGGTACTTGTGGCCAGTCCTGTGTTT 57
CTO             ATGGGAGACCACC---TGGACCTTCTCCTAGGAGTGGTGCTTGTGGCCAGTCCTGTGTTT 57
CJA             ATGGGAGACCACC---TGGACCTTCTCCTAAGAGTGGTGCTTGTGGCCAGTCCTGTGTTT 57
TSY             ATGGGAGGCCGCC---TTGACCTTCTCTTAGGAGTGGTGCTCATGGTCAGTCCTGTGTTT 57
CHI             ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
OAR             ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCCGTCCTGCACTT 57
RRU             ATGGGAGATTGCC---TTGACCTTCTCTTAGGAGTCRTACTCCTGACCAATCCTGCACTT 57
OGA             ATGGGAGACTGCC---TTGACCTTCTCTTTGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
OLE             ATGGGAGACTGCC---TTGACCTTCTCTTTGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
ODA             ATGGGAGACTGCC---TTGACCTTCTCTTTGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BBU1            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU2            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU3            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU4            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU5            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU8            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU9            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU12           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU14           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU16           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU18           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BCA             ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU7            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU11           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU13           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU17           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU15           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU6            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
BBU10           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
SCA1            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAATCCTGCACTT 57
SCA2            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAATCCTGCACTT 57
BTA10           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA16           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA7            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA3            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA1            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA2            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA4            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA6            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA9            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA15           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA12           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA11           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA14           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
```

```
BGR             ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA5            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA13           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA8            ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA17           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BTA18           ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BBI             ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
BJA             ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
TIM             ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
TST             ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTTGTACTCCTGACCAGTCCTGCACTT 57
GCA             ATGAGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
OHE             ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCARTCCTGCACTT 57
OVI             ATGGGAGACTGCC---TTGACCTTCTCTTAGGAGTCGTACTCCTGACCAGTCCTGCACTT 57
SSC             ATGGGAGACTGCC---TGGTCCTGCTCTT---GACCTTGCTCGTGGCCAGTCCTGCACTT 54
PAL             ATGGGAGATCACC---TTGACCTTCTCCTGGGAGTGTTGCTCGTGGCCAGTCCTGTGCTT 57
AME             ATGGGAGGCCACC---TGGACCTTCTGTTCGGGGTGATGCTTGCGGCCAGCCCTGTGCTT 57
MPU             ATGGGAGGCTACC---TGGACCTTCTTTTGGGGGTAGTGCTCGTGGTCAGCCCTGTGCTA 57
CLU             ATGGGCCGCCAGC---TGGGCCGCGCACTGGGGCTGCTGCTTGTGGCCGGCGCCGTGGCC 57
ETE             ATGAGAGACCACC---TCGAACTCCTCTTAGGAGTGGTGCTCGTCACCGGTCCTGCGCTT 57
OPR             ATGGCAGATCACC---TTGACCTTCTCATAGGAGTGGTGCTCATGGTGAGTGCTGTGTTT 57
MMU             ATGGCATGTCAAC---TTGACTTGCTCATAGGTGTGATCTTCATGGCCAGCCCCGTGTTG 57
MDO             ATGGGCCACCTCC---TTGCATTTCTCTTGGGATTGGTATTTAAAGCCACTTCTGTGTAT 57
SHA             ATGGGCCATCT------TGCATTTCTCTTGGGATTGCTATTTGAAGCCACCTCTATATGT 54
OAN             ATGTGGCTCCCCC---TGGTGCTCTTCTCGGGAATGCTGTTGGGAGCCAGCCCTGCACGA 57
GGA             ATGTTACATCAACGGCTAATAATTGTCTTTGGAATAGCACT---AGCTGGAGATATATGT 57
GLA             ATGTTACATCAACGGCTAATAATTGTCTTTGGAATAGCACT---AGCTGGAGATATATGT 57
MGA             ATGTTACATCAACGGCTAATAATTGTCTTCAGAATATCACT---AGCTGGAGATATATGT 57
PCO             ATGTTACATCAACGGCTAATAATTGTCTTTGGAATAGCACT---AGCTGGAGATATATGT 57
NME             ATGTTACATCAACGGCTAATAATTGTCTTTGGAATAGCACT---AGCTGGAGATATATGT 57
TGU             ATGTTGTGCCATCAGGTCCTCTTTGTCTTTGGGCTGTCGCT---AGCTAGTGGTGTGGGT 57
                ***                                     *

PPA             GGAATTCCTTCCTGCTCCTTTGATGGCCGAATAGCCTTTTATCGTTTCTGCAGCCTCACC 117
PTR             GGAATTCCTTCCTGCTCCTTTGATGGCAGAATAGCCTTTTATCGTTTCTGCAGCCTCACC 117
HSA             GGAATTCCTTCCTGCTCCTTTGATGGCCGAATAGCCTTTTATCGTTTCTGCAACCTCACC 117
GGO             GGAATTCCTTCCTGCTCCTTTGATGGCCGAATAGCCTTTTATCGTTTCTGCAACCTCACC 117
PPY             GGAATTCCTTCCTGCTCCTTTGATGGCCAAATAGCCTTTTATCGTTTCTGCAACCTCACC 117
MFA             GGATTTCCTTCCTGCTCCTTTGATGGCCGAATAGCCTTTTATCGTTTCTGCAACCTCACC 117
MMUL            GGATTTCCTTCCTGCTCCTTTGATGGCCGAATAGCCTTTTATCGTTTCTGCAACCTCACC 117
CTO             GGATTTCCTTCCTGCTCCTTTGATGGCCGAATAGCCTTTTATCGTTTCTGCAACCTCACC 117
CJA             GGAATTCCTTCCTGCTCCTCTGATGGTCGGATAGCTTTATATCGTTTCTGCAACCTCACC 117
TSY             GGAATTTCTTCCTGCTCCTTTGATGGTCAGATAGCCTTATATCGTTCCTGCAACCTCACC 117
CHI             GGAATTTCTTCCTGCTTCTTCAATGGTTGGAGAGCCCTCTATCTTTCCTGCAACCTCACC 117
OAR             GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
RRU             GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCCTCTATCTTTCCTGTAACCTCACC 117
OGA             GGAATTTCTTCCTGCTTCTTCAATGGTTGGAGAGCCCTCTATCTTTCCTGCAACCTCACC 117
OLE             GGAATTTCTTCCTGCTTCTTCAATGGTTGGAGAGCCCTCTATCTTTCCTGCAACCTCACC 117
ODA             GGAATTTCTTCCTGCTTCTTCAATGGTTGGAGAGCCCTCTATCTTTCCTGCAACCTCACC 117
BBU1            GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU2            GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU3            GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU4            GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU5            GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU8            GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU9            GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU12           GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU14           GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU16           GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU18           GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BCA             GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU7            GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU11           GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU13           GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU17           GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU15           GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU6            GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBU10           GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
```

```
SCA1                 GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
SCA2                 GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA10                GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA16                GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA7                 GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA3                 GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA1                 GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA2                 GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA4                 GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA6                 GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA9                 GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA15                GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA12                GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA11                GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA14                GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BGR                  GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA5                 GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA13                GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA8                 GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA17                GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BTA18                GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BBI                  GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
BJA                  GGAATGTCTTCCTGCTTCTTTGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
TIM                  GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTTCCTGCAACCTCACC 117
TST                  GGAATTTCTTCCTGCTTCTTCGATGGTTGGAGAGCCATCTATCTTKCCTGCAACCTCACC 117
GCA                  GGAGTTTCTTCCTGCTTCTTTGATGGTTGGAGAGCCCTCTATCTTTCCTGCAACCTCACC 117
OHE                  GGAATTTCTTCCTGCTTCTTCAATGGTTGGAGAGCCGTCTATCTTTCCTGCAACCTCACC 117
OVI                  GGAATTTCTTCCTGCTTCTTCAATGGTTGGAGAGCCGTCTATCTTTCCTGCAACCTCACC 117
SSC                  GGAATGCCTTCCTGCTTCTTTGATGGCCAGAGGGCTATCTATCGTGGCTGCAACCTCACC 114
PAL                  GGAATTTCTTCCTGCTCCTCTGATGGTCGGATGGCCTTATATCGTTTCTGCAACCTCACC 117
AME                  GCGATTCCTTCCTGCGCCTCCGACGGTCAGAGGGCCTTGTATCGCTCCTGCAACCTCACC 117
MPU                  ACAATTCCTTCCTGCACCTCTGATGGCCAGAGGGCCTTGTATCGATCCTGCAACCTAACC 117
CLU                  GCGGCATCCTGCTGCGTGGCTGACGGCCGGAGGGCCCTGTACCGCTCCTGCAACCTCAGC 117
ETE                  GGCATCTCTCCCTGCTCCTTTGATCATGGGGTAGCCTTATACCGTTTCTGCAACCTCACC 117
OPR                  GGAATTGTTCCCTGCTCCTTTGACGGGCAGGTGGCTTTCTATCGTTTCTGCAACCTCACC 117
MMU                  GTAATATCTCCCTGTTCTTCAGACGGCAGGATAGCCTTTTTCCGAGGCTGTAACCTCACC 117
MDO                  GGAATTCCTTCTTGCTCAGCTGATGGACAGCTCGCCTTTTATCGTTTCTGCAACCTCACC 117
SHA                  GGAATTCCTTTTTGCTCAGATGACGGACAACTTGCCTTCTATAATTCCTGCAACCTCACC 114
OAN                  GGAGTTCTGCCCTGCTCCACCACGGGACCCATTGCCGTGTACCATTTCTGCAACCTCACT 117
GGA                  GCATCTAGAAGCTGCTATTCAGAAGATCAGGTCTCCATGTATAATTCTTGCAACCTCACA 117
GLA                  GCATCTAGAAGCTGCTATTCAGAAGATCAAGTCTCCATGTATAATTCTTGCAACCTCACA 117
MGA                  GCATCTAGAAGCTGCTATTCAGAAGACCAGGTGTCCATGTATAATTCTTGCAACCTCACA 117
PCO                  GCATCTAGAAGCTGCTATTCAGAAGATCAGGTCTCCATGTATAATTTCTGCAACCTCACA 117
NME                  GCATCTAGAAGCTGCTATTCAGAAGATCAGGTCTCCATGTATAGTTCCTGCAACCTCACA 117
TGU                  GCATCTAGAAAGTGCTACTCAGAAGCCCAGGTCTCCATATATTTTTTCTGTGGCCTCACA 117
                                 **                    *  * *        **   *** *

PPA                  CAGGTCCCCCAGGTCCTCAACAC---CACTGAGAGGCTCCTGCTGAGCTTCAACTATATC 174
PTR                  CAGGTCCCCCAGGTCCTCAACAC---CACTGAGAGGCTCCTGCTGAGCTTCAACTATATC 174
HSA                  CAGGTCCCCCAGGTCCTCAACAC---CACTGAGAGGCTCCTGCTGAGCTTCAACTATATC 174
GGO                  CAGGTCCCCCAGGTCCTCAACAC---CACTGAGAGGCTCCTGCTGAGCTTCAACTATATC 174
PPY                  CAGGTCCCCCAGGTCCTCAACAC---CACTGAGAGGCTCCTGCTGAGCTTCAACTATATC 174
MFA                  CAGGTCCCCCAGGTCCTCAACAC---CACTGAGAGGCTCCTGTTGAGCTTCAACTATATC 174
MMUL                 CAGGTCCCCCAGGTCCTCAACAC---CACTGAGAGGCTCCTGCTGAGCTTCAACTATATC 174
CTO                  CAGGTCCCCCAGGTCCTCAACAC---CACTGAGAGGCTCCTGCTGAGCTTCAACTATATC 174
CJA                  CAGGTCCCCCAGGTCCTCAACAC---CACTGAGAGGCTCCTGCTGAGCTTCAACTATATC 174
TSY                  CAGGTCCCCCAGGTCCTCAACAC---CACCGAGAGACTCCTGCTAAGCTTCAACTACATC 174
CHI                  CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
OAR                  CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
RRU                  CAAGTGCCCCAGGTCCCCAATAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
OGA                  CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTTTATC 174
OLE                  CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTTTATC 174
ODA                  CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTTTATC 174
BBU1                 CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU2                 CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU3                 CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU4                 CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
```

```
BBU5                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU8                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU9                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU12               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU14               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU16               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU18               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BCA                 CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU7                CAAGTGCCCCAGGTCCCCAACAS---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU11               CAAGTGCCCCAGGTCCCCAACAS---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU13               CAAGTGCCCCAGGTCCCCAACAS---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU17               CAAGTGCCCCAGGTCCCCAACAS---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU15               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU6                CAAGTGCCCCAGGTCCCCAACAS---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBU10               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
SCA1                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
SCA2                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA10               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA16               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA7                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA3                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA1                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA2                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA4                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA6                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA9                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA15               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA12               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA11               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA14               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BGR                 CAAGTGCCCCAGGTCCCCAACAC---CACCAAGGGCCTCCTGCTCAGCTTCAACTATATC 174
BTA5                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA13               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA8                CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA17               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BTA18               CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BBI                 CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
BJA                 CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
TIM                 CAAGTGCCCCAGGTTCCCAGCAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
TST                 CAAGTGCCYCAGGTCCCCAGCAC---CACCAAGAGCCTYCTGCTCAGCTTCAACTATATC 174
GCA                 CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGCTTCAACTATATC 174
OHE                 CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGTTTCAACTATATC 174
OVI                 CAAGTGCCCCAGGTCCCCAACAC---CACCAAGAGCCTCCTGCTCAGTTTCAACTATATC 174
SSC                 CAGGTTCCCCAGGTCCCCAGTGG---CACCAAGAGCCTCCTGCTCAGCTTCAACTACATC 171
PAL                 CAGATACCCCGGGTCCTCAACAC---CACTGAGAGCCTCCTGCTAAGCTTCAACTATATC 174
AME                 CAGGTGCCGCCGGTCCCCAGCAC---CACCCAGGTCCTCCTGCTCAGCTTCAACTATATC 174
MPU                 CAGGTGCCGCCAGTCCCCAGCAC---CACCCAGATCCTCCTGCTTAGCTTCAACTATATC 174
CLU                 CAGGTGCCCCCGGTCCCCAGCAC---CACCGAGATCCTCCTGCTGAGCTTCAACTACATC 174
ETE                 CAAGTTCCCCACATCCCTCCAAC---CATGAAAATCCTCCTCCTGAGCTTCAACTCGATC 174
OPR                 CAGGTCCCGCAGGTCCTCAACAG---CACAGAGAGTCTTCTGCTAAACTTCAACTATATC 174
MMU                 CAGATTCCCTGGATCCTCAATACTACCACTGAGAGGCTCCTGCTCAGCTTCAACTATATC 177
MDO                 CAAGTCCCCCAAGTGCCAAATAC---TACAACAAAGCTGTTGTTAAGTTTCAACTACATC 174
SHA                 GAAGTCCCCCGAGTACCAAACAC---CATTATTAAGCTATTCTTAAGTTATAACTATATC 171
OAN                 CGGGTGCCCCTGGTCGCTAACAC---CACAGTGAGGCTTCTGTTGGCCTTCAACCATATC 174
GGA                 GGTGTTCCACCTGTGCCAAAGGA---CACTGCAAAGCTTTTTCTAACTTACAACTATATC 174
GLA                 GGTGTCCCACCTGTGCCGAAGGA---CACTGCAAAGCTTTTTCTAACTTACAACTATATC 174
MGA                 AGTGTTCCACCTGTGCCAAAGGA---CACTGCAAAGCTTTTTCTAACTTACAACTATATC 174
PCO                 AGTGTTCCACCTGTGCCAAAGGA---CACTGCAAAGCTTTTTCTAACTTACAACTATATC 174
NME                 GGTGTTCCACTTGTGCCAAAGGA---CACTGCAAAGCTTTTTCTAACTTACAACTATATC 174
TGU                 GATGTTCCACCTGTGCCAAAGGA---TACAATGAAGCTTTTCCTGACTTACAACTACATC 174
                        * **     *             *        **  *  *    *  ***   ***

PPA                 AGGACAGTCACTGCTTCATCC--TTCCCCTTTCTGGAACAGCTGCAGCTGCTGGAGCTCG 232
PTR                 AGGACAGTCACTGCTTCATCC--TTCCCCTTTCTGGAACAGCTGCAGCTGCTGGAGCTCG 232
HSA                 AGGACAGTCACTGCTTCATCC--TTCCCCTTTCTGGAACAGCTGCAGCTGCTGGAGCTCG 232
GGO                 AGGACAGTCACTGCTTCATCC--TTCCCCTTTCTGGAACAGCTGCAGCTGCTAGAGCTCG 232
PPY                 AGGACAGTCACTGCTTCATCC--TTCCCCTTTCTGGAACAGCTGCAGCTGCTGGAGCTCG 232
```

```
MFA             CGGACAGTCACTGTTTCATCC--TTCCCCTTTCTGGAACAGCTGCAGCTGCTGGAGCTCG 232
MMUL            CGGACAGTCACTGTTTCATCC--TTCCCCTTTCTGGAACAGCTGCAGCTGCTGGAGCTCG 232
CTO             CGGACAGTCACTGTTTCATCC--TTCCCCTTTCTGGAACAGCTGCAGCTGCTGGAGCTCG 232
CJA             AGGACAGTCACTGCTTCATCC--TTCCCCTTCCTGGAGCAGCTGCAGCTGCTGGAGCTCG 232
TSY             AGGAAAGTCACTTCCTCATCA--TTCCCCTACCTGGAGCAGCTGCAGCTGCTAGAGCTGG 232
CHI             AGGACAGTCAGAACCACATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
OAR             AGGACAGTCAGAACCACATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
RRU             AGGACAGTCAGAACTACATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
OGA             AGGACAGTCAGAACYACATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
OLE             AGGACAGTCAGAACCACATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
ODA             AGGACAGTCAGAACCACATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU1            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU2            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU3            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU4            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU5            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU8            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU9            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU12           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU14           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU16           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU18           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BCA             AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU7            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU11           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU13           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU17           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU15           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU6            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBU10           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
SCA1            ATGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGTTGCTGGAGCTGG 232
SCA2            AAGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGTTGCTGGAGCTGG 232
BTA10           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA16           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA7            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA3            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA1            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA2            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA4            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA6            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA9            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA15           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA12           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA11           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA14           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BGR             AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA5            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA13           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA8            AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA17           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BTA18           AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BBI             AGGACAGTCACAACCGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
BJA             AGGACAGTCACAACCRCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
TIM             AGGACAGTCACAAACGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
TST             AGGACAGTCACAAACGCATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
GCA             AGGACAGTCACAACCACATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
OHE             AGAACAGTCACARCCACATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
OVI             AGAACAGTCACAGCCACATCC--TTCCCCTTCCTGGAGCAGTTGCAGCTGCTGGAGCTGG 232
SSC             AGGACGGTCACAGCTGGTTCC--TTCCCCTTCCTGGAGGGGCTGCAGCTGCTGGAGCTCG 229
PAL             AAGACAGTCACAGCCGCGTCT--TTCCCCTTCCTGGAGCGGCTGCAGCTGCTGGAGCTCG 232
AME             CGGACTGTCACAACCACGTCC--TTCCCCTTCCTGGAGCAGCTGCAGCTGCTGGAGCTCG 232
MPU             CGGACTGTGACAACCACGTCT--TTCCCCTTCCTGGAGCAGCTGCAGCTGCTGGAGCTTG 232
CLU             CGGGCCGTCAC--CCGCGCCTCGTTCCCCCTCCTGGAGCGGCTGCAGCTGCTGGAGCTGG 232
ETE             AGGACCATCACACCCACGTCC--TTCCCCTTCTTGGAGCAGCTGCAGCTGCTGGAACTTG 232
OPR             AGGACAGTCACCACCTCGTCC--TTCCCCCTCCTGGAGCAGTTGCAGCTGCTGGAGCTTG 232
MMU             AGTATGGTGGTTGCCACATCA--TTTCCACTCCTGGAGCGGCTCCAGTTGCTGGAGCTGG 235
MDO             AGGGTAGTTAATGCCACTTCA--TTCCCTCTATTGGATCAGCTTCAATTTCTAGAGCTAG 232
```

```
SHA           AGGATGATTAATGCTACTTCA--TTCCCTCTATTGGAGATGCTCCAATTGCTACAGCTAG 229
OAN           AGGACAGTGAACGCCACCTCC--TTCCCTCTGCTGGAGAAGCTGGAGCTGCTGGAGCTCG 232
GGA           AGACAAGTGACTGCAACTTCA--TTTCCACTGCTGGAGGATTTGTTCTTGTTGGAAATTG 232
GLA           AGACGAGTGACTGCAACTTCA--TTTCCACTGCTGGAGGATTTGTTCTTGTTGGAAATTG 232
MGA           AGACAAGTGACTGCAACTTCA--TTTCCACTGCTGGAGGATTTCTTCTTGTTGGAAATTG 232
PCO           AGACAAGTGACCACAACTTCA--TTTCCACTGCTGGAGAATTTGTTCTTGTTGGAAATTG 232
NME           AGACAAGTGACTGCAACTTCA--TTTCCACTGCTGGAGGATTTGTTCTTGTTGGAAATTG 232
TGU           AGACGAGTGAC------TTGG--TTTCCAGTGCTGGAGCACCTGTGGCTGTTGGAAATCG 226
                    *            ** **    ****   *    *  * * * *

PPA           GGAGCCAGTATAC---CCCCTTGACTATTGACAAGGAGGCCTTCAGAAACCTGCCCAACC 289
PTR           GGAGCCAGTATAC---CCCCTTGACTATTGACAAGGAGGCCTTCAGAAACCTGCCCAACC 289
HSA           GGAGCCAGTATAC---CCCCTTGACTATTGACAAGGAGGCCTTCAGAAACCTGCCCAACC 289
GGO           GGAGCCAGTATAC---CCCCTTGACTATTGACAAGGAGGCCTTCAGAAACCTGCCCAACC 289
PPY           GGAGCCAGTATAC---CCCCTTAAGTATTGACAAGGAGGCCTTCAGAAACCTGCCCAACC 289
MFA           GGAACCAGTATAC---CCCCTTGACTATTGACAAGGAGGCCTTCAGAAACCTGCCCAACC 289
MMUL          GGAACCAGTATAC---CCCCTTGACTATTGACAAGGAGGCCTTCAGAAACCTGCCCAACC 289
CTO           GGAACCAGTATAC---CCCCTTGACTATTGACAAGGAGGCCTTCAGAAACCTGCCCAACC 289
CJA           GGAGCCAGTATAC---CCCCTTGACCATTGACAAGGAGGCCTTCAGAAACCTGCCCAACC 289
TSY           GGACCCAGTGGAC---CCCCTTGACTATTGACAAGGAGGCCTTCATAAATCTGCCCAACC 289
CHI           GAACTCAGTTTAC---TTCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
OAR           GAACTCAGTTTAC---TTCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
RRU           GAACTCAGTTTAC---TTCCTTGACCATTAACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
OGA           GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
OLE           GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
ODA           GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU1          GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU2          GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU3          GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU4          GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU5          GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU8          GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU9          GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU12         GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU14         GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU16         GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU18         GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BCA           GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU7          GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU11         GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU13         GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU17         GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU15         GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU6          GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBU10         GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
SCA1          GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
SCA2          GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA10         GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA16         GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA7          GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA3          GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA1          GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA2          GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA4          GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA6          GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA9          GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA15         GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA12         GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA11         GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA14         GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BGR           GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA5          GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA13         GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA8          GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA17         GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BTA18         GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
BBI           GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
```

```
BJA               GAACTCAGTTTAC---CCCCTTGACAATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
TIM               GAACTCAGTTTAC---CCCCTTGACCATTTATGGAGAAGCCTTCCGAAACCTGCCCAATC 289
TST               GAACTCAGTTTAC---CCCCTTGACCATTTATGGAGAAGCCTTCCGAAACCTGCCCAATC 289
GCA               GAACTCAGTTTAC---CCCCTTGACCATTTACAGAGAAGCCTTCCGAAACCTGCCCAATC 289
OHE               GAACTCAGTTTAC---CCCCTTGACCATTTCCAGAGAAGCCTTCCGAAACCTGCCCAATC 289
OVI               GAACTCAGTTTAC---CCCCTTGACCATTTCCAGAGAAGCCTTCCGAAACCTGCCCAATC 289
SSC               GGACTCAGTTGAC---TCCCTTGAGCATTGACAGGGAAGCCTTCAGGAACCTGCCCAATC 286
PAL               GAACTCAGTTTTC---ATCCTTAACTATTGACAAAGAGGCGTTCAGAAACCTGCCCAATC 289
AME               GGACTCAGTTTAC---CCCCTTCACCATTGGCAGAGAAGCCTTCAGAAACCTGCCCAACC 289
MPU               GGACTCAGTTTAC---CCCCTTTACCATCGGCAGAGAGGCCTTCAGAAACCTGCCCAACC 289
CLU               GGACGCAGCAGAC---GCCCTTCAGCGTCGACAGAGAAGCCTTCAGGAACCTGCCCAACC 289
ETE               GGACCCAGTTTAC---ACCCTTGACTATTGAAAAAGAGGCCTTCCGAAACCTGCCCAACC 289
OPR               GGACCCAGTACAC---GCCCTTGACCATTGCCAAAGATGCCTTCAGGAACCTGCCCAACC 289
MMU               GGACCCAGTATGC---TAACTTGACCATTGGTCCAGGGGCTTTCAGAAACCTGCCCAATC 292
MDO               GAACTCAGAACAT---TCCTCTGACCATAGAGAGAGAAGCTTTCAGAAACCTGCCCAACC 289
SHA               GAACTCAGCACAC---TCCTCTAATCATTGAGAGAGAAGCTTTCAGAAACTTGCCCAACC 286
OAN               GGAACCAAACCGC---TGCTCTGGCCATCCACAGAGACGCTTTCAGGAACCTGCCCAATC 289
GGA               GAACACAACGCGTCTTTCCTCTTTACATAGGAAAAGAAGCTTTCAGGAACCTGCCAAATC 292
GLA               GAACACAACACATCTTTCCTCTTTACATAGGAAAAGAAGCTTTCAGGAACCTGCCAAATC 292
MGA               GAACACAACGTGTCTTTCCTCTTTACATAGGAAAAGAAGCTTTCAAGAACCTGCCAAATC 292
PCO               GAACACAACATGTCTTTCCTCTTTACATAGGAAAAGAAGCTTTCAGGAACTTGCCAAACC 292
NME               GAACACAACATGTCTTTCCTCTTTATATAGGAAAAGAAGCTTTCAGGAACCTGCCAAACC 292
TGU               GAACCCAGTTAGTCCATCCTGTTACCATAGGAAAAGGAGCGTTCAGGAACCTGCCAAACC 286
                  * *  **              *     *       *  ** ***   **  **** ** *

PPA               TTAGAATCTTGGACCTGGGAAGTAGTAAGATACACTTCTTGCATCCAGATGCTTTTCAGG 349
PTR               TTAGAATCTTGGACCTGGGAAGTAGTAAGATACACTTCTTGCATCCAGATGCTTTTCAGG 349
HSA               TTAGAATCTTGGACCTGGGAAGTAGTAAGATATACTTCTTGCATCCAGATGCTTTTCAGG 349
GGO               TTAGAATCTTGGACCTGGGAAGTAGTAAGATATACTTCTTGCATCCAGATGTTTTTCAGG 349
PPY               TTAGAATCCTGGACCTGGGAAGTAGTAAGATATACTTCTTGCATCCAGATGCTTTTCAGG 349
MFA               TTAGAATCTTGGACCTGGGAAGTAGTCAGATATACTTCTTGCATCCAGATGCTTTTCAGG 349
MMUL              TTAGAATCTTGGACCTGGGAAGTAGTCAGATATACTTCTTGCATCCAGATGCTTTTCAGG 349
CTO               TTAGAATCTTGGACCTGGGAAGTAGTCAGATATACTTCTTGCATCCAGATGCTTTTCAGG 349
CJA               TTAGAATCTTGGACCTGGGAGATAGTCAGATAAACTTCTTGCACCCAGATGCTTTTCAGG 349
TSY               TTAAAATCTTAGACCTGGGCAAAAGCCAGATCGACTTCTTGCATCTGGATGCTTTTCAGG 349
CHI               TCAGGATCCTGGACCTGGGTGGAAGTCAGATAGAATTCTTGCATCCAGACGCTTTTCAGG 349
OAR               TCAGGATCCTGGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGACGCTTTTCAGG 349
RRU               TCAGGATCCTGGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGACGCTTTTCAGG 349
OGA               TCAGGATCCTGGACCTGGGTGGAAGTCGGATAGACTTCTTGCATCCAGACGCTTTTCAGG 349
OLE               TCAGGATCCTGGACCTGGGTGGAAGTCGGATAGACTTCTTGCATCCAGACGCTTTTCAGG 349
ODA               TCAGGATCCTGGACCTGGGTGGAAGTCGGATAGACTTCTTGCATCCAGACGCTTTTCAGG 349
BBU1              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU2              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU3              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU4              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU5              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU8              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU9              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU12             TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU14             TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU16             TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU18             TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BCA               TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU7              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU11             TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU13             TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU17             TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU15             TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU6              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BBU10             TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
SCA1              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
SCA2              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA10             TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA16             TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA7              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA3              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA1              TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
```

```
BTA2            TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA4            TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA6            TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA9            TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA15           TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA12           TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA11           TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA14           TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BGR             TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA5            TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA13           TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA8            TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA17           TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BTA18           TCAGGATCCTAGACCTGGGTGGAAGTCAGATAAACTTCTTGCATCCAGATGCTTTTCAGG 349
BBI             TCAGGATCCTAGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
BJA             TCAGGATCCTAGACCTGGGTGGAAGTCAGATARACTTCTTGCATCCAGATGCTTTTCAGG 349
TIM             TCAGGATCCTGGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
TST             TCAGGATCCTGGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
GCA             TCAGGATCCTGGACCTGGGTGGAAGTCGGATAGACTTCTTGCATCCAGATGCTTTTCAGG 349
OHE             TCAGGATCCTGGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGACGCTTTTCAGG 349
OVI             TCAGGATCCTGGACCTGGGTGGAAGTCAGATAGACTTCTTGCATCCAGACGCTTTTCAGG 349
SSC             TCAGGATCTTGGACCTGGGCCATAGTCAGATCGCATTCTTGCACCCAGATGCATTTCAGG 346
PAL             TTCGAATCTTGGACTTGGGCAAAAGTCAGATAGACTTCTTGCATCCGGATGCTTTTCAGG 349
AME             TGAGGGTCTTGGACCTGGGCAATAGTCAGGTGGATTTCCTGCATCCCGATGCTTTTCAGG 349
MPU             TCAGGGTGTTGGACCTGGGCAAGAGTCAGGTGGATTTCCTGCATCCCGATGCTTTCCAGG 349
CLU             TGCGCACCCTGGACCTGGGCAACAGCCGGGTGGATTTCCTGCATCCCGACGCCTTCCAGG 349
ETE             TTTCCATCTTGGATCTGGGCAGAAGTCAGATCAGCTTCTTGCATCCCGATGCTTTCCAGG 349
OPR             TTAAGATCTTGGACTTGGGCCAAAATCAGTTCAGCGTCTTGCATCCAGATGCCTTCCAGG 349
MMU             TTAGGATCTTGGACTTGGGCCAAAGCCAGATCGAAGTCTTGAATCGAGATGCCTTTCAAG 352
MDO             TTTTAGTCTTGGATATTGGCAACACTAAAATTCAGTTTTTGCATACTGATGCTTTTCAAG 349
SHA             TTAGAATCTTGGATATTGGCTATAGTAAAATTCAATTTTTGCATATTGATGCTTTTCAAG 346
OAN             TCAAAGTCTTGGACTTGGGATACAATCCAAAGCTCTTCTTGGATCCCGACGCTTTCCGGG 349
GGA             TTCGTGTCTTGGACCTGGGGTTCAATAACATTCTTCTGCTGGATCTTGATTCTTTTGCGG 352
GLA             TTCGTGTCTTGGACCTGGGGTTCAATAACATTCTTCTGCTGGATCTTGATTCTTTTGCGG 352
MGA             TTCGTGTCTTGGACCTGGGGTTCAATAACATTCTTCTGCTGGATCTTGATTCTTTTGCGG 352
PCO             TTCGTGTCTTGGACCTGGGGTTCAATAACATTCTTCTGCTGGATCTTGATTCTTTTGCAG 352
NME             TTCGTGTCTTGGATCTGGGATTCAATAACATTCTTCTGCTGGATCTCGATTCTTTTGTGG 352
TGU             TTCGTATCTTAGACCTGGGAGACAATAAGATTCTTCAACTGGATCTTGATGCTTTTGTGG 346
                *        * **  * **    *               ** *    **    **    *

PPA             GACTGTTCCATCTGTTTGAACTTAGACTGTATTTCTGTGGTCTCTCTGATGCTGTATTAA 409
PTR             GACTGTTCCATCTGTTTGAACTTAGACTGTATTTCTGTGGTCTCTCTGATGCTGTATTAA 409
HSA             GACTGTTCCATCTGTTTGAACTTAGACTGTATTTCTGTGGTCTCTCTGATGCTGTATTGA 409
GGO             GACTGTTCCATCTGTTTGAACTTAGACTGTATTTCTGTGGTCTCTCTGATGCTGTATTAA 409
PPY             GACTGTTCCATCTGTTTGAACTTAGACTGTATTTCTGTGGTCTCTCTGATGCTGTATTAA 409
MFA             GACTGTTCCATCTGTTTGAACTTAGACTGTATTTCTGTGGTCTCTCCGATGCTGTATTGA 409
MMUL            GACTGTTCCATCTGTTTGAACTTAGACTGTATTTCTGTGGTCTCTCCGATGCTGTATTGA 409
CTO             GACTGTTCCATCTGTTTGAACTTAGACTGTATTTCTGTGGTCTCTCCGATGCTGTATTGA 409
CJA             GACTGTTCCACCTGTTTGAACTTAGACTGTTTTTCTGTGGTCTCTCCGATGCTATATTAA 409
TSY             GATTGTCCCATCTATTTGAACTTAGACTATTTGCCTGTGGTCTCTCTGATGCTGTATTAC 409
CHI             GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
OAR             GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
RRU             GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
OGA             GACTGCCCCACCTCACTGAACTGCGACTGTTTTTCTGTGGTCTCTCYGATGCTGTATTAA 409
OLE             GACTGCCTCACCTCACTGAACTGCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
ODA             GACTGCCTCACCTCACTGAACTGCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU1            GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU2            GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU3            GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU4            GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU5            GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU8            GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU9            GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU12           GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU14           GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU16           GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU18           GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
```

```
BCA             GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU7            GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU11           GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU13           GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU17           GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU15           GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BBU6            GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCYGATGCTGTATTAA 409
BBU10           GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCYGATGCTGTATTAA 409
SCA1            GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
SCA2            GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA10           GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA16           GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA7            GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA3            GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA1            GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA2            GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA4            GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA6            GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA9            GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA15           GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA12           GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA11           GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA14           GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BGR             GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA5            GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA13           GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA8            GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA17           GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BTA18           GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BBI             GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCGATGCTGTATTAA 409
BJA             GACTGCCCCACCTCACTAAACTTCGACTGTTTTCCTGTGGTCTCTCCRATGCTGTATTAA 409
TIM             GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
TST             GACTGCCCCACCTCACTGAACTTCGACTGTTTTTCTGTGGTCTCTCCGATGCTGTATTAA 409
GCA             GACTGCCCCACCTCATTGAACTTCGACTGTTTTTCTGTGGTCTCTCTGATGCTGTATTAA 409
OHE             GGCTGTCCCACCTCGCTGAACTTCGACTGTTTTACTGTGGTCTCTCTGATGCTGTATTAA 409
OVI             GGCTGTCCCACCTCGCTGAACTTCGACTGTTTTACTGTGGTCTCTCTGATGCTGTATTAA 409
SSC             AACTGCCCCATCTTTCTGAACTTCGACTGTTTTCCTGTGGTCTCTCTGATGCTATCTTAA 406
PAL             GACTGCCCCATCTGTTTGAACTTAGACTGTTCTCCTGCGGTCTCTCCGACGCTGTGTTAA 409
AME             GGCTGCCCCACCTGCTTGAACTAAGACTCCTCTACTGTGGTCTGTCCGATACTGTGTTAC 409
MPU             GGCTGCCCCGCCTGCAGGAACTTAGACTCTTCCACTGTGGTCTGTCTGATAAGACATTAA 409
CLU             GGCTGCCCCACCTGCAGGAACTCCGGCTGTTCGCCTGTGGCCTCTCCGACGTCGTGTTGA 409
ETE             GACTACCTCATCTTGTTGAACTTCGACTGTTTTACTGCGGCCTCTCGGACACTGTGTTGA 409
OPR             GGCTACCCCATCTGATTGAACTTCGGTTATTTGGCTGTGGTCTCTCTGATATTGTATTAA 409
MMU             GTCTGCCCCATCTCTTGGAACTTCGGCTGTTTTCCTGTGGACTCTCCAGTGCTGTGTTAA 412
MDO             GCTTGTTCAATTTGGTTCAACTACAGCTATATTATTGTCATCTCTCAGATTCCATTCTAA 409
SHA             GCTTGCCCAACTTGTTTGAATTACGTCTATTTTTCTGTAATCTCTCAGATTCAATTCTAA 406
OAN             GACTGTCCAATCTGCTCGAGCTACGTCTCTTCTACTGCGGCCTCTCGGAGTCCGTGCTCA 409
GGA             GTTTGCAACGTTTGACCATACTCCGTCTGTTTCAGAACAACCTTGGAGATTCCATCCTGG 412
GLA             GTTTGCAACGTTTGACCATACTCCGTCTGTTTCAGAACAACCTTGGAGATTCCATCCTGG 412
MGA             GTTTGCAACGTTTGACCATACTCCGTCTGTTTCAGAACAACCTTGGAGATTCCATCCTGG 412
PCO             GTTTGCAACGTTTGACCATACTCCGTCTGTTTCAAAACAACCTTGGAGATTCCATCCTGG 412
NME             GTTTGCAACGTTTGACCATCCTCCAGCTGTTTCGTAACAACCTTGGGGATTCCATCCTGG 412
TGU             GCTTGCCAAACCTGACTGTCCTCCGTCTGTTTCACAACTACCTTGGAGATTCCATCCTGG 406
                   *        *        *     *             **              *

PPA             AAGATGGTTATTTCAGAAATTTAAAGGCTTTAACTCGCTTGGATCTATCCAAAAATCAGA 469
PTR             AAGATGGTTATTTCAGAAATTTAAAGGCTTTAACTCGCTTGGATCTATCCAAAAATCAGA 469
HSA             AAGATGGTTATTTCAGAAATTTAAAGGCTTTAACTCGCTTGGATCTATCCAAAAATCAGA 469
GGO             AAGATGGTTATTTCAGAAATTTAAAGGCTTTAACTCGCTTGGATCTATCCAAAAATCAGA 469
PPY             AAGATGGTTATTTCAGAAATTTAAAGGCTTTAACTCGCTTGGATCTATCCAAAAATCAGA 469
MFA             AAAATGGTTATTTCAGAAATTTAAAGTCTTTAACTCGCTTGGATCTATCCAAAAATCAGA 469
MMUL            AAAATGGTTATTTCAGAAATTTAAAGTCTTTAACTCGCTTGGATCTATCCAAAAATCAGA 469
CTO             AAGATGGTTATTTCAGAAATTTAAAGTCTTTAACTCGCTTGGATCTATCCAAAAATCAGA 469
CJA             AAGATGGTTATTTCAGAAATTTAAAGTCTTTAACTCGCTTGGATCTATCCAAAAATCAGA 469
TSY             GAGATGGTTATTTCAGAAATTTAAACTCTTTAATTCGCTTGGATCTGTCAAAAAATCAGA 469
CHI             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCGCTTGGACCTATCCAAAAATCAAA 469
OAR             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCGCTTGGACCTATCCAAAAATCAAA 469
```

```
RRU               AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCGCTTGGACCTATCCAAAAATCAAA 469
OGA               AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCGCTTGGACCTATCCAAAAATCAAA 469
OLE               AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCGCTTGGACCTATCCAAAAATCAAA 469
ODA               AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCGCTTGGACCTATCCAAAAATCAAA 469
BBU1              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU2              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU3              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU4              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU5              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU8              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU9              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU12             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU14             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU16             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU18             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BCA               AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU7              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU11             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU13             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU17             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU15             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU6              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBU10             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
SCA1              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
SCA2              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA10             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA16             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA7              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA3              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA1              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA2              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA4              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA6              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA9              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA15             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA12             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA11             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA14             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BGR               TAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA5              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA13             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA8              AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA17             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BTA18             AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
BBI               AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATGAAA 469
BJA               AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
TIM               AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
TST               AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATAAAA 469
GCA               AAGATGGCTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATCAAA 469
OHE               AAGATGGTTATTTCAGAAATTTGGMATCTTTGACTCACTTGGACCTATCCAAAAATCAAA 469
OVI               AAGATGGTTATTTCAGAAATTTGGCATCTTTGACTCACTTGGACCTATCCAAAAATCAAA 469
SSC               AAGATGGTTATTTCAGAAATTTGGCATCTTTAACTCGCTTGGACCTATCCAAAAATCAGA 466
PAL               AAGATGGTTATTTCAGAAATTTGGGGTCTTTGTCTCGCCTGGACCTGTCCACAAATCAGA 469
AME               AAGATGGTTATTTCAGAAACTTAGGGTCTTTGTCTCGCCTGGACCTGTCCAAAAATGAGA 469
MPU               AAGATGGTTATTTCAGAAATTTGGAGTCTTTGTCTCGCCTGGACCTGTCCAAAAATCAGA 469
CLU               CAGACGGTTATTTCAGAAACCTGGGGGCTTTGTCGCGCCTGGACCTGTCCAAAAATCAGA 469
ETE               AAGGTGGCTATTTCAGAAATTTAGACTCCTTAGCTCACCTAGACCTATCAAAAAACCAGA 469
OPR               AAGATGGTTATTTCCGAAATTTAAATTCCTTGTCTCGCTTGGACCTATCCATCAATCAGA 469
MMU               GTGACGGTTACTTCAGAAATCTATATTCATTAGCTCGCTTAGACCTATCTGGCAACCAGA 472
MDO               AAGATGGCTATTTTAGAAATTTAAGTTCTTTAGCTATATTGGACCTATCAAGAAATGAAA 469
SHA               AAGATGGTTATTTTAGAAATTTAAGTTCTTTATCTGTGTTGGACCTATCTAAAAATGCCA 466
OAN               GGGACGGCCATTTGCGGGACTTACGTTCCTTGATCCGCTTGGATCTGTCCACAAACCGCA 469
GGA               AGGAGCGTTACTTTCAAGACTTGAGATCATTAGAAGAATTGGATCTTTCAGGAAACCAAA 472
GLA               AGGAGCGTTACTTTCAAGATTTGAGATCATTAGAAGAATTGGATCTTTCAGGAAACCAAA 472
MGA               AGGAGCGTTACTTTCAAGATTTGAGCTCATTAGAAGAATTGGATCTTTCAGGAAACCAAA 472
PCO               AGGAGCGTTACTTTCAAGATTTGAGCTCATTAGAAGAATTGGATCTTTCAGGAAACCAAA 472
NME               AGGAGCGTTACTTTCAAGATTTGAGCTCATTAGAAGAATTGAATCTTTCAGGAAACCAAA 472
```

```
TGU             AAGAATGTTACTTTCAAGATTTGAGGTCATTGGAAGAATTGGATCTTTCTGAGAATGAAA 466
                      *  * **     *  *     * **        *  * ** **    **    *

PPA             TTCGTAGCCTTTACCTTCATCCTTCATTTGGGAAGTTGAATTCCTTAAAGTCCATAGATT 529
PTR             TTCGTAGCCTTTACCTTCATCCTTCATTTGGGAAGTTGAATTCCTTAAAGTCCATAGATT 529
HSA             TTCGTAGCCTTTACCTTCATCCTTCATTTGGGAAGTTGAATTCCTTAAAGTCCATAGATT 529
GGO             TTCATAGCCTTTACCTTCATCCTTCATTTGGGAAGTTGAATTCCTTAAAGTCCATAGATT 529
PPY             TTCGTAGCCTTTACCTTCATCCTTCATTTGGGAAGTTGAATTCCTTAAAGTCCATAGATT 529
MFA             TTCGTAGCCTTTACCTTCATCCTTCATTTGGGAAGCTGAATTCCTTGAAGTCCATAGATT 529
MMUL            TTCGTAGCCTTTACCTTCATCCTTCATTTGGGAAGCTGAATTCCTTGAAGTCCATAGATT 529
CTO             TTCGTAGCCTTTACCTTCATCCTTCATTTGGGAAGCTGAATTCCTTGAAGTCCATAGATT 529
CJA             TTCGTAGCCTTTACCTTCATCCTTCATTTGGGGAGTTGAATTCCTTAGAGTCCATAGATT 529
TSY             TTCACAGCCTTTACCTTCATCCTTCATTTGGGGAACTGAATTCCTTAAAGTCCATAGATT 529
CHI             TTCAGAGTCTTCATCTTCATCCCTCTTTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
OAR             TTCAGAGTCTTCATCTTCATCCCTCTTTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
RRU             TTCAGAGTCTTTATCTTCATCCCTCTTTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
OGA             TTCAGAGTCTTTACCTTCATCCCTCATTCCAGGAACTGAATTCCTTGAAGTCCATTGATT 529
OLE             TTCAGAGTCTTTACCTTCATCCCTCATTCCAGGAACTGAATTCCTTGAAGTCCATTGATT 529
ODA             TTCAGAGTCTTTACCTTCATCCCTCATTCCAGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU1            TTCAAAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU2            TTCAAAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU3            TTCAAAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU4            TTCAAAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU5            TTCAAAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU8            TTCAAAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU9            TTCAAAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU12           TTCAAAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU14           TTCAAAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU16           TTCAAAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU18           TTCAAAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BCA             TTCAAAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU7            TTCARAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU11           TTCARAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU13           TTCARAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU17           TTCARAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU15           TTCARAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU6            TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
BBU10           TTCAAAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
SCA1            TTCAGAGTCTTTACCTTCATCCCTCATTCCAGGAACTGAATTCCTTGAAGTCCATTGATT 529
SCA2            TTCAGAGTCTTTACCTTCATCCCTCATTCCAGGAACTGAATTCCTTGAAGTCCATTGATT 529
BTA10           TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA16           TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA7            TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA3            TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA1            TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA2            TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA4            TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA6            TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA9            TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA15           TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA12           TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA11           TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA14           TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BGR             TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA5            TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA13           TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA8            YTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA17           TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGACT 529
BTA18           TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGARCTGAATTCCTTGAAGTCCATTGACT 529
BBI             TTCAGAGTCTTTACCTTCATCCCTCATTCCAGGAACTGAATTCCTTGAAGTCCATTGACT 529
BJA             TTCAGAGTCTTTACCTTCATCCCTCATTCCRGGAACTGAATTCCTTGAAGTCCATTGACT 529
TIM             TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
TST             TTCAGAGTCTTTACCTTCATCCTTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
GCA             TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCCATTGATT 529
OHE             TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCTATTGATT 529
OVI             TTCAGAGTCTTTACCTTCATCCCTCATTCCGGGAACTGAATTCCTTGAAGTCTATTGATT 529
SSC             TTCAGAGTCTTCACCTTCATCCTTCATTCCAGGAACTGAATTCCTTGAAGGCCATTGATC 526
```

```
PAL             TTCGCAGCCTTTCCCCCCATCCTTCGTTCAGGGAATTGAATTCCTTGAAGTCCATCGATT 529
AME             TTCGTAGCCTTAAGCTTCATCCTTCATTCTGGGAATTGAATTCCCTGAAGTCCATTGATT 529
MPU             TTCAAAGCCTTAACCTTCACCCTTCATTCTGGGAATTAAATTCCCTGAAGTCCATTGATT 529
CLU             TTGGGAGCCTCGAGCTTCACGCCTCCTTCCGGGAGCTGGGTTCCCTGAGGTCCGTGGACT 529
ETE             TTGGCAGCCTTCACCTCCATCCTTCCTTCCGAGAGTTGAATGCCTTGAAGTCCATAGACT 529
OPR             TTCAAAGTCTTTCCCTTCATGCTTCATTTGCAGACTTGAATTCCTTAAAGTCGGTAGACA 529
MMU             TTCACAGCCTCCGCCTCCATTCTTCATTCCGGGAACTGAATTCCTTAAGCGACGTAAATT 532
MDO             TAGAAAATCTCCAGCTTCATCCTTCTTTTGGAAATCTGGAATCCTTGAAATCCATAGATT 529
SHA             TCCAGAATATCCACCTTCATCCTTCTTTTGAAGATCTGAAATCTTTGGAATCTATAGACT 526
OAN             TCCAAAGTCTTCCCCTTCACGCCTCGTTTCGGGAGTTGAGATCTCTGGAGACCCTGGACC 529
GGA             TCACAAAACTTCATCCACACCCCTTATTTTATAATCTAACCATCTTGAAAGCTGTGAACC 532
GLA             TCACAAAACTTCATCCACACCCCTTATTTTATAATCTAACCATCTTGAAAGCTGTGGACC 532
MGA             TCACAAAACTTCATCCACACCCCTTATTTTATAATCTAACCATCTTGAAAGCTGTGAACC 532
PCO             TCACAAAACTTCATCCACACCCCTTATTTTATAATCTAACCATCTTAAAAGTTGTGAACC 532
NME             TCACAAAACTTCATCCACACCCCTTATTTTATAATCTAACCATCTTGAAAGCTGTGGACC 532
TGU             TCACAAAACTTCATCCCCATCCCTTATTTTATAATCTAACAGCCTTGAAAAGTGTGAACC 526
                     *   *    *  **  * *  **     *  *        *        *  *

PPA             TTTCCTCCAACCAAATATTCCTTGTATGTGAACATGAGCTCGAGCCCCTGCAAGGGAAAA 589
PTR             TTTCCTCCAACCAAATATTCCTTGTATGTGAACATGAGCTCGAGCCCCTGCAAGGGAAAA 589
HSA             TTTCCTCCAACCAAATATTCCTTGTATGTGAACATGAGCTCGAGCCCCTACAAGGGAAAA 589
GGO             TTTCCTCCAACCAAATATTCCTTGTATGTGAACATGAGCTCGAGCCCCTGCAAGGGAAAA 589
PPY             TTTCCTCCAACCAAATATTCCTTGTATGTGAACATGAGCTCGAGCCCCTGCAAGGGAAAA 589
MFA             TTTCCTCCAACCAAATATTTCTTGTATGTGAACATGAGCTCGAGCCCCTCCAAGGGAAAA 589
MMUL            TTTCCTCCAACCAAATATTTCTTGTATGTGAACATGAGCTCGAGCCCCTCCAAGGGAAAA 589
CTO             TTTCCTCCAACCAAATATTTCTTGTATGTGAACATGAGCTCGAGCCCCTCCAAGGGAAAA 589
CJA             TTTCCTCTAACCAAATATTCCTCGTATGTGAACATGAGCTCAGGCCCCTCCACGGGAAAA 589
TSY             TTTCCCTCAACCAGATATCCATTGTCTGTGAGAACAACCTAAAGCTCCTCCAAGGGAAAA 589
CHI             TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
OAR             TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
RRU             TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
OGA             TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
OLE             TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
ODA             TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU1            TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU2            TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU3            TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU4            TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU5            TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU8            TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU9            TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU12           TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU14           TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU16           TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU18           TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BCA             TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU7            TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU11           TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU13           TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU17           TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU15           TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU6            TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBU10           TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
SCA1            TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
SCA2            TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA10           TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA16           TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA7            TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA3            TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA1            TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA2            TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA4            TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA6            TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA9            TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA15           TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA12           TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA11           TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
```

```
BTA14             TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BGR               TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA5              TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA13             TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA8              TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA17             TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BTA18             TTTCCTTCAACRAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BBI               TTTCCTTCAACAAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
BJA               TTTCCTTCAACRAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
TIM               TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
TST               TTTCCCTCAACCAAATACCTATTGTATGTGAGCAGGAGTTCAAACCCCTCCAAGGGAAAA 589
GCA               TTTCCCTCAACCAAATACCTATTGTATGTGAGCAAGAACTCAAACCCCTCCAAGGGAAAA 589
OHE               TTTCCCTCAACAATATATCTATTGTATGTGAGCACGAGCTCAAACCCCTCCAAGGGAAAA 589
OVI               TTTCCCTCAACAATATATCTATTGTATGTGAGCACGAGCTCAAACCCCTCCAAGGGAAAA 589
SSC               TGTCCCTCAACCAGATACCCCTTGTGTGCGAGCAGGGGCTCAAACCCCTCCAAGGGAAAA 586
PAL               TCTTCCTCAACCAAATACCCACAGTGTGTGAGCACGAGCTCAAGCCCCTCCGAGGGAAAA 589
AME               TTTCCCTCAACCAGATCCCCATCGTGTGTGAACACGAGCTCCAGCCGCTCCAAGGGAAAA 589
MPU               TTTCCCTCAACCAGATACCCGTCGTGTGTGAACACGAGCTTCAGCCGCTGCAAGGGAAAA 589
CLU               TTTCCCTCAACCGGATCCCGGCTGCGTGTGAGCAGGGGCTCAGGCCCCTGCAGGGCAAGG 589
ETE               TTTCCCTCAACCAAGTCGCTTCGGTATGCGAGAGGGAGCTCAAGCCCCTGCAAGGTAAGG 589
OPR               TCTCCCTCAATCAAATATTAGTTGTGTGTGAGAGTGAGCTCCAGCCCCTCCAGGGGAAAG 589
MMU               TTGCTTTCAACCAAATATTCACTATATGTGAAGATGAACTCGAGCCTCTGCAGGGCAAAA 592
MDO               TGTCCCTGAACCACATATCCCTCATATGTAAGAGAGATCTTGAGGTTCTCCAAGGGAAAA 589
SHA               TGTCTCAAAACCAAATATCCCATGTATGTGAAAGAGATCTTAAACTCCTCCAAGGGAAAA 586
OAN               TGTCAAAAAACCAGATCACCTCCGTGTGCGAAAGGGATCTCCAGAGCCTCTGGGGAAAAC 589
GGA               TGAAATTCAACAAGATATCCAACCTGTGTGAAAGTAATCTTACCAGCTTCCAAGGAAAAC 592
GLA               TGAAATTCAACAAGATATCCAACCTGTGTGAAAGTAATCTTACCAGCTTCCAAGGAAAAC 592
MGA               TGAAATTCAACAAGATATCCAACCTGTGTGAAAGTAATCTTACCAGCTTCCAAGGAAAAC 592
PCO               TGAAATTCAACAAGATATCCAACCTGTGTGAAAGTAATCTTACCAGCTTCCAAGGAAAAC 592
NME               TGAAATTCAACAAGATATCCAACCTGTGTGAAAGCAATCTTACCAGCTTCCAAGGAAAAC 592
TGU               TGAAAGACAACAAGATATCCAACTTTTGTCAAAGTAATCTTACCAGCTTCCAAGGAAAGC 586
                  *       **     *          **  *        *        *    ** **

PPA               CGCTCTCCTTTTTTAGCCTCGCAGCTAA-TAGCTTGTATAGCAGAGTCTCAGTGGACTGG 648
PTR               CGCTCTCCTTTTTTAGCCTCGCAGCTAA-TAGCTTGTATAGCAGAGTCTCAGTGGACTGG 648
HSA               CGCTCTCCTTTTTTAGCCTCGCAGCTAA-TAGCTTGTATAGCAGAGTCTCAGTGGACTGG 648
GGO               CGCTCTCCTTTTTTAGCCTCGCAGCTAA-TAGCTTGTATAGCAGAGTCTCAGTGGACTGG 648
PPY               CACTCTCCTTTTTTAGCCTCGCAGCTAA-TAACTTGTACAGCAGAGTCTCAGTGGACTGG 648
MFA               TGCTCTCCTTTTTCAGCCTCGCAGCTAA-TAACTTGTATAGCAGAGTCTCAGTGGACTGG 648
MMUL              TGCTCTCCTTTTTCAGCCTCGCAGCTAA-TAACTTGTATAGCAGAGTCTCAGTGGACTGG 648
CTO               TGCTCTCCTTTTTCAGCCTCGCAGCTAA-TAACTTGTATAGCAGAGTCTCAGTGGACTGG 648
CJA               CGCTCTCCTTCCTTAGCCTGGCGGCTAA-CAGCTTGTACAGCAGAGTCTCAGTGGACTGG 648
TSY               CACTCTCCTTTTTAAGCCTCGCAGCTAA-TAGCCTATATAGCAAAGTCTCCATGGACTGG 648
CHI               CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACTTGTACAGCAGGGTGTCAGTGGACTGG 648
OAR               CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACTTGTACAGCAGGGTGTCAGTGGACTGG 648
RRU               CACTCTCCTTCTTAAGCCTTGCTGATAA-CCATTTGTACAGCAGGGTCTCAGTGGACTGG 648
OGA               CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACTTGTACAGCAGGGTCTCAGTGGACTGG 648
OLE               CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACTTGTACAGCAGGGTCTCAGTGGACTGG 648
ODA               CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACTTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU1              CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU2              CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU3              CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU4              CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU5              CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU8              CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU9              CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU12             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU14             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU16             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU18             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BCA               CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU7              CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU11             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU13             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU17             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU15             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBU6              CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
```

```
BBU10           CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
SCA1            CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
SCA2            CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA10           CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA16           CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA7            CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA3            CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA1            CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA2            CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA4            CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA6            CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA9            CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA15           CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA12           CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA11           CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA14           CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BGR             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA5            CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA13           CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA8            CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA17           CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BTA18           CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGGGTCTCAGTGGACTGG 648
BBI             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
BJA             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCAGCTGTACAGCAGRGTCTCAGTGGACTGG 648
TIM             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
TST             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
GCA             CACTCTCCTTCTTAAGCCTTGCTGATAA-CCACCTGTACAGCAGGGTCTCAGTGGACTGG 648
OHE             CACTCTCCTTCTTAAGCCTTGCTGCTAA-CCACCTCTACAGCAKSGTCTCCGTGGACTGG 648
OVI             CACTCTCCTTCTTAAGCCTTGCTGCTAA-CCACCTCTACAGCAGCGTCTCCATGGACTGG 648
SSC             CGCTCTCCTTTTTAAGCCTTGCGGATAA-TAACCTGTACAGTAGGGTCTCGGTGGATTGG 645
PAL             CGCTCTCATTTTTGAGACTCGCTGCTAA-CAACCTGTACAGCAGGGTCTCGGTGGACTGG 648
AME             CCCTCTCCCTGTTCAACCTCGCTGCCAA-TCACCTGTACAGTAGGGTCTCCGTGGACTGG 648
MPU             CGCTCTCACTGTTAAACCTCGCCGCCAA-TCAGTTGTACAGCAGGGGCTCCATGGACTGG 648
CLU             CGCTCTCCCTTCTGAACCTCGCGGCCAA-TGGCCTGTACAGCCGGGCCCCCGTGGACTGG 648
ETE             TGCTCTCCTTCTTCAGCCTCGCATCTAA-CAACCTGTACAGCAGAATCTCAGTGGACTGG 648
OPR             AGTTCTCTTTCTTCAATCTGGCAAACAA-TAACCTGTACAGCAGAGTGCCCGTGGCCTGG 648
MMU             CACTGTCTTTCTTTGGCCTCA-AATTAACTAAGCTGTTCAGCAGAGTCTCTGTGGGCTGG 651
MDO             GATTCTCTTTGTTTAACCTTGCTTCCAA-TAACCTCTATAGTAAGGTCTCAGTTAACTGG 648
SHA             GATTTTCTTTGTTTAACCTTTCTTCCAA-TATCCTCTTTAGCAGGATCTCAGTCAACTGG 645
OAN             ACTTCTTCCTGTTGAACCTTGCCGACAA-CCAGCTGTTCAGCCGCAGGTCTGTCGACTGG 648
GGA             ACTTTTCATTCTTTAGCCTCAGTACTAA-CACTCTGTATAAGACAGATAAAATGATCTGG 651
GLA             ACTTTTCATTCTTTAGCCTCAGTACTAA-CACTCTGTATAAGACAGATAAAATGGTCTGG 651
MGA             ACTTTTCATTCTTCAGCCTCAGTTCTAA-CACTCTGTATAAGACAGATAAAATGGTCTGG 651
PCO             ACTTTTCATTTTTCAGCCTCAATTCTAA-CTCTTTGTATAAGACAGATAAAATGGTCTGG 651
NME             ACTTTTCATTTTTTAACCTCAGTTCTAA-CACTTTGTATAACACAGATAAAGTGGTCTGG 651
TGU             ACTTTTTATTTTTTAACCTCGGTTCTAA-TCAGCTGCACAAAACAGAAGATGTGGCCTGG 645
                   * *   *  *    **       **      *    *            *    ***

PPA             GGAAAATGTATGAACCCATTCAGAAACATGGTGCTGGAGATACTAGATGTTTCTGGAAAT 708
PTR             GGAAAATGTATGAACCCATTCAGAAACATGGTGCTGGAGATACTAGATGTTTCTGGAAAT 708
HSA             GGAAAATGTATGAACCCATTCAGAAACATGGTGCTGGAGATACTAGATGTTTCTGGAAAT 708
GGO             GGAAAATGTATGAACCCATTCAGAAACATGGTGCTGGAGATACTAGATGTTTCTGGAAAT 708
PPY             GGAAAATGTATGAACCCATTCAGAAACATGGTGCTGCAGACACTAGATGTTTCTGGAAAT 708
MFA             GGAAAATGTATGAACCCGTTCAGAAACATGGTGCTGGAGACACTAGATGTTTCTGGAAAT 708
MMUL            GGAAAATGTATGAACCCGTTCAGAAACATGGTGCTGGAGACACTAGATGTTTCTGGAAAT 708
CTO             GGAAAATGTATGAACCCGTTCAGAAACATGGTGCTGGAGACACTAGATGTTTCTGGAAAT 708
CJA             GGGAAATGTATGAACCCCTTCAGAAACATGGTGCTGGAGACTCTAGATGTTTCTGGAAAT 708
TSY             GGGAAATGTATGAACCCATTCAGAAACATGGTGCTGGAAACCTTAGATGTTTCTGGCAAT 708
CHI             AATAGGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
OAR             AAGAGGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
RRU             AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
OGA             AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
OLE             AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGAAAT 708
ODA             AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGAAAT 708
BBU1            AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU2            AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU3            AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
```

```
BBU4            AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU5            AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU8            AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU9            AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU12           AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU14           AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU16           AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU18           AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BCA             AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU7            AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU11           AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU13           AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU17           AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU15           AAGAAGTGTCTGAACCCATTCAGAAACATGGTYCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU6            AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBU10           AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
SCA1            AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
SCA2            AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA10           AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA16           AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA7            AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA3            AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA1            AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA2            AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA4            AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA6            AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA9            AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA15           AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA12           AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA11           AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA14           AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BGR             AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA5            AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA13           AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA8            AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA17           AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BTA18           AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BBI             AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
BJA             AACAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
TIM             AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACTCTAGATGTTTCTGGCAAT 708
TST             AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACTCTAGATGTTTCTGGCAAT 708
GCA             AAGAAGTGTCTGAACCCATTCAGAAATATGGTCCTGGAAACCCTAGATGTTTCTGGCAAT 708
OHE             ARGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACACTAGATGTTTCTGGCAAT 708
OVI             AAGAAGTGTCTGAACCCATTCAGAAACATGGTCCTGGAAACACTAGATGTTTCTGGCAAT 708
SSC             GGGAAGTGTATGAACCCTTTCAGAAACATGGCCTTGGAAATGCTAGATGTTTCTGGCAAT 705
PAL             GGGAGGTGCATGAACCCGTTCAGAGACGTGATCCTGGAAACCCTAGACGTTTCTGGCAAT 708
AME             GGCGCGTGCATGAACCCGTTCACAGACATGGTCCTGGAAACCCTGGACGTTTCTGGCAAT 708
MPU             GGCGCATGCATGAACCCATTCAAGAACATGGTCTTGGAGACCCTGGATGTTTCTGGCAAT 708
CLU             GGGCGGTGCGGGAACCCGTTCAGGAACGTGGTCCTGGAGACCCTGGACGTGTCTAACAAC 708
ETE             AGCAAGTGCATGAACCCATTCAAAAATATGGTCTTGGATACCCTCGATGTTTCTGACAAT 708
OPR             GAGACATGTCGGAATCCATTCAGAGACATGGTGCTGGAGACCTTGGACGTTTCGGGCAAT 708
MMU             GAGACATGCAGGAACCCCTTCAGAGGCGTGAGGCTAGAAACTCTAGATCTTTCTGAAAAT 711
MDO             AAAGAATGCATGAATCCTTTCAAAAATATGTCCTTTGAGATCTTAGATGTCTCAAGCAAT 708
SHA             GAAGAGTGCATGAATCCTTTCAAAAATATGTTCCTTGAGATCCTGGATGTCTCAGACAAT 705
OAN             GGAGCGTGTGGGAACCCGTTCAGGAACATCCTCCTCGACACCCTGGACGTTTCAGGGAAC 708
GGA             GCCAAATGCCCAAATCCTTTCAGAAATATTACATTTAACTCACTGGACGTTAGTGAGAAT 711
GLA             GCCAAATGCCCAAATCCTTTCAGAAATATTACATTTAACTCACTGGATGTTAGTGAGAAT 711
MGA             GCCAAATGCCCAAATCCTTTCAGAAATATTACATTTAACTCACTGGACGTTAGTGAGAAT 711
PCO             GCCAAATGCCCCAATCCTTTCAGAAATATTACATTTAACTCACTGGACGTTAGTGAGAAC 711
NME             GCCAAATGCCCAAATCCTTTCAGAAATATTACCTTTAATTCACTGGACGTTAGCGAGAAT 711
TGU             GCCAAGTGCCCCAATCCTTTCAAAAATATTACATTTAGCTCACTAGACCTTAGTGACAGT 705
                      **    ** ** ****      *     *        * **  *       *

PPA             GGCTGGACAGTGGACATCACAGGAAACTTTAGCAATGCCATCAGCAAAAGCCAGGCCTTC 768
PTR             GGCTGGACAGTGGACATCACAGGAAACTTTAGCAATGCCATCAGCAAAAGCCAGGCCTTC 768
HSA             GGCTGGACAGTGGACATCACAGGAAACTTTAGCAATGCCATCAGCAAAAGCCAGGCCTTC 768
GGO             GGCTGGACAGTGGACATCACAGGAAACTTTAGCAATGCCATCAGCAAAAGCCAGGCCTTC 768
```

```
PPY              GGCTGGACAGTGGACATCACAGGAAACTTTAGCAATGCCATCAGCAAAAGCCAGGCCTTC 768
MFA              GGCTGGACAGTGGATATCACAGGAAACTTTAGCAATGCCATCAGCAAAAGCCAGGCCTTC 768
MMUL             GGCTGGACAGTGGATATCACAGGAAACTTTAGCAATGCCATCAGCAAAAGCCAGGCCTTC 768
CTO              GACTGGACAGTGGATATCACAGGAAACTTTAGCAATGCCATCAGCAAAAGCCAGGCCTTC 768
CJA              GGCTGGACAGTGGACATCACAGGAAACTTCAGCAATGCCATCAGCGGAAGTCAGGCCTTC 768
TSY              GGCTGGACAGTGGACATCACAGGAAACTTCAGCAATGCCATTAGTGGAAGCCAGACTTCC 768
CHI              GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
OAR              GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
RRU              GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
OGA              GGCTGGGGGGTRGACATCATGAGAAACTTCAGCAGTGCCATCAATGGGAGCCAGATTTTC 768
OLE              GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAGTGCCATCAATGGGAGCCAGATTTTC 768
ODA              GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAGTGCCATCAATGGGAGCCAGATTTTC 768
BBU1             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU2             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU3             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU4             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU5             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU8             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU9             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU12            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU14            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU16            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU18            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BCA              GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU7             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU11            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU13            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU17            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU15            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU6             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBU10            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
SCA1             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
SCA2             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA10            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA16            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA7             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA3             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA1             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA2             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA4             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA6             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA9             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA15            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA12            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA11            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA14            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BGR              GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA5             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA13            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA8             GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA17            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BTA18            GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BBI              GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
BJA              GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
TIM              GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
TST              GGCTGGGGGGTGGACATCATGAGAAACTTCAGCAATGTCATCAATGRGAGCCAGATTTTC 768
GCA              GGCTGGGGGGTGGACGTCATGAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
OHE              GGCTGGGGGGTGGATGTCACAAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
OVI              GGCTGGGGGGTGGATGTCACAAGAAACTTCAGCAATGCCATCAATGGGAGCCAGATTTTC 768
SSC              GGCTGGACAGCGGACACCACAAGGAACTTCAGCCAGGCCGTCAATGGAAGCCAGATTTCC 765
PAL              GGCTGGACCGTGGACATCACAAGGAACTTTAGCAACGCCATCAACGGAAGCCAGGTTTTC 768
AME              GGCTGGACCGCGGACATCACAGGGAACTTCAGCAGGGCCATCAGCGGGAGCCGGATCTCC 768
MPU              GGCTGGACTGCAGACATCACAGGCAACTTCAGCAGGGCTGTCAGTGGGAGCCAGATCTCC 768
CLU              GGCTGGACCGCAGACGTCACGGGCAACGTCACCAGGGCCATCGGTGGGAGCCAGATCTCC 768
ETE              GGCTGGGCAGTGGACACCATGAGAAACTTTAGCAATGCCATCAATGGAAGCGAGATTTTC 768
OPR              GGCTGGACTGCAGACATCACTGGAAACTTCAGCCAGGCCATCAGTGGGAGCCAGACTTCC 768
MMU              GGCTGGACGGTGGACATCACAAGGAACTTCAGCAACATCATCCAGGGAAGCCAGATTTCC 771
```

```
MDO             GGCTGGACAGTAGATATTGTACGAGACTTTTGTCATGCCATCCAGGGAACCAGGATTTCT 768
SHA             GGCTGGACAGTAGATATCATCCAAAACTTCTCTCGTGCTACCAATGGAACCAAGATTCTT 765
OAN             GGCTGGTCTGCCGACATCACGCGAGACTTCTGTGCCGCCATCAACGGGACACGGGTGTCC 768
GGA             GGCTGGAGCACAGAGACAGTCCAGTACTTCTGCACAGCTATTAAGGGGACTCAAATCAAT 771
GLA             GGCTGGAGCACAGAGACAGTCCAGTACTTCTGCACAGCTATTAAGGGGACTCAAATCAAT 771
MGA             GGCTGGAGCACAGAGACAGTCCAATATTTCTGTACAGCTATTAAGGGGACTCAAATCAAC 771
PCO             GGCTGGAGCACAGAGACAGTCCAGTATTTCTGCACAGCTATTAAGGGGACTCAAATCAAT 771
NME             GGCTGGAACACGGAGACAGTCCAGTATTTCTGTACAGCCATTAAGGGTACTCAAATCAAT 771
TGU             GGCTGGAGCACAGAGAGAGTCCAGTATTTCTGCACAGCCATTGAAGGGACTCAAATAAGT 765
                * ****      **           *  *                   *

PPA             TCTTTGATTCTTGCCCACCACATCATGGGTGCCGGGTTTGGCTTCCATAACATCAAAGAT 828
PTR             TCTTTGATTCTTGCCCACCACATCATGGGTGCCGGGTTTGGCTTCCATAACATCAAAGAT 828
HSA             TCTTTGATTCTTGCCCACCACATCATGGGTGCCGGGTTTGGCTTCCATAACATCAAAGAT 828
GGO             TCTTTGATTCTTGCCCACCACATCATGGGTGCCGGGTTTGGCTTCCATAACATCAAAGAT 828
PPY             TCTTTGATTCTTGCCCACCACATCATGGGTGCTGGGTTTGGCTTCCATAACATCAAAGAT 828
MFA             TCTTTGATTCTTGCCCACCACATCATGGGTGCCGGGTTTGGCTTCCATAACATCAAAGAT 828
MMUL            TCTTTGATTCTTGCCCACCACATCATGGGTGCCGGGTTTGGCTTCCATAACATCAAAGAT 828
CTO             TCTTTGATTCTTGCCCACCACATCATGGGTGCCGGGTTTGGCTTCCATAACATCAAAGAT 828
CJA             TCTCTGACTCTTGCCTACCACATCATGGGTGCCACATTTGGCTTCCATAACATGAAAGAC 828
TSY             TCACTGATTCTTTCCTACCACATCATGGGTTCTGGATTTGGCTTCAATAACCTCAAAGAT 828
CHI             TCTTTGGTTCTTACCCATCACATTATGGGTTCTTCGTTTGGCTTCTCCAACCTGAAGGAT 828
OAR             TCTTTGGTTCTTACCCATCACATTATGGGTTCTTCGTTTGGCTTCTCCAACCTGAAGGAT 828
RRU             TCTTTGGTTCTTACCCATCACATTATGGGTTCTTCRTTTGGCTTCTCCAACCTGAAGGAT 828
OGA             TCTTTGGTTCTTACCCATCACATTATGGGTTCTTCGTTTGGCTTCTCCAACCTGAAGGAT 828
OLE             TCTTTGGTTCTTACCCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
ODA             TCTTTGGTTCTTACCCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU1            TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU2            TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU3            TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU4            TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU5            TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU8            TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU9            TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU12           TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU14           TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU16           TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU18           TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BCA             TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU7            TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU11           TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU13           TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU17           TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU15           TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU6            TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BBU10           TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
SCA1            TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
SCA2            TCTTTGGTTCTTACTCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA10           TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA16           TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA7            TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA3            TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA1            TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA2            TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA4            TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA6            TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA9            TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA15           TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA12           TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA11           TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA14           TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BGR             TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA5            TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA13           TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA8            TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA17           TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BTA18           TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
```

```
BBI             TCTTTGGTTCTTACTCGTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
BJA             TCTTTGGTTCTTACTCRTCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
TIM             TCTTTGGTTCTTACCCATCACATTATGGGTTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
TST             TCTTTGGTTCTTACCCATCATATTATGGGTTCTTCATTTGGCTTCTCTAACCTGAAGGAT 828
GCA             TCTTTGGTTCTTACCCATCATATTATGGGTTCTTCGTTTGGCTTCTCCAACCTGAAGGAT 828
OHE             TCTTTGGTTCTTACCCRTCACACTATGGGGTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
OVI             TCTTTGGTTCTTACCCGTCACACTATGGGGTCTTCATTTGGCTTCTCCAACCTGAAGGAT 828
SSC             TCCTTGGTTCTCGCCCACCACATTATGGGTTCTGGGTTTGGCTTCCATAACATCAAAGAT 825
PAL             TCCTTGGTTCTTGGCTACCACAATATGGGTTCTGGGTTTGGCTTCCACAACATCAAAGAT 828
AME             TCCCTGGTTCTGGCCCACCACATCATGGGGCCCGGGTTTGGCTTCCAGAACATCAGGGAC 828
MPU             TCCCTGGTGCTGGCCCACCATATTATGGGGCCCGGGTTTGGCTTCCAGAACATCAGGGAC 828
CLU             TCCTTGGTGCTCGCCCACCACATCATGGGGCAGGGGTTTGGCTTCCGGAACATCCGGGAC 828
ETE             TCTCTGGTTCTTTCCCACCACATCATGGGCTCAGGGTTTGGCTTCCATAACCTCAAGGAC 828
OPR             TCTCTGATTCTCGCCTACCACAATATGGGTGCTGGATTTGGCTTCAACAACATCAGAGAC 828
MMU             TCTTTGATTCTTAAACACCACATCATGGGTCCTGGCTTTGGCTTCCAGAACATCAGAGAT 831
MDO             TCTTTGCTTCTCAACTACCATATCATGGGTGGAGGGTTTGGTTTTCATAACCTAAAAGAA 828
SHA             TCTTTGTTTCTTAAAAACCATATTATGGGGGCAGGATTTGGTTTTCATAACATAAAGGAA 825
OAN             TCGCTGGTGCTCCGCCACCACATCATGGGCTCGGGATTTGGGTTTGATAACATCAAGGAC 828
GGA             TATTTATCATTTCGCTCTCATACAATGGGCTCAGGATTTGGCTTTAATAACTTAAAAAAT 831
GLA             TATTTATCATTTCGCTCTCATACAATGGGCTCAGGATTTGGCTTTAATAACTTAAAAAAT 831
MGA             TATTTATCATTTCGCCTTCATACAATGGGCTCAGGATTTGGCTTTAATAACTTAAAAAAT 831
PCO             TATTTATCATTTCGCTTTCATATAATGGGCTCAGGATTTGGCTTTAATAACTTAAAAAAT 831
NME             TATTTAACATTTCGCTCTCATACAATGGGCTCAGGATTTGGCTTTAATAACTTAAAAAAT 831
TGU             TCTTTAATATTTAGCTCTACTATAATGGGTTCAGGATTTGGCTTTAATAACTTTAAAAAT 825
                *   *     *          *  *****       ***** **    *** *     *

PPA             CCTGACCAGAACACATTTGCTGGCCTGGCCAGAAGTTCAGTGAGACACCTGGATCTTTCA 888
PTR             CCTGACCAGAACACATTTGCTGGCCTGGCCAGAAGTTCAGTGAGACACCTGGATCTTTCA 888
HSA             CCTGACCAGAACACATTTGCTGGCCTGGCCAGAAGTTCAGTGAGACACCTGGATCTTTCA 888
GGO             CCTGACCAGAGCACATTTGCTGGCCTGGCCAGAAGTTCAGTGAGACACCTGGATCTTTCA 888
PPY             CCTGACCAGAACACATTTGCTGGCCTGGCCAGAAGTTCAGTGAGACACTTGGATCTTTCA 888
MFA             CCTGACCAGAACACATTTGCTGGCCTGGCCAGAAGTTCAGTGAGACACCTGGACCTTTCA 888
MMUL            CCTGACCAGAACACATTTGCTGGCCTGGCCAGAAGTTCAGTGAGACACCTGGACCTTTCA 888
CTO             CCTGACCAGAACACATTTGCTGGCCTGGCCAGAAGTTCAGTGAGACACCTGGACCTTTCA 888
CJA             CCTGACCAGAGCACATTCGCCGGCCTGGCCAGATGTTCCGTGAGACTCCTGGATCTTTCA 888
TSY             CCTGACCAGAACACATTTGCTGGCCTGGCCCGAAACTCTGTGATACGTCTGGATCTTTCA 888
CHI             CCTGACCAGCACACCTTTGCTGGGCTAGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
OAR             CCTGACCAGCACACCTTTGCTGGGCTAGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
RRU             CCTGACCAGCACACCTTTGCTGGGCTAGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
OGA             CCTGACCAGCACACCTTTGCTGGGCTAGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
OLE             CCTGACCAGCACACCTTTGCTGGGCTAGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
ODA             CCTGACCAGCACACCTTTGCTGGGCTAGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU1            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU2            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU3            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU4            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU5            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU8            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU9            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU12           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU14           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU16           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU18           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BCA             CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU7            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU11           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU13           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU17           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU15           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU6            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBU10           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
SCA1            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
SCA2            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA10           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA16           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA7            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA3            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
```

```
BTA1            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA2            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA4            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA6            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA9            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA15           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA12           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA11           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA14           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BGR             CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA5            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA13           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA8            CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA17           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BTA18           CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
BBI             CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGTTCGATGATACAGCTGGACATTTCA 888
BJA             CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
TIM             CCTGACTACCTCACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
TST             CCTGACTACCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
GCA             CCTGACCAGCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
OHE             CCTGACCAGCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
OVI             CCTGACCAGCACACCTTTGCTGGGCTGGCCAGGAGCTCGATGATACAGCTGGACATTTCA 888
SSC             CCTGACCATCACACCTTTGCCAGCCTGGGCAGAAGCTCCCTGATACAGCTGGACCTTTCT 885
PAL             CCTGACCAGAGCACGTTTGCCGGCCTGGCCGGAAGCTCAGTGGCACAGCTGGACCTCTCC 888
AME             CCTGACCGGGACACGTTTGCCGGCCTGGCCGGGAGCGCGGTACTGCGGCTGGATCTGTCC 888
MPU             CCCAACCGGGACACGTTTGCAGGCCTGGCCAGGAGCACGCTGCTGTGGCTGGACCTGTCC 888
CLU             CCTGACCGGAGCACGTTCGCGGGGCTGGCCGGGAGCTCGGTGCTGCGGCTGGATCTGTCG 888
ETE             CCTGACCAGAGCACATTCGCTGGCCTGGCCAGGAGTTCATTGATCAAGCTCGACCTTTCA 888
OPR             CCTAACCAGAGCACATTTGCTGGCCTGGCCAGAAGCTCAGTGTTGAGTTTGGATCTGTCG 888
MMU             CCTGACCAGAGCACATTTGCCAGCCTGGCCAGAAGTTCGGTGCTGCAACTGGACCTTTCG 891
MDO             CCTGACCAAGACACATTTGCTGCACTGGGCATGAGTTCAGTGATAAAAATGGATATTTCC 888
SHA             CCTGACCAGGACACATTTGCTGCCCTGGGCATGAGTTCAATGATAAAAATGGATATTTCA 885
OAN             CCCAACAGCGACACCTTCTCAGGGCTCGAGAGAAGTTCGGCGGTTCAGCTGGACCTCTCA 888
GGA             CCAGATACTGATACATTTACAGGACTAGCAAGAAGTGATCTTCATTTGCTTGATATTTCC 891
GLA             CCAGATAATGATACATTTACAGGACTAGCAAGAAGTGATCTTCATTTGCTTGATATTTCC 891
MGA             CCAGATACTGATACATTTACAGGACTAGCAAGAAGTGATCTTCGTTTGCTTGATATTTCC 891
PCO             CCAGATAAGGATACATTTACAGGACTAGCAAGAAGTGATCTTCGTTTGCTTGATATTTCC 891
NME             CCAGATCAGGATACATTTACAGGACTAGCAAGAAGTGGTCTTCAGTTGCTTGATATTTCC 891
TGU             CCAGATGATTCTACTTTTGCAGGCCTAGGAAGAAGTAATCTTAGGTTCTTTGACATTTCT 885
                **  *       ** **  *    ** *                     * **  * **

PPA             CATGGGTTTGTCTTCTCCCTGAACTCACGAGTCTTTGAGACACTCAAGGATTTGAAGGTT 948
PTR             CATGGGTTTGTCTTCTCCCTGAACTCACGAGTCTTTGAGACACTCAAGGATTTGAAGGTT 948
HSA             CATGGGTTTGTCTTCTCCCTGAACTCACGAGTCTTTGAGACACTCAAGGATTTGAAGGTT 948
GGO             CATGGGTTTGTCTTCTCCCTGAACTCACGAGTCTTTGAGACACTCAAGGATTTGAAGGTT 948
PPY             CATGGGTTTATCTTCTCCCTGAACTCACGTGTCTTTGAGACACTCAAGGATTTGAAGGTT 948
MFA             CATGGGTTTATCTTCTCCCTGAACTCCCGAGTCTTTGAGACACTCCAGGATTTGCAGGTT 948
MMUL            CATGGGTTTATCTTCTCCCTGAACTCCCGAGTCTTTGAGACACTCCAGGATTTGCAGGTT 948
CTO             CATGGGTTTATCTTCTCCCTGAACTCACGAGTCTTTGAGACACTCCAGGATTTGCAGGTT 948
CJA             CATGGGTTTATCTTCTCCCTGAACTCCCGAGTCTTTGAGAGACTCAGGGATTTGAAGGTT 948
TSY             TATGGGTTTATCTTCTCCCTGAACCGTCGACTCTTTGAGACACTCAAGGACTTGAAGGTT 948
CHI             CATGGGTATATCTTCTCCCTGAACTCCGGAGTCTTTGAAACGCTCCAGGAGCTGAAGGTC 948
OAR             CATGGGTATATCTTCTCCCTGAACTCCAGAGTCTTTGAAACGCTCCAGGAGCTGAAGGTC 948
RRU             CATGGGTATATCTTCTCCCTGAACTCCGGAGTCTTTGAAACGCTCCAGGAGCTGAAGGTC 948
OGA             CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACRCTCCAGGAGCTGAAGGTC 948
OLE             CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGAYGCTCCAGGAGCTGAAGGTC 948
ODA             CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACGCTCCAGGAGCTGAAGGTC 948
BBU1            CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGAA 948
BBU2            CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGAA 948
BBU3            CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGAA 948
BBU4            CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGAA 948
BBU5            CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGAA 948
BBU8            CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGAA 948
BBU9            CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGAA 948
BBU12           CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGAA 948
BBU14           CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGAA 948
BBU16           CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGAA 948
```

```
BBU18                CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGAA 948
BCA                  CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGAA 948
BBU7                 CATGGGTATATCTTCTCCYTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGWM 948
BBU11                CATGGGTATATCTTCTCCYTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGWM 948
BBU13                CATGGGTATATCTTCTCCYTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGWM 948
BBU17                CATGGGTATATCTTCTCCYTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGWM 948
BBU15                CATGGGTATATCTTCTCCYTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGWM 948
BBU6                 CATGGGTATATCTTCTCCTTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BBU10                CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGAA 948
SCA1                 CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGTC 948
SCA2                 CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA10                CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA16                CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA7                 CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA3                 CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA1                 CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA2                 CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA4                 CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA6                 CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA9                 CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA15                CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA12                CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA11                CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA14                CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BGR                  CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA5                 CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA13                CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA8                 CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA17                CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BTA18                CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BBI                  CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
BJA                  CATGGGTATATCTTCTCCCTGAACTTCCGAATCTTTGAGACACTCCAGGAGCTGAAGGTC 948
TIM                  CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAAACACTCCAGGAGCTGAAGGTC 948
TST                  CATGGGTATATCTTCTCCCTGAACTTCCGAGTCTTTGAAACACTCCAGGAGCTGAAGGTC 948
GCA                  CATGGGTATATCTTCTCCCTGAATTTCCGAGTCTTTGAGACGCTCCAGGAGCTGAAGTTC 948
OHE                  CATGGGCATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAAGAGCTGAAGGTC 948
OVI                  CATGGGCATATCTTCTCCCTGAACTTCCGAGTCTTTGAGACACTCCAAGAGCTGAAGGTC 948
SSC                  CATGGGTTTATCTTCTCCCTGAACTTCCGACTCTTTGGGACCCTCAAGGAGCTGAAAGTT 945
PAL                  CACGGCTTCGTCTTCTCCCTGAACTCCCGACTCTTTGAGACCCTCGCGGAGCTGAAGGTT 948
AME                  CATGGCTTTATCTTCTCCCTGAACTTCCGACTCTTTGAGGCCCTCAAGGCCTTGAAGCTC 948
MPU                  TATGGCTTCATCTTCTCCCTGAACTTCCGAGTCTTTGAGGCCCTCAAGGACTTGAAGCTC 948
CLU                  CACGGCTTCGTCTTCTCCCTGAACGCCCGACTGTTCGAGGTGCTCGGGGACCTGAAGCTC 948
ETE                  CATGGGTTCATCTTCTCCCTCAACGTCCGGCTCTTTGAGACCCTCACCGAGTTGAAAGTT 948
OPR                  CACGGATTTATCTTCTCCCTGAACCGCAGACTCTTTGAGGCTCTTACAGCTTTGAAGGTT 948
MMU                  CACGGCTTTATCTTCTCCTTGAATCCTCGACTGTTTGGGACACTGAAGGATTTGAAGATG 951
MDO                  CATGGCTTTATCTTTTCCTTGAACTTTCATCTGTTTGAGACTCTCAGAGAGTTGAAAGTT 948
SHA                  CATGGCTTTATCTTCTCCTTGAATTCTCACCTGTTCGAGACCCTCAAAAAGTTGAAACTT 945
OAN                  CATGGCTTTATCTTTTCTCTCGGGGACCGGCTCTTTTGGGCCCTCAAAAAACTAAAAGTC 948
GGA                  AATGGATTCATTTTCTCTCTCAATTCTTTAATCTTTGAAAGTCTTCGTAATCTGGAATTT 951
GLA                  AATGGATTCATTTTCTCTCTCAATTCTTTAATCTTTGAAAGTCTTCGTAATCTGGAATTT 951
MGA                  AATGGATTCATTTTCTCTCTCAATTCTTTAATCTTTGAAAGTCTTCGTAATCTGGAATTT 951
PCO                  AATGGATTCATTTTCTCTCTCAATTCTTTAATCTTTAAAAGCCTTGGTAATCTGGAAGTT 951
NME                  AGAGGTTACATTTTCTCTCTCAATTCTTTAATCTTTAAAGGCCTTGGTAATCTGGAATTT 951
TGU                  CAGGGTTATGTTTTTCTCTCAATTCTTTAGTCTTTCAAAGTCTTGGCAATCTGGAATCA 945
                        **     * ** **  *           * **       **        *  *

PPA                  CTGAACCTTGCCTACAACAAGATAAATAAGATTGCAGATGAAGCATTTTACGGACTTGAC 1008
PTR                  CTGAACCTTGCCTACAACAAGATAAATAAGATTGCAGATGAAGCATTTTACGGACTTGAC 1008
HSA                  CTGAACCTTGCCTACAACAAGATAAATAAGATTGCAGATGAAGCATTTTACGGACTTGAC 1008
GGO                  CTGAACCTTGCCTACAACAAGATAAATAAGATTGCAGATGAAGCATTTTACGGACTTGAC 1008
PPY                  CTGAACCTTGCCTACAACAAGATAAATAAGATTGCAGATGAAGCATTTTACGGACTTGAC 1008
MFA                  CTGAACCTTGCCTACAACAAGATAAATAAGATTGCGGTTGAAGCATTTTACGGACTTGAC 1008
MMUL                 CTGAACCTTGCCTACAACAAGATAAATAAGATTGCGGTTGAAGCATTTTACGGACTTGAC 1008
CTO                  CTGAACCTTGCCTACAACAAGATAAATAAGATTGCGGTTGAAGCATTTTACGGACTTGAC 1008
CJA                  CTGAACCTTGCCTACAACAAGATCAATAAGATTGCAGATGAAGCATTTGATGGACTTGAC 1008
TSY                  CTAAATCTTGCCCACAACAAGATAAACAAGATTGCACGTGAAGCATTTAATGGACTTGAC 1008
CHI                  CTAAACCTCGCCTACAACAAGATAAACAGTATTTTGAGGAATGCGTTTTATGGACTCGAC 1008
```

```
OAR             CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAACGCGTTTTATGGACTCGAC 1008
RRU             CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
OGA             CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCAAC 1008
OLE             CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCAAC 1008
ODA             CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCAAC 1008
BBU1            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BBU2            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BBU3            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BBU4            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BBU5            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BBU8            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BBU9            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BBU12           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BBU14           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BBU16           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BBU18           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BCA             CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BBU7            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCRAGGAATGCGTTTTATGGACTCGAC 1008
BBU11           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCRAGGAATGCGTTTTATGGACTCGAC 1008
BBU13           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCRAGGAATGCGTTTTATGGACTCGAC 1008
BBU17           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCRAGGAATGCGTTTTATGGACTCGAC 1008
BBU15           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCRAGGAATGCGTTTTATGGACTCGAC 1008
BBU6            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCAAGGAATGCGTTTTATGGACTCGAC 1008
BBU10           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
SCA1            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
SCA2            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA10           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA16           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA7            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA3            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA1            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA2            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA4            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA6            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA9            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA15           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA12           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA11           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA14           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BGR             CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCATTTTATGGACTCGAC 1008
BTA5            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA13           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA8            CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA17           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BTA18           CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BBI             CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
BJA             CTAAACCTCGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTYGAC 1008
TIM             CTAAACCTTGCCTACAACAAGATAAACAGTATTTCGAGGAATGCGTTTTATGGACTCGAC 1008
TST             CTAAACCTTGCCTACAACAAGATAAACAGTATTTCAAGGAATGCGTTTTATGGACTCGAC 1008
GCA             CTGAACCTCGCCTACAACAAGATAAACACTATTTCGAGGAATGCATTTTATGGACTTGAC 1008
OHE             CTTAACCTCGCCTGCAACAAGATAAACAGTATTTTGAGGAATGCATTTTATGGACTTGAC 1008
OVI             CTTAACCTCGCCTGCAACAAGATAAACAGTATTTTGAGGAATGCATTTTATGGACTTGAC 1008
SSC             CTGAACCTGGCCTTCAACAAGATAAACAAGATTGCAGACCAAGCATTTCATGGACTTGAC 1005
PAL             CTGAACGTTGCCCACAACAAGATAAACAAGATTGCACACGAGGCGTTTTACGGACTCGAC 1008
AME             CTGAACCTGGCCCACAACAAGATAAACAGGATTGCGGGAGAAGCATTTTATGGCCTTGAC 1008
MPU             CTGCAACTGGCCCACAACAAGATCAACAGGATTGCAGAAGAAGCGTTTTATGGCCTCGAC 1008
CLU             CTGGACCTCGCCCACAACAAGATCAACAGGATCGCGGGAGAAGCGTTTCACGGCCTCGGC 1008
ETE             CTAAACCTGGCCCACAACAAGATTAACAAAATTGTAGAAGGAGCCTTTTATGGACTTGAT 1008
OPR             TTGAACCTCGCCCACAACAAGATAAATAAGATTGCAAGTGAGGCCTTCTATGGACTTAAC 1008
MMU             CTGAACCTTGCCTTCAACAAGATAAACAAGATTGGAGAGAATGCCTTTTATGGGCTTGAC 1011
MDO             ATGAACCTTTCACATAACAAGGTAAACAAGATTGCTAATGGAGCATTTTATGGCCTTGAT 1008
SHA             ATAAACCTTTCATATAACAAAGTAAATCAGATTGCTAAAGAAGCATTTTATGGCCTTGAT 1005
OAN             CTAAGTCTCACCCACAACAAGATAAACAGGTTTGAAAAAGGAGCATTTTATGGCCTCGAC 1008
GGA             CTAAACCTTTTCAGAAACAAGATAAATCAAATCCAAAAGCAAGCATTTTTTGGCTTGGAA 1011
GLA             CTAAACCTTTTCAGAAACAAGATAAATCAAATCCAAAAGCAAGCATTTTTTGGCTTGGAA 1011
MGA             CTAAACCTTTTCAGAAACAAGATAAATCAAATCCAAAAGCAAGCATTTTTTGGCTTGGAA 1011
PCO             CTAAACCTTTTCAGAAACAAGGTAAATCAAATCCAAGAGCAAGCATTTTTTGGGTTGGAA 1011
```

```
NME             CTGAACCTTTTCAAAAACAAGGTAAATCAAATCCAAAAGCAAGCATTTTTTGGCTTGGAA 1011
TGU             CTGAACCTTTTCAAAAACAAGATAAATCAAATCCAAAGGCAAGCATTTTTTGGCTTGGGC 1005
                 *     *       *****  * **     *          ** **    **  *

PPA             AACCTCCAAGTTCTCAATTTGTCATATAACCTTCTGGGGGAACTTTACAGTTCGAATTTC 1068
PTR             AACCTCCAAGTTCTCAATTTGTCATATAACCTTCTGGGGGAACTTTACAGTTCGAATTTC 1068
HSA             AACCTCCAAGTTCTCAATTTGTCATATAACCTTCTGGGGGAACTTTACAGTTCGAATTTC 1068
GGO             AACCTCCAAGTTCTCAATTTGTCATATAACCTTCTGGGGGAACTTTACAGTTCGAATTTC 1068
PPY             AACCTCCAAGTTCTCAATTTGTCATATAACCTTCTGGGGGAACTTTACAGTTCGAATTTC 1068
MFA             AACCTCCAAGTTCTCAATTTGTCGTATAACCTTCTGGGGGAACTTTACAGTTCGAATTTC 1068
MMUL            AACCTCCAAGTTCTCAATTTGTCGTATAACCTTCTGGGGGAACTTTACAGTTCGAATTTC 1068
CTO             AACCTCCAAGTTCTCAATTTGTCGTATAACCTTCTGGGGGAACTTTACAGTTCGAATTTC 1068
CJA             AACCTCCAAGTTCTCAATTTGTCATATAACCTTATAGGGGAACTTTACAATTTGAATTTC 1068
TSY             AACCTCCAAGTTCTCAATATGTCACATAACCTTCTGGGGGAACTTTACAATTCAAATTTC 1068
CHI             AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATCATGATTTC 1068
OAR             AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATCATGATTTC 1068
RRU             AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATCATGATTTC 1068
OGA             AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATCATGATTTC 1068
OLE             AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATCATGATTTC 1068
ODA             AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATCATGATTTC 1068
BBU1            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU2            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU3            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU4            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU5            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU8            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU9            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU12           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU14           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU16           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU18           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BCA             AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU7            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU11           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU13           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU17           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU15           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU6            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBU10           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
SCA1            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
SCA2            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA10           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA16           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA7            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA3            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA1            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA2            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA4            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA6            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA9            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA15           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA12           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA11           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA14           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BGR             AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA5            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA13           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA8            AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA17           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BTA18           AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BBI             AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
BJA             AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
TIM             AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
TST             AACCTCCAAGTTCTCAATATATCATATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
GCA             AACCTTCAAGTTCTCAATATATCACATAACCTTCTTGGGGAATTATATAATTATGATTTC 1068
OHE             AACCTCCAAGTTCTCAACATATCACATAACCTTCTTGGGGAACTATATAATTATAATTTC 1068
OVI             AACCTCCAAGTTCTCAACATATCACATAACCTTCTTGGGGAACTATATAATTATAATTTC 1068
```

```
SSC             AACCTCCAGATTCTCAACATGTCATATAACCTTCTGGGGGAACTATATAATTCTAATTTT 1065
PAL             AGTCTGCAGGTTCTCAATATGTCACACAACCTTCTTGGGGAGCTTTACAATTTTAACTTC 1068
AME             AGCCTCCAGGTTCTTAACATGTCATATAACCTTCTGGGGGAGCTTTACAATTCCGATTTC 1068
MPU             AGCCTCCAGGTTCTCAACATGTCCTACAACCTCCTGGGGGAGCTTTATGATTCTGATTTC 1068
CLU             AGCGTCCAGGTTCTCAACCTGTCGCACAATCTCCTGGGCGAGCTCTATGACTCTGACTTC 1068
ETE             AGACTCCAAGTTCTCAACCTGTCACATAACCTTCTAGGGGAACTTTATAACTCAAATTTC 1068
OPR             AAACTCCAGATTCTCAACATGTCGCATAACCTTCTGGGGGAGCTCTATAGTGCTGACTTT 1068
MMU             AGCCTCCAGGTTCTCAATCTATCCTATAATCTTTTGGGGGAACTCTATAATTCCAACTTC 1071
MDO             AATCTTCAGATTCTCAACCTGTCCTATAACCTTCTGGGAGAACTCTACCAATCTGATTTT 1068
SHA             AGTCTCCAAGTTCTCAATCTATCCTATAACCTACTAGGGGAACTATACAATTCTGATTTT 1065
OAN             ACTCTCCAAGTTCTCAACTTGTCATACAACCTGCTAGGTGAACTTTACAATTCCAATTTT 1068
GGA             AACCTAAAAATTCTCAATCTCTCAAGTAACCTTTTAGGTGAGTTGTACGATTATACTTTT 1071
GLA             AACCTAAAAATTCTCAATCTCTCAAGTAACCTTTTAGGTGAGTTGTACGATTATACTTTT 1071
MGA             AACCTAGAAATTCTCAATCTCTCAAGTAACCTTTTAGGTGAGTTGTACGATTATACTTTT 1071
PCO             AACCTAAAAATTCTCAATCTCTCAAGTAACCTTTTAGGTGAGTTGTACGACTATACTTTT 1071
NME             AATCTAAAAGTTCTCAATCTCTCAAGTAACCTTTTAGGTGAGTTGTACGATTATACTTTT 1071
TGU             AACCTAAAAATTCTCAATCTCTCAAGTAACCTTTTGGGTGAGTTGTACGATTATACTTTT 1065
                *   *  *  **** **  * **    ** **  * ** **  * **          **

PPA             TATGGACTACCTAAGGTAGCCTACATTGATTTGCAAAAGAATCACATTGGAATAATTCAA 1128
PTR             TATGGACTACCTAAGGTAGCCTACATTGATTTGCAAAAGAATCACATTGGAATAATTCAA 1128
HSA             TATGGACTACCTAAGGTAGCCTACATTGATTTGCAAAAGAATCACATTGCAATAATTCAA 1128
GGO             TATGGACTACCTAAAGTAGCCTACATTGATTTGCAAAAGAATCACATTGGAATAATTCAA 1128
PPY             TATGGACTACCTAAGGTAGCCTACATTGATTTGCAAAAGAATCACATTGGAATAATTCAA 1128
MFA             TATGGACTACCTAAGGTAGCCTACATTGATTTGCAAAAGAATCACATTGGAATAATTCAA 1128
MMUL            TATGGACTACCTAAGGTAGCCTACATTGATTTGCAAAAGAATCACATTGGAATAATTCAA 1128
CTO             TATGGACTACCTAAGGTAGCCTACATTGATTTGCAAAAGAATCACATTGGAATAATTCAA 1128
CJA             TATGGATTACCTAAGATAGCCAACATTGATTTGCAAAAGAATCACATTGGAATCATTCAG 1128
TSY             TATGGACTACCTAAGGTAGCCTATGTTGATCTGAAAAATAATCACATTGGGGTAATTCAA 1128
CHI             GATGGACTACCTAAGGTAGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
OAR             AATGGACTACCTAAGGTAGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
RRU             GATGGACTACCTAAGGTAGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
OGA             GATGGACTACCTAAGGTAGTCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
OLE             GATGGACTACCTAAGGTAGTCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
ODA             GATGGACTACCTAAGGTAGTCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU1            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU2            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU3            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU4            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU5            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU8            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU9            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU12           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU14           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU16           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU18           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BCA             GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU7            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU11           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU13           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU17           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU15           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU6            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBU10           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
SCA1            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
SCA2            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA10           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA16           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA7            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA3            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA1            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA2            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA4            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA6            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA9            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA15           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA12           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
```

```
BTA11           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA14           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BGR             GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA5            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA13           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA8            GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA17           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BTA18           GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BBI             GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
BJA             GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
TIM             GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
TST             GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
GCA             GATGGACTACCTAATGTGGCCTCTATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
OHE             GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
OVI             GATGGACTACCTAAGGTGGCCTATATTGACCTGCAGAAGAATCACATTGGGATCATTCAG 1128
SSC             GAAGGACTGCCTAAGCTCGCTTATATTGATCTGCAGAAGAATCACATTGGGATCATTCAG 1125
PAL             TACGGACTCGCTAACGTGGCCCACATCGACCTGCAGAGGAACCACATCGGGATCATTCAG 1128
AME             TACGGACTCCCTCAGGTAGCCTATATTGATCTTCAAAACAATCATATTGGGATCATTCAG 1128
MPU             TCCGGACTCCGTCAGGTAGCCTATATTGATCTCCAAAACAATCATATTGGGATCATTCAG 1128
CLU             TCGGGGCTCGCGGAGGTCGCCTACATTGACCTGCAGCACAATCACATCGGGATCATCCAG 1128
ETE             AATGGACTTCCAAGAGTGGCCTATGTCGACCTAAGGAAGAACCACATTGGGATCATCCAG 1128
OPR             GATGGCCTGTCTGAGCTCACCTACATCGATCTCCAAAAGAATCACATCGGCATCATCCAG 1128
MMU             TATGGGCTTCCTAGAGTAGCCTACGTTGACCTTCAAAGGAACCACATTGGGATCATTCAA 1131
MDO             GCTGGGCTGTCTAAAGTTGCTTATATTGATCTACAAAGAAATCATATTGGGATAATTGAA 1128
SHA             TACGGACTGCCTAATGTTGCTTATATTGATCTACAAAAAAACCATATTGGGGCAATTCAG 1125
OAN             GATGGCCTCCCTAACCTAAAGTATATTGATCTACAGCAAAATCACATTGGGGCAATTCAG 1128
GGA             GAGGGGCTACACAGTATAATGTATATTGATTTACAGCAAAATCATATTGGGATGATTGGT 1131
GLA             GAGGGGCTACACAGTATAATGTATATTGATTTACAGCAAAATCATATTGGGATGATTGGT 1131
MGA             GAGGGGCTACACAGTATAATGTATATTGATTTACAGCAAAATCATATTGGGATGATTGGT 1131
PCO             GAGGGGCTACACAGTATAATATATATTGATTTACAGCAAAATCATATTGGGATGATTGGT 1131
NME             GAGGGCCTACACAATGTAATGCATATTGATTTACAGCAAAATCATATTGGGATGATTGGT 1131
TGU             GAGGGTCTACATAGTGTAATGTATATTGATTTACAGCAAAATCATATTGGGATGATTGGT 1125
                   **  *        *        * **  *       ** ** ** *     **

PPA             GACCAAACATTCAAATTCCTGGAAAAATTACAGACCTTGGATCTCCGAGACAATGCTCTT 1188
PTR             GACCAAACATTCAAATTCCTGGAAAAATTACAGACCTTGGATCTCCGAGACAATGCTCTT 1188
HSA             GACCAAACATTCAAATTCCTGGAAAAATTACAGACCTTGGATCTCCGAGACAATGCTCTT 1188
GGO             GACCAAACATTCAAATTCCTGGAAAAATTACAGACCTTGGATCTCCGAGACAATGCTCTT 1188
PPY             GACCAAACTTTCAAATTCCTGGAAAAATTACAGACCTTGGATCTCCGAGACAATGCTCTT 1188
MFA             GACCAAACATTCAAATTCCTGGAAAACTTACAGACCTTGGATCTCCGAGACAATGCTCTT 1188
MMUL            GACCAAACATTCAAATTCCTGGAAAACTTACAGACCTTGGATCTCCGAGACAATGCTCTT 1188
CTO             GACCAAACATTCAAATTCCTGGAAAACTTACAGACCTTGGATCTCCGAGACAATGCTCTT 1188
CJA             GACCAAACATTCAAATTCCTGGAAAAATTACAGACCTTGGATCTCCGAGACAATGCCCTT 1188
TSY             GACCAAACTTTCAGAGTCCTGGAAAACTTAAGTACCTTGGATCTCCGGGACAACGCTCTT 1188
CHI             GACAAAACATTCAAATTCCTGGGGAAATTAAATACCCTGGACCTCCGGGATAATGCTCTT 1188
OAR             GACAAAACATTCAAATTCCTGGGGAAATTAAATACCCTGGACCTCCGGGATAATGCTCTT 1188
RRU             GACAAAACATTCAAATTCCTGGGGAAATTAAATACCCTGGACCTCCGGGATAATGCTCTT 1188
OGA             GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
OLE             GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
ODA             GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU1            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU2            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU3            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU4            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU5            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU8            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU9            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU12           GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU14           GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU16           GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU18           GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BCA             GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU7            GACAMAACATTCAAATTCCTGGGGAAATTRAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU11           GACAMAACATTCAAATTCCTGGGGAAATTRAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU13           GACAMAACATTCAAATTCCTGGGGAAATTRAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU17           GACAMAACATTCAAATTCCTGGGGAAATTRAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU15           GACAAAACATTCAAATTCCTGGGGAAATTRAATACCTTGGACCTCCGGGATAATGCTCTT 1188
```

```
BBU6            GACAMAACATTCAAATTCCTGGGGAAATTGAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBU10           GACAAAACATTCAAATTCCTGGGGAAATTRAATACCTTGGACCTCCGGGATAATGCTCTT 1188
SCA1            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
SCA2            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA10           GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA16           GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA7            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA3            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA1            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA2            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA4            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA6            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA9            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA15           GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA12           GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA11           GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA14           GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BGR             GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA5            GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA13           GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA8            GAYRAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA17           GAYRAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BTA18           GAYRAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BBI             GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
BJA             GACAAAACATTCAAATTCCTGGGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
TIM             GACAAAACATTCAAATTCCTGGGGAAATTAACTACCTTGGACCTCCGGGATAATGCTCTT 1188
TST             GACAAAACATTCAAATTCCTGGGGAAATTAACCACCTTGGACCTCCGGGATAATGCTCTT 1188
GCA             GACAAAACATTTAAATTCCTGTGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
OHE             GACAAAACATTCAAATTCCTGAGGAAATTAAATACCTTGGAYCTCCGGGATAATGCTCTT 1188
OVI             GACRAAACATTCAAATTCCTGAGGAAATTAAATACCTTGGACCTCCGGGATAATGCTCTT 1188
SSC             GACCAAACATTCAGGTTCCTAAAAAAATTAAATACCTTGGATCTCCGGGATAATGCTCTT 1185
PAL             GAAGAAACGTTCAGATTCCTGGAAAAGTTGAATACCTTGGACCTCCGAGACAATGCCCTC 1188
AME             GACCGGACCTTCAGGTTCCTGAAAACATTGCACACCTTGGATCTCCGGGACAATGCTCTT 1188
MPU             AGCCAGACCTTCAGGTTCCTGAAAACGTTACAGACCTTGGATCTGCGGGACAATGCTCTT 1188
CLU             GACCAGACGTTCAGATTCCTGGGGGCGCTTCGGACCCTGGATCTCCGCGACAACGCCCTC 1188
ETE             GACCAAACATTTAAGTCCCTGGGAAGTTTAAAGACCCTGGATCTCCGGGATAATGCTCTG 1188
OPR             ACCCGAACATTCCAATCCCTGGAAAAACTGAGTATGTTGGATCTCCGGGACAATGCGCTT 1188
MMU             GACCAAACATTCAGATTATTAAAAACGTTACAAACCTTAGATCTCCGTGACAATGCTCTT 1191
MDO             AAGCAGACATTCAAACACTTGAAAAATTTACAAACTTTAGACCTTCGTGACAATGCTATT 1188
SHA             GCACAGACGTTCAATCCCTTGAAAAATTTAAAAACTTTGGATCTTCGTGATAATGCTATT 1185
OAN             GACCAGACCTTCACCCACCTGAAAGAATTAAGAACCTTAGATCTCCGCGACAATGCTATT 1188
GGA             GAAAAATCTTTCAGTAACTTAGTAAATCTGAAAATAATTGATCTCCGAGACAATGCCATT 1191
GLA             GAAAAATCTTTCAGTAACTTAGTAAATCTGAAAATAATTGATCTCCGAGACAATGCCATT 1191
MGA             GAAAAATCTTTCAGTAACTTAGTAAATCTGAAAATAATTGATCTCCGAGACAATGCCATT 1191
PCO             CAAAAATCTTTCAGTAACTTAGTAAGTCTGAAAATAATTGATCTCCGAGACAATGCCTTA 1191
NME             GAAAAATCTTTCAGTAATTTACTAAGTCTGAAAATAATTGATCTCCGAGACAATGCCATT 1191
TGU             GGCAATTCATTCAGGAATTTAGTAAATCTGAAAATAATTGATCTCCGAGACAATGCCATT 1185
                       * **        *        *    *   * ** ** ** ** ** **  *

PPA             ACAACCATTCATTTTATTCCAAGCATACCTGATATCTTCTTGAGTGGCAATAAACTAGTG 1248
PTR             ACAACCATTCATTTTATTCCAAGCATACCTGATATCTTCTTGAGTGGCAATAAACTAGTG 1248
HSA             ACAACCATTCATTTTATTCCAAGCATACCCGATATCTTCTTGAGTGGCAATAAACTAGTG 1248
GGO             ACAACCATTCATTTTATTCCAAGCATACCCGATATCTTCTTGAGTGGCAATAAACTAGTG 1248
PPY             ACAACCATTCATTTTATTCCAAGCATACCTGATATCTTCTTGAGTGGCAATAAACTAGTG 1248
MFA             ACAACCATTCATTTTATTCCAAGCATACCTGATATCTTCTTGAGTGGCAATAAACTAGTG 1248
MMUL            ACAACCATTCATTTTATTCCAAGCATACCTGATATCTTCTTGAGTGGCAATAAACTAGTG 1248
CTO             ACAACCATTCATTTTATTCCAAGCATACCTGCTATCTTCTTAAGTGGCAATAAACTAGTG 1248
CJA             ACAACCATTTATTTTATTCCAAGCATACCTAATATCTTCTTGGGCGGAAATAAACTAGCA 1248
TSY             AAAACCATTAATTTTATTCCAAGCATATCTGATATCTTCTTGAGCAGCAATAAACTGGTG 1248
CHI             AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTGGGTGGCAATAAGCTGGTG 1248
OAR             AAAACAATTCATTTTCTTCCAAGCATTCCTAATATCTTCTTGGGTGGCAATAAGCTGGTG 1248
RRU             AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTGGGTGGCAATAAGCTGGTG 1248
OGA             AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTGGGTGGCAATAAGCTGGTG 1248
OLE             AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTGGGTGGCAATAAGCTGGTG 1248
ODA             AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTGGGTGGCAATAAGCTGGTG 1248
BBU1            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU2            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
```

```
BBU3            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU4            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU5            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU8            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU9            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU12           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU14           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU16           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU18           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BCA             AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU7            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU11           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU13           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU17           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU15           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU6            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBU10           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
SCA1            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
SCA2            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA10           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA16           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA7            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA3            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA1            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA2            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA4            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA6            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA9            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA15           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA12           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA11           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA14           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BGR             AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA5            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA13           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA8            AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA17           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BTA18           AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BBI             AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
BJA             AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGCAATAAGCTGATG 1248
TIM             AAAACAGTTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGTAATAAGCTGATG 1248
TST             AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTAAGTGGTAATAAGCTGATG 1248
GCA             AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTTTTGGGTGGCAATAAGCTGGTG 1248
OHE             AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTGGGTGGCAATAAGCTGGTG 1248
OVI             AAAACAATTTATTTTCTTCCAAGCATTCCTAATATCTTCTTGGGTGGCAATAAGCTGGTG 1248
SSC             AAAACAATTCAGTTTATTCCGAGCATACCTACTCTCTTCTTGGGCGGCAATAAACTGGTG 1245
PAL             AAAACCATTTATTTTATTCCCAGTATACCTAATATCTTTTTGGGTGGCAATAAACTGGTG 1248
AME             AAAACAATTTCTTTCCTGCCAAGCATAAATACTATCTTCTTGAGTAGCAATAAACTGGTG 1248
MPU             AAAACAATCTCTTTCCTGCCAAGCCTAGACACCATCTTCTTGGGTAGCAATAAGCTGGCG 1248
CLU             AAAACCGTTTCCTTCGTGCCCAGCATAGACACCATCTTCCTGGGCAACAACAAGCTGGAG 1248
ETE             GAAACCATCCATATTATTCCCAGCATACCTACTATCTACTTGGGTGGCAATAAGCTTGTG 1248
OPR             ACGACCATCTCTTCTCTTCCAAGCATTCCTACCCTCCTTTTGGCGAACAACAAACTAGCG 1248
MMU             AAGGCCATTGGTTTTATTCCAAGCATACAGATGGTCCTCCTGGGAGGCAATAAGCTGGTC 1251
MDO             AAAACAGTTTATTTTCTGCCAAGCGTACATACTGCCTTCCTAAGTGGCAATAAGTTGGTA 1248
SHA             AAAACAGTTGGTTTTCTTCCAAGCATAACTACTGTCTTCCTAAGTGGGAATAAATTAGTA 1245
OAN             AAAGAAATCCATTTTCTCCCAAGCATTGACAGTGCCTTTCTGGCTGGTAACAAACTGGTA 1248
GGA             AAAAAACTCCCTTCCTTCCCACATCTGACTTCTGCCTTTTTAGGTGACAATAAGCTGATG 1251
GLA             AAAAAACTCCCTTCCTTCCCACATCTGACTTCTGCCTTTTTAGGTGACAATAAGCTGATG 1251
MGA             AAAAAACTCCCTTCCTTCCCACATCTGACTACTGCCTTTTTAGGTGACAATAAGCTGATG 1251
PCO             AAAAAACTCCCTTCCTTTCCACATCTGACTACTGCCTTTTTAAGTGACAATAAGCTGATG 1251
NME             AAAAAACTCCCTTCCTTTCCACATCTGACTTCTGCCTTTTTAGGTGACAATAAGCTGATG 1251
TGU             AAAAGACTCCCCTCCTTTCCACATCTGACTTCTGCCTTTTTAGGTGACAATAAGCTAATG 1245
                       *        * **     *         *    *       ** **  *

PPA             ACTTT---GCCAAAGATCAACCTTACAGCGAACCTCATCTACTTATCAGAAAACAGGCTA 1305
PTR             ACTTT---GCCAAAGATCAACCTTACAGCGAACCTCATCTACTTATCAGAAAACAGGCTA 1305
HSA             ACTTT---GCCAAAGATCAACCTTACAGCGAACCTCATCCACTTATCAGAAAACAGGCTA 1305
```

```
GGO                 ACTTT---GCCAAAGATCAACCTTACAGCGAACCTCATCCACTTATCAGAAAACAGGCTA 1305
PPY                 ACTTT---GCCAAAGATCAACCTTACAGCCAACTTCATCCACTTATCAGAAAACAGGCTA 1305
MFA                 ACTTT---GTCAGAGATCAACCTTACAGCCAACTTCATCCACTTATCAGAAAACAGGCTA 1305
MMUL                ACTTT---GTCAGAGATCAACCTTACAGCCAACTTCATCCACTTATCAGAAAACAGGCTA 1305
CTO                 ACTTT---GTCAGAGATCAACCTTACAGCCAACTTCATCCACTTATCAGAAAACAGGCTA 1305
CJA                 ACTTT---GCCAAAGATCAACCTTACAGCCAACTTCATCCACTTATCAGAAAACAGGCTA 1305
TSY                 ACTTT---GCCAAACATCAGCCTTACAGCCAGCTTCATCCACTTATCAGAAAACAGGTTA 1305
CHI                 ACTTT---GCCAAACATCCCACTTACAGCCAATTTGATCCAATTATCAGAGAATAGGCTA 1305
OAR                 ACTTT---GCCAAACATCCCACTTACAGCCAATTTGATCCAATTATCAGAGAATAGGCTA 1305
RRU                 ACTTT---GCCAAACATCCCACTTACAGCCAATTTGATCCAATTATCAGAGAATAGGCTA 1305
OGA                 ACTTT---GCCAAACATCCCACTTACAGCCAATTTGATCCAATTATCAGAGAATAGGCTA 1305
OLE                 ACTTT---GCCAAACATCCCACTTACAGCCAATTTGATCCAATTATCAGAGAATAGGCTA 1305
ODA                 ACTTT---GCCAAACATCCCACTTACAGCCAATTTGATCCAATTATCAGAGAATAGGCTA 1305
BBU1                ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBU2                ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBU3                ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBU4                ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBU5                ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBU8                ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBU9                ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBU12               ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBU14               ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBU16               ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBU18               ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BCA                 ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBU7                ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCRATTATCAGAGAATAGGCTA 1305
BBU11               ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCRATTATCAGAGAATAGGCTA 1305
BBU13               ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCRATTATCAGAGAATAGGCTA 1305
BBU17               ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCRATTATCAGAGAATAGGCTA 1305
BBU15               ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBU6                ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBU10               ACTTT---GCCAAATATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
SCA1                ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
SCA2                ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA10               ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA16               ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA7                ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA3                ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA1                ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA2                ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA4                ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA6                ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA9                ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA15               ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA12               ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA11               ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA14               ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BGR                 ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA5                ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA13               ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA8                ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA17               ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BTA18               ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BBI                 ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
BJA                 ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
TIM                 ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
TST                 ACTTT---GCCAAACATCCCACTTACAGCCAATTTCATCCAATTATCAGAGAATAGGCTA 1305
GCA                 ACTTT---GCCAAACATCCCACTTAGAGCCAATTTCATCCACTTATCAGAGAATAGGCTA 1305
OHE                 ACTTT---GCCAAACATCCCACTTACAGCAAATTTCATCCAATTATCAGAGAATAGACTA 1305
OVI                 ACTTT---GCCAAACATCCCACTTACAGCAAATTTTCACCAATTATCAGAGAATAGACTA 1305
SSC                 ACTTT---GCCAAACATCAGGCTTACGGCCAACTTCATCCACTTATCAGAGAACAGGCTA 1302
PAL                 ACTTT---GCCAACCATCAGGTTCACAGCCAACTTCATCCACTTATCAGAGAACAGGCTA 1305
AME                 ACCTT---GCAGAACATGAGACTTAAAGCCAACTTCCTCCACTTATCAGAGAACAGGCTA 1305
MPU                 GCCTT---GCCGGACATGGAGCTTAAAGCCAGCTTCATCCACTTGTCAGAAAACAGGCTA 1305
CLU                 ACCGT---GTCCCACATGGACCTCACAGCCAGCTTCCTGGAGCTGTCGGACAACAGGCTG 1305
ETE                 AAGTT---GTCCCACATCAGCCTCGTGGCCGACATCATCCACTTAGCGGAGAACAGACTG 1305
OPR                 TCCTT---GTCAGACACTCACCTTACAGCCAAATTCCTCCAGTTAACAGAGAACAGATTA 1305
```

```
MMU             CATTT---GCCACACATCCACTTTACTGCCAACTTCCTAGAGTTATCTGAAAACAGGCTA 1308
MDO             CATATAGAAGAAAACATCAACATAACTGCCGGATTCCTTGATTTAGCAGAAAACAGATTG 1308
SHA             AGTTTTGAAAGGAG---AGGCATAACTGCTGAATTCCTTGATTTAGCAGAAAACAGGTTG 1302
OAN             CATCTGAAAGGCCGTATCAACT---CGGCGGAATTTCTACACTTGGCAGGAAACAGACTG 1305
GGA             TCTGT---AGCTCACACGGCAATAGTAGCAACACATATTGAATTAGAGAGAAACTGGCTC 1308
GLA             TCTGT---AGCTCACACGGCAATAGTAGCAACACATATTGAATTAGAGAGAAACTGGCTC 1308
MGA             TCTGT---AGCTCACACGGCAATAGCAGCAACACATATTGAATTAGAGAGAAATTGGCTC 1308
PCO             TCTGT---AGCTCACACAGCAATAGCAGCAACACATATTGAATTAGAGAGAAACTGGCTC 1308
NME             TCTGT---AGCTCACACAACAATAGCTGCAACACATATTGAATTAGAGAGAAATTGGCTA 1308
TGU             TCTAT---AGACAACATAGCAATAATTGCAACACACCTTGAATTAGAAAGAAATTGGTTG 1302
                    *                      **              *       **  *  *

PPA             GAAAATCTAGATATTCTCTACTTTCTCCTACGGGTACCTCATCTCCAGATTCTCATTTTA 1365
PTR             GAAAATCTAGATATTCTCTACTTTCTCCTACGGGTACCTCATCTCCGGATTCTCATTTTA 1365
HSA             GAAAATCTAGATATTCTCTACTTTCTCCTACGGGTACCTCATCTCCAGATTCTCATTTTA 1365
GGO             GAAAATCTAGATATTCTCTACTTTCTCCTACGGGTACCTCATCTCCAGATTCTCATTTTA 1365
PPY             GAAAATCTAGATATTCTCTACTTTCTCCTACGGGTACCTCATCTCCAGATTCTCATTTTA 1365
MFA             GAAAATCTAGATATTCTCTACTTTCTCCTACGGGTACCTCATCTCCAGATTCTCATTTTA 1365
MMUL            GAAAATCTAGATATTCTCTACTTTCTCCTACGGGTACCTCATCTCCAGATTCTCATTTTA 1365
CTO             GAAAATCTAGATATTCTCTACTTTCTCCTACGGGTACCTCATCTCCAGATTCTCATTTTA 1365
CJA             GAAAATCTAGATATTCTCTACTTTCTCCTAGAGGTTCCTCATCTCCAGATTCTCATTTTA 1365
TSY             GAACATTTGGATGTTCTGTACTTTCTTCTCCAAGTGCCTCGCCTCCAGATTCTCATTTTA 1365
CHI             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
OAR             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
RRU             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
OGA             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
OLE             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
ODA             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU1            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU2            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU3            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU4            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU5            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU8            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU9            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU12           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU14           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU16           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU18           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BCA             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU7            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU11           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU13           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU17           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU15           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU6            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBU10           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
SCA1            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
SCA2            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA10           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA16           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA7            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA3            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA1            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA2            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA4            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA6            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA9            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA15           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA12           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA11           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA14           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BGR             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA5            GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA13           GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA8            GAAAATCTGAATGATCTCYACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BTA17           GAAAATCTGAATGATCTCYACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
```

```
BTA18           GAAAATCTGAATGATCTCCACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BBI             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
BJA             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
TIM             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
TST             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
GCA             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTTATTTTA 1365
OHE             GAAAATCTGAATGATCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
OVI             GAAAATCTGAATGATCTCACTTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1365
SSC             GAAAATCTGGATAACCTCTACTTCCTTCTCCAGGTACCTCATCTCCAGATTCTCATTTTA 1362
PAL             GAAAGTCTGGATAATCTCTACTTCCTTCTCCAGGTGCCTCATCTCCAGATTCTCATTTTA 1365
AME             GAAGATCTGGACGATCTCTACTTCCTCCTCCGGGTCCCTGACCTCCAGGTCCTCATTCTG 1365
MPU             GAGGATCTGGATGATCTCTACTTCCTCCTCCAGGTCCCCAACCTCCAGGTCCTCATTCTG 1365
CLU             GAGGACCTGGGCGACCTCTACTCGCTCCTCCGGGTCCCTGCCCTGCAGGTCCTCATCCTC 1365
ETE             GAAAATCTAGCCGACCTCTACTTTCTTCTCCAAGTGCCTCACCTTCAGATTCTCATCCTC 1365
OPR             GAAAACCTGGATGAGCTCTACTTCCTCCTCCAGATACCCCAACTCCAGATTCTCATCTTG 1365
MMU             GAAAACCTGTCCGACCTCTACTTCCTCCTGCGAGTCCCCCAGCTCCAGTTTCTCATCTTG 1368
MDO             GCAAATCTAAATGATCTCTATATTCTCCTCCAGATTCCAGATCTGAAGTTCCTTATTTTA 1368
SHA             GAAACTCTGACAGATTTCTATACTCTTCTCCAGATTCCAGGTCTGAAGTTTCTCATTTTA 1362
OAN             GAAGATTTGGGAGATCTGTACCTCCTTCTCCAAATTCCAAATCTCCAGGTTCTCATTTTA 1365
GGA             GCAAACCTGGGTGACCTGTACGTTCTTTTCCAAGTTCCAGGTGTGCAGTATCTCCTCTTA 1368
GLA             GCAAACCTGGGTGACCTGTATGTTCTTTTCCAAGTTCCAGGTGTGCAGTATCTCCTCTTA 1368
MGA             GCAAACCTGGGTGACCTGTATGTTCTTTTCCAAGTTCCAGGTGTGCAGTATCTCTTCTTA 1368
PCO             GCAAATCTGGGTGACCTGTATGTTCTTTTCCAAGTTCCAGATATGCAGTATCTCTCCTTA 1368
NME             GCAAATCTGGGTGATCTGTATGTTCTTTTCCAAGTTCTGGATGTGCAGTATCTCTTCTTA 1368
TGU             GCAAACCTAGGTGACCTGTATTTTCTTTTCCAAATTCCAGATCTGCAATATATCTTCTTA 1362
                *      *        *       **  *     * *      *        *     *

PPA             AATCAAAATCGCTTATCCTCCTGTAGTGGAGATCAAACCCCTTCAGAGAATCCCAGCTTA 1425
PTR             AATCAAAATCGCTTATCCTCCTGTAGTGGAGATCAAACCCCTTCAGAGAATCCCAGCTTA 1425
HSA             AATCAAAATCGCTTCTCCTCCTGTAGTGGAGATCAAACCCCTTCAGAGAATCCCAGCTTA 1425
GGO             AATCAAAATCGCTTATCCTCCTGTAGTGGAGATCAAACCCCTTCAGAGAATCCCAGCTTA 1425
PPY             AATCAAAATCGCTTATCCTCCTGTAGTGGAGATCAAACCCCTTCAGAGAATCCCAGCTTA 1425
MFA             AATCAAAATCGCTTATCCTCTTGTAGTGGAGATCAAACCCCTTCAGAGAATCCCAGCTTA 1425
MMUL            AATCAAAATCGCTTATCCTCTTGTAGTGGAGCTCAAACCCCTTCAGAGAATCCCAGCTTA 1425
CTO             AATCGAAATCGCTTATCCTCCTGTAGTGGAGATCAAACACCTTCAGAGAATCCCAGCTTA 1425
CJA             AATCAAAACCGCTTATCCTCTTGTAACGGAGGTCAAACCCCTTCAGAGAATCCCAGCTTA 1425
TSY             AATCAAAATCGCTTATCCTTTTGTAGCCAAAGTCAGAGCACTTCAGAGAATCCAAGTTTG 1425
CHI             AATCAAAATCGCTTTTCCTTTTGTCCGCAAAACCATGCCCCTTCAAAGAATCCCAGCCTA 1425
OAR             AATCAAAATCGCTTTTCCTTTTGTCCACAAAACCATGCCCCTTCAGAGAATCCCAGCCTA 1425
RRU             AATCAAAATCGCTTTTCCTTTTGTCTGCAAAACCATGCCCCTTCAGAGAATCCCAGCCTA 1425
OGA             AATCAAAATCGCTTTTCTTTTTGTCAGCAAAACCATGCCCCTTCAGAGAATCCCAGCCTA 1425
OLE             AATCAAAATCGCTTTTCTTTTTGTCAGCAAAACCATGCCCCTTCAGAGAATCCCAGCCTA 1425
ODA             AATCAAAATCGCTTTTCTTTTTGTCAGCAAAACCATGCCCCTTCAGAGAATCCCAGCCTA 1425
BBU1            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU2            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU3            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU4            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU5            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU8            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU9            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU12           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU14           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU16           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU18           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BCA             AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU7            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU11           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU13           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU17           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU15           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU6            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBU10           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
SCA1            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
SCA2            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA10           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA16           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA7            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
```

```
BTA3            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA1            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA2            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA4            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA6            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA9            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA15           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA12           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA11           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA14           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BGR             AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA5            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA13           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA8            AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA17           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BTA18           AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BBI             AATCAAAATCGCTTTTCCTTTTGTTACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
BJA             AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATTCCAGCCTA 1425
TIM             AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATCCCAGCCTA 1425
TST             AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATCCCAGCCTA 1425
GCA             AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATCCCAGCCTA 1425
OHE             AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATCCCAGCCTA 1425
OVI             AATCAAAATCGCTTTTCCTTTTGTCACCAAAACCATGCCCCTTCAGAGAATCCCAGCCTA 1425
SSC             AATCAAAATCGCTTTTCCAATTGTAACCAGAGGCACGCGCCTTCAGAGAATCCCAGCTTG 1422
PAL             AATCAAAATCGCTCTTCCTCATGTAACCAAGGTCATGTCCATTCAGAGAGTCTCAGCTTA 1425
AME             AATCAAAATCGCTTTTCCTCTTGCAGCCGAGCTCACGGCCCTACAGGCAGCCGCAGCTTA 1425
MPU             AATCAAAACCGCTTTTCCTCTTGCAGCCGTGCTCGTGGCCCGGCAGGGAGCCTCAGCCTG 1425
CLU             AACCGCAACCGCCTGTCCGCGTGCCGTGGCGGACACGGCCCCACGGGCAGCGTCGGCCCA 1425
ETE             AACCAAAATCGTCTTTCCTCGTGCAGCCCGAGCCCTGCCCCCGCAGAGAGCCTCAGCCTA 1425
OPR             AATGAAAATCGCCTTTCTTCCTGTACGCAAAGTCACCCATTGACAGAGAATCTCAGCTTA 1425
MMU             AATCAGAATCGCCTTTCGTCATGCAAGGCAGCCCACACTCCCTCGGAGAACCCAAGCTTA 1428
MDO             AATAAAAATCGATTTTCCTTCTGTAACCAACAGTATGGTCCTTCAAAGAATCACACCTTA 1428
SHA             AATAAAAATCGATTTTCCATTTGCTACCAACACTATTCTTCTTCAAAGAACTATACCTTA 1422
OAN             AATCAAAATCGGTTTTCCTATTGTTATGAAAATTATCATTTCAAAGAGAACTTCAGCTTG 1425
GGA             AAACAGAATCGCTTCTCTTACTGTGTGAAACATGTTGATGCTATAGAAAATAACCAGTTG 1428
GLA             AAACAGAATCGCTTCTCTTACTGTGTGAAACATGTTGATGCTATAGAAAATAACCAGTTG 1428
MGA             AAACAGAATCGTTTCTCTTACTGTGTGAAACATGTTAATGCTATAGAAAATAGCCAGTTG 1428
PCO             AAACAGAATCGCTTCTCTTACTGTGAAAAACATGTTAATGCTATAGAAAATAACCAGTTG 1428
NME             AAACAGAATCGCTTCTCTTACTGTGTGAAAAGTGTTAATGCTATAGAAAATAACCAGTTA 1428
TGU             AAACAGAACCGGTTCTCTTACTGTAAGGAGAGTGCTAATGTTATAGAAAACAATCAGTTA 1422
                **    ** **    **    **                         *

PPA             GAACAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGAGCTCTGTTGG 1485
PTR             GAACAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGAGCTCTGTTGG 1485
HSA             GAACAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGAGCTCTGTTGG 1485
GGO             GAACGGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGAGCTCTGTTGG 1485
PPY             GAACAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGAGCTCTGTTGG 1485
MFA             GAACAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGAGCTCTGTTGG 1485
MMUL            GAACAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGAGCTCTGTTGG 1485
CTO             GAACAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTCAGCTCTGTTGG 1485
CJA             GAACAGCTTTTCCTTGGAGAAAATATGTTGCAACTGGCCTGGGAAACTGAGCTCTGCTGG 1485
TSY             GAACAACTTTTCCTTGGAGAAAATATGTTACAGCTTGCCTGGGAAACTGGACTGTGCTGG 1485
CHI             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACCGAGTCATGTTGG 1485
OAR             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACCAAGTCATGTTGG 1485
RRU             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACCGAGTCATGTTGG 1485
OGA             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGAGTCATGCTGG 1485
OLE             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGAGTCATGCTGG 1485
ODA             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGAGTCATGCTGG 1485
BBU1            GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU2            GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU3            GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU4            GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU5            GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU8            GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU9            GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU12           GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU14           GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
```

```
BBU16           GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU18           GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BCA             GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU7            GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU11           GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU13           GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU17           GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU15           GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU6            GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBU10           GAAAAGCTTTACCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
SCA1            GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
SCA2            GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA10           GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA16           GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA7            GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA3            GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA1            GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA2            GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA4            GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA6            GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA9            GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA15           GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA12           GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA11           GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA14           GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BGR             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA5            GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA13           GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA8            GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA17           GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BTA18           GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BBI             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
BJA             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAGCTTGCCTGGGAAACTGGGTCATGTTGG 1485
TIM             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
TST             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAACTGGGTCATGTTGG 1485
GCA             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAGCCGGCTCATGTTGG 1485
OHE             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAGCCGGGTCATGTTGG 1485
OVI             GAAAAGCTTTTCCTTGGAGAAAATATGTTGCAACTTGCCTGGGAAGCCGGGTCATGTTGG 1485
SSC             GAACAGCTTTTCCTCGGAGAAAATATGTTGCAACTTGCCTGGGAAGCCGGCTTCTGTTGG 1482
PAL             GAGAAGCTTTTCCTCGGAGAAAATATGTTGCAACTTGCCTGGGAGACCGGCTCCTGTTGG 1485
AME             GAAAAGCTTTTCCTTGGAGGAAACATGTTGCAGCTTGCCTGGGAAACCGGCTTCTGCTGG 1485
MPU             GAAATGCTTTTCCTCGGAAGAAACATGTTGCAGCTTGTCTGGGAAACCGGCTTCTGCTGG 1485
CLU             GAGAGGCTCTTCCTCGGGAGCAACATGCTGCAGCTGGCCTGGGAGACCGGGCGGTGCTGG 1485
ETE             GAACAGCTCTTCCTTGGAGAAAACATGCTGCAGCTTGCCTGGGAAACGGGGTTCTGTTGG 1485
OPR             GAACAACTTTTCCTTACCGGAAATATGTTGCAGCTGGCCTGGGAATCCGGGTGTGGCTGG 1485
MMU             GAACAGCTTTTCCTTACAGAGAATATGCTGCAGCTGGCCTGGGAGACCGGCCTCTGTTGG 1488
MDO             GAGCAGCTTTATCTTTCAGAAAATATGTTGCAACTTATCTGGGAAGCAGGAAAATGTTGG 1488
SHA             GAGAAGCTTTATCTTTCAGAAAACATGCTGGAACTTGTCTGGCAAACAGGATCATGTTGG 1482
OAN             ATGCAGCTTTTTCTCGGGGAAAATATGTTGCAACTTGTCTGGGAGTCAGGGTCGTGCTGG 1485
GGA             ATTTATATGGACCTAGGAGAAAACATGTTGCAGCTTGTGTGGGAGAGAGGTTTATGTTTG 1488
GLA             ATTTATATGGACCTAGGAGAAAACATGTTGCAGCTTGTGTGGGAGAGAGGTTTATGTTTG 1488
MGA             ATTTATATGGATCTAGGAGAAAACATGTTACAGCTTGTGTGGGAGAGAGGTTTATGTTTG 1488
PCO             ATTTATATGGATCTAGGAGAAAACATGTTACAGCTTGTGTGGGAGAGAGGTTTATGTTTG 1488
NME             ATTTATATGGATCTAGGAGAAAACATGTTACAGCTTGTGTGGGAGAGAGGTTTGTGTTTG 1488
TGU             GTATATTTGGATCTAGGTGAAAATATGTTACAGTTGGTGTGGGAGAGAGATTTATGTTTG 1482
                       *    **       ** *** *  *  *    *** *           * * *

PPA             GATG-TTTTTGAGGGACTT-TCTCATCTTCAAG-TTCTGTATTTGAATCATAACTATCTT 1542
PTR             GATG-TTTTTGAGGGACTT-TCTCATCTTCAAG-TTCTGTATTTGAATCATAACTATCTT 1542
HSA             GATG-TTTTTGAGGGACTT-TCTCATCTTCAAG-TTCTGTATTTGAATCATAACTATCTT 1542
GGO             GATG-TTTTTGAGGGACTT-TCTCATCTTCAAG-TTCTGTATTTGAATAATAACTATCTT 1542
PPY             GATG-TTTTTGAAGGACTG-TCTCATCTTCAAG-TTCTGTATTTGAATAATAACTATCTT 1542
MFA             GATG-TTTTTGAGGGACTT-TCTAATCTTCAAG-TTCTGTATTTGAATAATAACTATCTT 1542
MMUL            GATG-TTTTTGAGGGACTT-TCTAATCTTCAAG-TTCTGTATTTGAATAATAACTATCTT 1542
CTO             GATG-TTTTTGAGGGACTT-TCTAATCTTCAAG-TTCTGTATTTGAATAATAACTATCTT 1542
CJA             GATG-TTTTTGAGGGACTT-TCTCATCTGCAAG-TTCTGTATTTGAATAATAACTATCTT 1542
TSY             AATG-TTTTTAAGGGACTT-TCCCATCTCCAAG-TTCTGTATTTGAATAATAACTACCTT 1542
```

```
CHI              GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTGAATAAAAACTACCTG 1542
OAR              GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTGAATCAAAACTACCTG 1542
RRU              GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTGAATAAAAACTACCTG 1542
OGA              GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAG-TCCTCTATCTGAATAAAAACTACCTG 1542
OLE              GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAG-TCCTCTATCTGAATAAAAACTACCTG 1542
ODA              GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAG-TCCTCTATCTGAATAAAAACTACCTG 1542
BBU1             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU2             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU3             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU4             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU5             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU8             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU9             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU12            GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU14            GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU16            GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU18            GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BCA              GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU7             GATA-TTTTTAAGGGKCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU11            GATA-TTTTTAAGGGKCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU13            GATA-TTTTTAAGGGKCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU17            GATA-TTTTTAAGGGKCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU15            GATA-TTTTTAAGGGKCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU6             GATA-TTTTTAAGGGTCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBU10            GATA-TTTTTAAGGGKCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
SCA1             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
SCA2             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA10            GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA16            GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA7             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA3             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA1             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA2             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA4             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA6             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA9             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA15            GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA12            GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA11            GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA14            GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BGR              GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA5             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA13            GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA8             GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA17            GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BTA18            GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BBI              GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
BJA              GATA-TTTTTAAGGGGCTT-TCTCATCTYCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
TIM              GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAY-TCCTCTATCTAAATAAAAACTACCTG 1542
TST              GATA-TTTTTAAGGGGCTT-TCTCATCTCCAAC-TCCTCTATCTAAATAAAAACTACCTG 1542
GCA              GATG-TTTTTAAGGGGCTT-TCCCATCTCCAGC-TCCTCTATCTGAATAAAAACTACCTG 1542
OHE              GATG-TTTTTAAGGGGCTT-TCCCATCTCCAAA-TCCTCTATCTGAATAAAAACTACCTG 1542
OVI              GATG-TTTTTAAGGGGCTT-TCCCATCTCCAAA-TCCTCTATCTGAATAAAAACTACCTG 1542
SSC              GATG-TTTTTAAGGGGCTT-TCTCATCTCCAAG-TCCTGTATTTGAATAACAACTACCTG 1539
PAL              GATG-TTTTTAAGGGGCTT-TCCCGTCTCCAGG-TCCTATATTTGAATAATAACTACCTG 1542
AME              GATG-TGTTCAAGGGGCTC-TCCCGGCTCCAGA-TCCTTTATCTGAACAACAACTACTTG 1542
MPU              GATG-TGTTCAAGGGACTT-TCACGGCTCCGGG-TCCTGTATCTGAACAATAACTACCTG 1542
CLU              GACG-TGTTCCGGGGGCTG-CCCCGGCTCCGGG-TGCTGCACCTGAACCACAACTACCTG 1542
ETE              GATG-TTTTCAAGGGGCTG-CCTCACCTCCAGT-TTCTGTACCTGAACAACAACCACCTG 1542
OPR              GATC-TTTTCCAAGGGCTT-TCTCACCTACAAA-TTCTGTATCTGGATGATAACTATCTG 1542
MMU              GATG-TTTTTCAAGGCCTT-TCCCGCCTCCAGA-TTCTTTACCTGAGTAATAACTACCTT 1545
MDO              GATG-TGTTTAAAAGACTT-TCCCACCTTAAAA-TCCTCTTCCTCAATAATAATTACCTT 1545
SHA              AATA-TGTTCAAGGGACTT-TACCAGCTGAAAG-TTCTCTTCCTGAATAATAATTACCTC 1539
OAN              GATG-TTTTTAAGGGGCTT-TCTCATCTCAGAG-TTCTCTATCTGAATAGCAACTACCTC 1542
GGA              GATG-TGTTCAGGACACTG-TCTAAACTTCAGG-TTCTACACCTGAACAACAACTACCTT 1545
GLA              GATG-TGTTCAGGACACTG-TCTAAACTTCAGG-TTCTACACCTGAACAACAACTACCTT 1545
MGA              GATGGTGTTCAGGTCACTGGTCTAAACTTCAGGGTTCTACACCTGAACAACAACTACCTT 1548
```

```
PCO             GATG-TGTTCAGGACACTG-TCTAAACTTCAGA-TTCTATTCCTGAACAACAACTACCTT 1545
NME             GACG-TGTTCAGGACCCTG-TCCAAACTTCAGG-TTCTACACCTGAACAACAACTACCTT 1545
TGU             GATG-TGTTTGGGGCATTG-CCCAAACTTCAGG-TTCTACATCTGAATAACAACTACCTT 1539
                 *   * **        *        **      * **     *       **  *  *

PPA             AATTCCCTTCCACCAGGAGTATTTAGCCATCTGACTGCATTAAGGAGACTAAGGCTCAAC 1602
PTR             AATTCCCTTCCACCAGGAGTATTTAGCCATCTGACTGCATTAAGGAGACTAAGGCTCAAC 1602
HSA             AATTCCCTTCCACCAGGAGTATTTAGCCATCTGACTGCATTAAGGGGACTAAGCCTCAAC 1602
GGO             AATTCCCTTCCGCCAGGAGTATTTAGCCATCTGACTGCATTAAGGGGACTAAGCCTCAAC 1602
PPY             AATTCCCTTCCACCAGGAGTATTTAGCCATCTGACTGCATTAAGGGGACTAAGCCTCAAC 1602
MFA             AATTCCCTTCCACCAGGAGTATTTAAACATCTGACTGCATTAAAGGGACTAAGCCTCAAC 1602
MMUL            AATTCCCTTCCACCAGGAGTATTTAAACATCTGACTGCATTAAAGGGACTAAGCCTCAAC 1602
CTO             AATTCCCTTCCACCAGGAGTATTTAAACATCTGACTGCATTAAAGGGACTAAGCCTCAAC 1602
CJA             AATTTCCTTCCACCAGGAATATTTAGCCATCTGACTGCATTAAGGGGACTAAGCCTCAAC 1602
TSY             AATTTCCTCCCACCAGGAATATTTAGCAGTCTGATCGCATTAAGGGGACTGAGCCTCAAC 1602
CHI             AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAGA 1602
OAR             AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAGA 1602
RRU             AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
OGA             AATTTCCTTCCACCAGGAGTATTTCATCATCTGACGGCACTGAGGGGACTCAGCCTCAGG 1602
OLE             AATTTCCTTCCACCAGGAGTATTTCATCATCTGACGGCACTGAGGGGACTCAGCCTCAGG 1602
ODA             AATTTCCTTCCACCAGGAGTATTTCATCATCTGACGGCACTGAGGGGACTCAGCCTCAGG 1602
BBU1            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU2            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU3            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU4            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU5            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU8            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU9            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU12           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU14           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU16           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU18           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BCA             AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU7            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU11           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU13           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU17           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU15           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU6            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBU10           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
SCA1            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
SCA2            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA10           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA16           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA7            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA3            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA1            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA2            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA4            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA6            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA9            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA15           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA12           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA11           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA14           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BGR             AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA5            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA13           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA8            AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA17           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BTA18           AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BBI             AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
BJA             AATTTCCTTCCACCAAGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
TIM             AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
TST             AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
GCA             AATTTCCTTCCACCAGGAGTATTTCGTCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
OHE             AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
```

```
OVI             AATTTCCTTCCACCAGGAGTATTTCATCATCTGACTGCACTGAGGGGACTCAGCCTCAAA 1602
SSC             AATTTCCTTCCACCAGGAGTCTTTCGCCATCTGACTGCACTGAGGGGACTCAGCCTCAGC 1599
PAL             ACTTTTCTCCCGCCAGGAGTATTTAGCGATCTGACTGCCTTAAGGGGACTCAGCCTCAAC 1602
AME             ACCTTCCTCCCGCCGGGGGCACTTAGTGATCTGACTGCTCTGAGGGGCCTCGACCTCAAC 1602
MPU             ACCTTCATCCCGCCGGGGGCCCTTGGCGATCTGAGTGCGCTGAGGGGTCTCGACCTCAGC 1602
CLU             GCCGCCCTCCCGCCGGGGCTGCTGCGGGACCTCACGGCGCTGAGGGGCCTCGACCTGAGC 1602
ETE             AGTTTCCTGCCCCCAGGGGTGTTCAGTGGCCTGGCCGCTCTGAGAGAACTGTACCTCAAC 1602
OPR             AATTTCCTTCCACCTGGACTGTTTAGCAACCTGACTGCCTTGAAGATCCTTAACCTCAGC 1602
MMU             AATTTCCTTCCACCTGGGATATTTAACGACCTGGTTGCATTACGGATGCTTAGTCTTAGT 1605
MDO             AATTTCCTTCCACCTGATGTTTTCAGTGATTTGACTGCATTACAAATCCTTAGCCTGGAT 1605
SHA             AGTTTCCTTCCACCTGATGTTTTCAGTGATCTGACTGCATTACAAATCCTTAGCCTGCAT 1599
OAN             AGTTTCCTTCCACCGGGTGTTTTCAGTAACTTGAAATCACTTCAGATCCTTAGCCTGAAT 1602
GGA             AGTGCTCTTCCACAGGAGATTTTTAATGGTCTAACATCTCTAAAAAGACTTAATCTAGCT 1605
GLA             AGTGCTCTTCCACAGGAGATTTTTAATGGTCTAACATCTCTAAAAAGACTTAATCTAGCT 1605
MGA             AGTGCTCTTCCACAGGAGATTTTTAATGGTCTAACATCTCTAAAAAGACTTAATCTAGCT 1608
PCO             AGTGCTCTTCCACAGGAGATTTTTAGTGGTCTAACATCTCTCAAAATACTTAATCTAGCC 1605
NME             AGTGCTCTTCCACAGGAGATTTTTAGTGGTCTAACATCTCTAAAAAGACTTAATCTAGCT 1605
TGU             AGTGCTCTTCCACAGGAGATTTTCAGAGGTCTAACATCTCTTAAAAAACTTAACCTGGCT 1599
                       * ** *         *        *     *  *       **    **

PPA             TCCAACAGGCTGACAGTTCTTTCTCACAATGATTTACCTGCTAATTTAGAGATCCTGGAC 1662
PTR             TCCAACAGGCTGACAGTTCTTTCTCACAATGATTTACCTGCTAATTTAGAGATCCTGGAC 1662
HSA             TCCAACAGGCTGACAGTTCTTTCTCACAATGATTTACCTGCTAATTTAGAGATCCTGGAC 1662
GGO             TCCAACAGGCTGACAGTTCTTTCTCACAATGATTTACCTGCTAATTTAGAGATCCTGGAC 1662
PPY             TCCAACAGGCTGACAGTTCTTTCTCACAATGATTTACCTGCTAATTTAGAGATCCTGGAC 1662
MFA             TCCAACAGGCTGACAGTTCTTTCTCACAATGATTTACCTGCTAATTTAGAGATCCTGGAC 1662
MMUL            TCCAACAGGCTGACAGTTCTTTCTCACAATGATTTACCTGCTAATTTAGAGATCCTGGAC 1662
CTO             TCCAACAGGCTGACAGTTCTTTCTCACAATGATTTACCTGCTAATTTAGAGATCCTTGAC 1662
CJA             TCCAACAGGCTGACAGTGCTTTCTCACAATGACTTACCTGCTAATTTAGAGATCCTGGAC 1662
TSY             TCCAACAGGCTGACCGTTCTTTCCTTTGGTGATTTACCTGCTAATTTAGAAATCCTGGAT 1662
CHI             GACAACAGGCTGACTGTTCTTTCTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
OAR             GACAACAGGCTGACTGTTCTTTCTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
RRU             GACAACAGGCTGACTGTTCTTTCTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
OGA             GACAACAGGCTGACTGTTCTTTCTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
OLE             GACAACAGGCTGACTGTTCTTTCTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
ODA             GACAACAGGCTGACTGTTCTTTCTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU1            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU2            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU3            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU4            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU5            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU8            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU9            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU12           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU14           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU16           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU18           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BCA             GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU7            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU11           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU13           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU17           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU15           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU6            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBU10           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
SCA1            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
SCA2            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA10           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA16           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA7            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA3            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA1            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA2            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA4            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA6            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA9            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA15           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
```

```
BTA12           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA11           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA14           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BGR             GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA5            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA13           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA8            GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA17           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BTA18           GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BBI             GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
BJA             GACAACAGGCTGACTGTTCTTTTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
TIM             GACAACAGGCTGACTGTTCTTCTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
TST             GACAACAGGCTGACTGTTCTTCTTCCTGGCGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
GCA             GACAACAGGCTTACTGTTCTTTCTCCTGGTGACTTACCTGCTAACTTAGAGATCCTGGAT 1662
OHE             GACAATAGACTGACTGTTCTTTCTCCTGGCGATTTACCTGCTAACTTAGAGATCCTGGAT 1662
OVI             GACAATAGACTGACTGTTCTTTCTCCTGGCGATTTACCTGCTAACTTAGAGATCCTGGAT 1662
SSC             TACAACAGGCTAACAGTTCTTTATCCGGGTGACTTACCTGCTCACCTCGAGGTCCTGGAT 1659
PAL             TCCAACAGGCTGACGGTCCTCTCCCCTGGCGACTTACCGCCTAACTTAGAGATCCTGGAT 1662
AME             TCCAACAGGCTGACGGCTCTTGCTCCTGGCGACTTGCCTGCGAACCTGGAGGTGCTGGAC 1662
MPU             TCCAACAGGCTGATGGCACTTGCTCCTGGTGACCTGCCCGCCAACCTGGAGGTGCTAGAC 1662
CLU             GCCAACAGGCTGAGCACGCTGTCCCGGGGCGACCTGCCTGCTGCCTTGGAGGTGCTGGAT 1662
ETE             TTCAACCGGCTGACGTCTCTTTCGCCGGGCGATCTCCCGGCTCAGCTCGAGTTCCTGGAC 1662
OPR             TCCAACAGGCTGACAGCTCTTGCCCCCGGCAGCTTCCCTGCCAGTTTAGAGAGTTTGGAT 1662
MMU             GCTAACAAGCTGACCGTGCTCTCTCCGGGCAGTTTACCTGCTAATTTAGAGATTCTCGAC 1665
MDO             GGCAACAAGCTGATATCTCTTTCTCCTGGTGTTCTACCTGAAAATTTAAGAGTCTTGTCT 1665
SHA             GCTAACAAGTTGACATCTCTTTCTCCTGGTGTTCTACCTGCAAATTTAAGAGTCTTGATT 1659
OAN             GCCAATCGATTGATTTCCCTCTCCCATGGTGATTTACCTAACACTTTAGTCTTCTTGGAT 1662
GGA             TCCAACCTATTGTCTCACCTCTCTCTCAGGGTTTTTCCACAAAGCCTAATAAACCTAAAC 1665
GLA             TCCAACCTATTGTCTCACCTCTCCCTCAGGGTTTTTCCACAAAGCCTAATAAACCTAAAC 1665
MGA             TCCAACCTATTGTCTCACCTCTCTCTCAGGGTTTTTCCACAAAGCCTAATAAACCTAAAC 1668
PCO             TCCAACCTATTGTCTCACCTCTCTCTTGGGGTTTTTCCACGAAGCCTAATAAACCTAAAC 1665
NME             TCCAACCTATTGTCTCACCTCTCCCTCGGGGTTTTTCCACAAGGCCTAATAAACCTAAAC 1665
TGU             TCCAACCTGTTGTCTCATCTTTCTCCTGGGCTTTTCCCACAAAGCCTAACAAACCTAAAC 1659
                   **     *       **              * **        *        *

PPA             ATATCCAGGAACCAGCTCCTAGCTCCCGATCCTGATGTATTTGTATCACTTAGTGTCTTG 1722
PTR             ATATCCAGGAACCAGCTCCTAGCTCCCGATCCTGATGTATTTGTATCACTTAGTGTCTTG 1722
HSA             ATATCCAGGAACCAGCTCCTAGCTCCTAATCCTGATGTATTTGTATCACTTAGTGTCTTG 1722
GGO             ATATCCAGGAACCAGCTCCTAGCTCCCGATCCTGATGTATTTGTATCACTTAGTGTCTTG 1722
PPY             ATATCCAGGAACCAGCTCCTAGCTCCCGATCCTGATGTATTTGTATCACTTAGTGTCTTG 1722
MFA             ATATCTGGGAATCAGCTCCTAGCTCCCGATCCTGATGTATTTGTATCACTTAGTGTCTTG 1722
MMUL            ATATCTGGGAATCAGCTCCTAGCTCCCGATCCTGATGTATTTGTATCACTTAGTGTCTTG 1722
CTO             ATATCTGGGAATCAGCTCCTAGCTCCCGATCCTGATTTATTTGTATCACTTAGTGTCTTG 1722
CJA             ATATCCAGAAACCAGCTCCTAGCTCCCGATCCTAATTTCTTTGTATCACTTAGTATCTTG 1722
TSY             GTATCCAGAAACCAGCTCCTAGTTCCCAGCCCTAATTTATTTTTATCACTTAGTGCCTTG 1722
CHI             ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATG 1722
OAR             ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATG 1722
RRU             ATATCTGGAAACCAGCTCCTGTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATG 1722
OGA             ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTAATGTATTTGCATCACTGAGTGCCATG 1722
OLE             ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTAATGTATTTGCATCACTGAGTGCCATG 1722
ODA             TTATCTGGAAACCAGCTCCTCTCTCCTGATCCTAATGTATTTGCATCACTGAGTGCCATG 1722
BBU1            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU2            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU3            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU4            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU5            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU8            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU9            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU12           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU14           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU16           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU18           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BCA             ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU7            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU11           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU13           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU17           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
```

```
BBU15           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU6            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBU10           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
SCA1            ATATCTGGAAACCATCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
SCA2            ATATCTGGAAACCAKCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA10           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA16           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA7            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA3            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA1            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA2            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA4            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA6            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA9            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA15           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA12           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA11           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA14           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BGR             ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA5            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA13           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA8            ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA17           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BTA18           ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BBI             ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
BJA             ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
TIM             ATATCTAGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGGATCACTGAGTGCCATA 1722
TST             ATATCTAGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCATA 1722
GCA             ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTACATCACTGAGTGCCGTG 1722
OHE             ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCGTG 1722
OVI             ATATCTGGAAACCAGCTCCTCTCTCCTGATCCTGATTTATTTGCATCACTGAGTGCCGTG 1722
SSC             CTATCCAGAAACCAGCTCCTCTCTCCCGATCCTGACTTATTCACCTCACTAAGTGCCGTG 1719
PAL             GTATCCAGAAACCAGCTCCTGTCTCCTGATCCTGATGTATTTGCATCACTTCATTTCGTG 1722
AME             GTGTCCAGGAACCAGCTCCTGTCCCTGGACCCCGACTTGTTTGCGTCCCTCAGGGCCGTG 1722
MPU             GTGTCCAGAAACCAGCTCCTGACCCTGGACCCCAACCTGCTGGCGTCCCTCACCGCCGTG 1722
CLU             GTGTCCAGGAACCAGCTCCTGTCCCTGGACCCCGGGCTGCTCGCCCCGCTCAGAGCCGTG 1722
ETE             GTGTCCTGGAACCAGCTCCTGGCTCCAGACCCCGCTGTGTTCGCCTCACTCCGGGCGGTG 1722
OPR             GTGTCCAGAAACCAGCTGCTCTCTCCTGATCCTGATTTATTTGCCTCACTTCGCATCTTG 1722
MMU             ATATCTAGAAATCAGCTTTTCTCTCCTGACCCTGCTTTGTTTTCTTCGCTTCGTGTTTTG 1725
MDO             TTATCCCAGAACCACCTACTATCTCCTGACCCTACTGTATTTGCATCACTGAGCTACCTA 1725
SHA             TTATCCCATAACCTCCTACTATCCCCTGACCCATCCATATTTGCATCACTGAGCCACTTA 1719
OAN             TTATCCAGAAACCAGTTGTTTTCTCCTGATCCTAACCTCTTCATGTCCCTGCAAGTTCTG 1722
GGA             TTGTCTGGAAATCAGCTTTTTTCCCCTAAGCCTGAAGTCTTTATGACTTTGAGTATTCTG 1725
GLA             TTGTCTGGAAATCAGCTTTTTTCCCCTAAGCCTGAAGTCTTTATGACTTTGAGTATTCTG 1725
MGA             TTGTCTGGAAATCAGCTTTTTTCCCCTAAGCCTGAAGTCTTTATGACTTTGAGTATTCTG 1728
PCO             TTGTCTGGAAACCAGCTTTTTTCCCCTAAGCCTGAAGTCTTTATGACTTTGAGTATTCTG 1725
NME             TTGTCTGGAAACCAGCTTTTTTCCCCTGAGCCTGAAGTCTTTATGACTTTGAGTATTCTG 1725
TGU             TTATCTGGAAACCAGCTATTTTCCCCTGAGCCTGAAGTCTTTATGACTTTGAGTATTCTG 1719
                 * **    ** *   *  *    *     **     *  *     *  *        *

PPA             GATATAACTCATAACAAGTTCATTTGTGAATGTGAACTTAGCACTTTTATCAAGTGGCTT 1782
PTR             GATATAACTCATAACAAGTTCATTTGTGAATGTGAACTTAGCACTTTTATCAAGTGGCTT 1782
HSA             GATATAACTCATAACAAGTTCATTTGTGAATGTGAACTTAGCACTTTTATCAATTGGCTT 1782
GGO             GATATAACTCATAACAAGTTCATTTGTGAATGTGAACTTAGCACTTTTATCAATTGGCTT 1782
PPY             GATATAACTCATAACAAGTTCATTTGTGAATGTGAACTTAGCACTTTTATCAATTGGCTT 1782
MFA             GATATAACTCATAACAAGTTCATTTGTGAATGTGCACTTAGCACTTTTATCCATTGGCTT 1782
MMUL            GATATAACTCATAACAAGTTCATTTGTGAATGTGCACTTAGCACTTTTATCCATTGGCTT 1782
CTO             GATATAACTCATAACAAGTTCATTTGTGAATGTGCACTTAGCACTTTTATCCATTGGCTT 1782
CJA             GATATAACTCATAACAAGTTCATTTGTGAATGTGAACTTAGCGCTTTTATCAACTGGCTT 1782
TSY             GATATAACGCATAATAAGTTCATTTGTGAGTGTGAACTTAGCACTTTTATCAGTTGGCTT 1782
CHI             GACATAACTCATAACAAATTCATCTGTGATTGTGAACTTAGTGCTTTTATCCATTGGGTC 1782
OAR             GACATAACTCATAACAAATTCATCTGTGATTGTGAACTTAGTGCTTTTATCCATTGGGTC 1782
RRU             GACATAACTCATAACAAATTCATCTGTGATTGTGAACTTAGTGCTTTTATCCATTGGGTC 1782
OGA             GACATAACTCATAACAAATTCATCTGTGATTGTGAACTTAGTGCTTTTATCCATTGGGTC 1782
OLE             GACATAACTCATAACAAATTCATCTGTGATTGTGAACTTAGTGCTTTTATCCATTGGGTC 1782
ODA             GACATAACTCATAACAAATTCATCTGTGACTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU1            GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
```

```
BBU2                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU3                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU4                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU5                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU8                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU9                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU12                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU14                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU16                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU18                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BCA                  GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU7                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU11                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU13                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU17                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU15                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU6                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBU10                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
SCA1                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
SCA2                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BTA10                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BTA16                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BTA7                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BTA3                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BTA1                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BTA2                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTCAGTGCTTTTATCCATTGGCTC 1782
BTA4                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTCAGTGCTTTTATCCATTGGCTC 1782
BTA6                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTCAGTGCTTTTATCCATTGGCTC 1782
BTA9                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTCAGTGCTTTTATCCATTGGCTC 1782
BTA15                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTCAGTGCTTTTATCCATTGGCTC 1782
BTA12                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTYAGTGCTTTTATCCATTGGCTC 1782
BTA11                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTCAGTGCTTTTATCCATTGGCTC 1782
BTA14                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTCAGTGCTTTTATCCATTGGCTC 1782
BGR                  GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTCAGTGCTTTTATCCATTGGCTC 1782
BTA5                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTCAGTGCTTTTATCCATTGGCTC 1782
BTA13                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTYAGTGCTTTTATCCATTGGCTC 1782
BTA8                 GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BTA17                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTYAGTGCTTTTATCCATTGGCTC 1782
BTA18                GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BBI                  GACATAACTCATAACAATTTTATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
BJA                  GACATAACTCATAACAATTTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
TIM                  GACATAACTCATAACAATTTCATCTGTGACTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
TST                  GACATAACTCATAACAATTTCATCTGTGACTGTGAACTTAGTGCTTTTATCCACTGGCTC 1782
GCA                  GACATAACTCATAACAAATTCATCTGTGAGTGTGAACTTAGTACTTTTATCCATTGGCTC 1782
OHE                  GACCTAACTCATAACAAATTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
OVI                  GACCTAACTCATAACAAATTCATCTGTGAGTGTGAACTTAGTGCTTTTATCCATTGGCTC 1782
SSC                  GACCTGAGTCATAACAAGTTTGTTTGTGACTGTGAACTTAGCACTTTTATCAATTGGCTC 1779
PAL                  GACATAACTCATAACAAGTTCATCTGTGAGTGTGAACTTAGCGCTTTCATCAGGTGGCTC 1782
AME                  GACATAACGCACAACAGGTTCATCTGTGAGTGTGACCTCCGTCCTCTCATCACTTGGCTC 1782
MPU                  GACATAACACACAACAAATTCATCTGTGAGTGTGACCTCCGTTCTCTCGTTGTTTGGCTC 1782
CLU                  GACCTAACGCACAACAAGTTCATCTGCGGCTGCGAGCTCCGTCCCTTGGTGAGGTGGCTC 1782
ETE                  GACCTCCGGCATAACCAGTTCATCTGTGCGTGTGAACTGAGCGCCTTTATCAGCTGGCTC 1782
OPR                  GACATTACCCATAACAAGTTCATCTGTGTGTGTGAACTTAGCAAGTTTATCAGTTGGCTT 1782
MMU                  GACATAACTCATAACGAGTTCGTCTGCAACTGTGAACTTAGCACTTTTATCTCCTGGCTC 1785
MDO                  GATATAACCCATAACAAATATATCTGTGAGTGTGAAGCCAGAAATTTTATACTTTGGTTG 1785
SHA                  GATATAAGCCACAATCAATATATTTGTGATTGTGAAGTCAAAAATTTTATCCTTTGGCTG 1779
OAN                  GATATAACCCATAACAGGTACATCTGTGAGTGTGAGCTCAGAGACTTTCTAGGCTGGCTA 1782
GGA                  GATATAACACATAACAAGTATGTCTGTGACTGTGCTTTAAAAAGCCTATTAGTGTGGCTA 1785
GLA                  GATATAACACATAACAAGTATGTCTGTGATTGTGCTTTAAAAAGCCTACTAGTGTGGCTA 1785
MGA                  GATATAACACATAACAAGTATGTCTGTGACTGTGCTTTAAAAAGCCTACTAGTGTGGCTA 1788
PCO                  GATATAACACATAACAAATATGTCTGTGATTGTGCTTTAAAAAGCCTACTAGTGTGGCTA 1785
NME                  GATATAACACATAACAATTATGTCTGTGACTGTGCTTTAAAAAGCCTGCTAGTCTGGCTA 1785
TGU                  GATATAACACATAATAATTATGTCTGTGATTGTGCTTTAAAGAGCCTGCTAGTGTGGTTG 1779
                     **  *    ** **    *   * **    ** *            *  *    *** *

PPA                  AATCACACCAATGTCACTATAGCTGGGCCTCCTGCAGACATATATTGTGTGTACCCTGAC 1842
PTR                  AATCACACCAATGTCACTATAGCTGGGCCTCCTGCAGACATATATTGTGTGTACCCTGAC 1842
```

```
HSA             AATCACACCAATGTCACTATAGCTGGGCCTCCTGCAGACATATATTGTGTGTACCCTGAC 1842
GGO             AATCACACCAATGTCACTATAGCTGGGCCTCCTGCAGACATATATTGTGTGTACCCTGAC 1842
PPY             AATCACACCAATGTCACTATAGCTGGGCCTCCTGCAGACATATATTGTGTGTACCCTGAC 1842
MFA             AATCACACCAATGTCACTATAGCTGGGCCTCCTGCAGACATACATTGCGTGTACCCTGAC 1842
MMUL            AATCACACCAATGTCACTATAGCTGGGCCTCCTGCAGACATACATTGCGTGTACCCTGAC 1842
CTO             AATCACACCAATGTCACTATAGCTGGGCCTCCTGCAGACATACATTGTGTGTACCCTGAC 1842
CJA             AATCATACCAATGTCACTGTAGCTGGACCTCCTGCGGACATATATTGTGTGTACCCTGAT 1842
TSY             AATCATACCAATGTCACTATATTTGGGTCTCCTGCAGACATCTACTGCATGTACCCTAAC 1842
CHI             AATCAAACCAATATCACAATATCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
OAR             AATCAAACCAATATCACAATATCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
RRU             AATCAAACCAATATCACAATATCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
OGA             AATCAAACCAATATCACAATATCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
OLE             AATCAAACCAATATCACAATATCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
ODA             AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU1            AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU2            AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU3            AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU4            AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU5            AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU8            AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU9            AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU12           AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU14           AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU16           AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU18           AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BCA             AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU7            AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU11           AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU13           AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU17           AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU15           AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU6            AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBU10           AATCAAACCAATATCACAATAGCTGGATCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
SCA1            AATCAAACCCAAATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
SCA2            AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA10           AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA16           AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA7            AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA3            AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA1            AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA2            AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA4            AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA6            AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA9            AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA15           AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA12           AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA11           AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA14           AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BGR             AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA5            AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA13           AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA8            AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA17           AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BTA18           AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BBI             AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
BJA             AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
TIM             AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
TST             AATCAAACCAATATCACAATAGCTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
GCA             AATCAAACCAATATCACAATATTTGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
OHE             AATCAAACCAACATCACAATATATGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
OVI             AATCAAACCAACATCACAATATATGGGTCTCCAGCAGACATGTACTGCATGTACCCAAAC 1842
SSC             AATCAAACCAATGTCACGATATTTGGGTCTCGAGATGATATATACTGCATGTATCCGAGC 1839
PAL             AATCAAACCAATGTCACTATATTTGGGTCTCACGCAGACATATACTGCATGTACCCAAAC 1842
AME             AACCAGACCAACGTCACTGTATTCGGGTCTCATGCAGACATCTACTGCATGTACCCCAAC 1842
MPU             AACCAGACCAACGTCACTGTGTTTGGGTCTGGTGCAGACATCTCCTGCACGTACCCCAAC 1842
CLU             AACCGGACCAACGTCACTGTGTTCGGGTCCCGCGCAGACGTGCGCTGCGCCTACCCCAGC 1842
ETE             AATCACACGAATGCCACTCTGCGGGGTGCTCCTGCGGACAGATACTGCATGTTCCCCGAG 1842
```

```
OPR             AATCAAACCAACGTCTCTGTATTTGGATCTCCTGCAGACCTCTACTGCATGTACCCCGAC 1842
MMU             AACCAAACCAACGTCACCCTGTTCGGCTCTCCTGCAGACGTGTATTGCATGTACCCTAAC 1845
MDO             AACCAAACCAAAGTCAACATGCTTGGGTCCCCTGAGGATGTCTACTGCACATACCCTGAC 1845
SHA             AATCAAACCAATGTTACCATGCTTGGGTCCCCTGAGGATGTTTACTGCACATACCCTGGC 1839
OAN             AACCAGTCAAATGTCACTTTTTTGGGGTCACCCAAGGACATGTACTGTGTGTATCCAGAC 1842
GGA             AATGAAACCAATGTAACCCTAGCTGGCTCGGAGTCTGACAGGTACTGTGTGTACCCACCT 1845
GLA             AATGAAACCAATGTAACCCTAGCTGGCTCGGAGTCTGACAGGTACTGTGTGTACCCACCT 1845
MGA             AATGAAACCAATGTAACCCTAGCTGGCTCAGAGTCTGACAGGTACTGTGTGTACCCACCT 1848
PCO             AATGAAACCAATGTAACCCTAGCTGGCTCAGAGTCTGACAGGTACTGTGTATACCCACCT 1845
NME             AATGAAACCAATGTAACCCTAGTTGGCTCAGAGTCTGACAGGTACTGTGTATACCCACCT 1845
TGU             AATGAAACCAATGTAACCCTGGCTGGCTCCCAGTCTGACAGGTACTGTGTGTACCCCCCT 1839
                **     *  *        *    **  *       **       **    *  **

PPA             TCACTCTCTGGGGTTTCCCTCTTCTCTCTTTCCACGGAAGGTTGTGATGAAGAGGAAGTC 1902
PTR             TCACTCTCTGGGGTTTCCCTCTTCTCTCTTTCCACGGAAGGTTGTGATGAAGAGGAAGTC 1902
HSA             TCGTTCTCTGGGGTTTCCCTCTTCTCTCTTTCCACGGAAGGTTGTGATGAAGAGGAAGTC 1902
GGO             TCGCTTTCTGGGGTTTCCCTCTTCTCTCTTTCCACAGAAGGTTGTGATGAAGAGGAAGTC 1902
PPY             TCGCTCTCTGGGGTTTCCCTCTTCTCTCTTTCCACAGAAGGTTGTGATGAAGAGAAAGTC 1902
MFA             TCGCTCTCCGGGGTTTCCCTCTTCTCTCTTTCCACGGAAGCTTGTGATGAAGAGGAAGTC 1902
MMUL            TCGCTCTCCGGGGTTTCCCTCTTCTCTCTTTCCACGGAAGCTTGTGATGAAGAGGAAGTC 1902
CTO             TCGCTCTCTGGGGTTTCCCTCTTCTCTCTTTCCACGGAAGCTTGTGATGAAGAGGAAGTC 1902
CJA             TCGTTCTCTGGGGTTTCCCTCTTCTCTCTTTCCACAGAAGACTGTGATGAAGAGGCAATC 1902
TSY             TCGCTCTTTGGGGTTTCCCTTTACTCTGTGTCCACGGAAGATTGTGATGAAGAGGAAGTC 1902
CHI             TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAGGTTGCGAAGAAGAAGAATTT 1902
OAR             TCTCTGGCTGGGGTGTCCATTTACAGTCTTTCCACAGAAGGTTGTGAAGAAGAAGAATTT 1902
RRU             TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAGGTTGTGAAGAAGAAGAATTT 1902
OGA             TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAGGTTGCGAAGAAGAAGAATTC 1902
OLE             TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAGGTTGCGAAGAAGAAGAATTC 1902
ODA             TTTCTGGCTAGGGTTTCCATTTACAGTCTTTCCACAGAAGGCTGTGAAGAAGAAGAAGTT 1902
BBU1            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU2            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU3            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU4            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU5            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU8            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU9            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU12           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU14           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU16           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU18           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BCA             TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU7            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU11           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU13           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU17           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU15           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU6            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBU10           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
SCA1            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
SCA2            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA10           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA16           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA7            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA3            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA1            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA2            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA4            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA6            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA9            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA15           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA12           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA11           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA14           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BGR             TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA5            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA13           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA8            TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
```

```
BTA17           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BTA18           TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BBI             TCTCTGGCTGGGGTTTCCATTTACAGTCTTTCCACAGAAAGTTGTGAAGAAGAAGAAGTT 1902
BJA             TTTCTGGCTAGGGTTTCCATTTACAGTCTTTCCACAGAAGGCTGTGAAGAAGAAGAAGTT 1902
TIM             TTTCTGGCTAGGGTTTCCATTTACAGTCTTTCCACAGAAGGCTGTGAAGAAGAAGAAGTT 1902
TST             TTTCTGGCTAGGGTTTCCATTTACAGTCTTTCCACAGAAGGCTGTGAAGAAGAAGAAGTT 1902
GCA             TCTCTGGCTGGGGTTTCCCTTTACAGTCTTTCCACAGAAGGTTGCGAAGAAGAAGAAGTT 1902
OHE             TCTCTGGCTGGGGTTTCCCTTTACAGTTTTTCCACAGAAGGTTGTGAAGAAGAAGAAGTT 1902
OVI             TCTCTGGCTGGGGTTTCCCTTTACAGTTTTTCCACAGAAGGTTGTGAAGAAGAAGAAGTT 1902
SSC             TCGCTCGCTGGGAGTCCCCTCAACACCGTTTCCATGGCAGGTTGCAGTGAAGAGGAAGTC 1899
PAL             TCGCTCTCTGGGACTTCCCTCTACTCCGTGTCCACGGACGGTTGTGACGAAGAGGAAATC 1902
AME             GAGCTCGCGGGGACCCCCCTCTCCTCTGTGTCCATGGAGGACTGCGATGAGGAGGAGGTC 1902
MPU             GCACTCGCAGGGACCCCCCTCTCCTCTGTCTCCATGGAGGACTGTGATGAAGAGGAGGTC 1902
CLU             TTGCTTGCGGGGACGCCCCTGTCCTCTGTCTCCATGGAGGGCTGTGACGACGAGGAGGCC 1902
ETE             GCATTTGCTGGGGTCCCCCTGGACTCTATTTCCACGGATGGGTGTGACGAAGAGAAAGCC 1902
OPR             TCGCTCTTGGGGGCCTCACTCTACTCTATCTCCACTGAGGGTTGTGATGAAGAGAAAATC 1902
MMU             TCACTGCTAGGGGGCTCCCTCTACAACATATCCACCGAAGACTGCGATGAAGAGGAAGCC 1905
MDO             TCATTCTCTGGGGTCTCACTCTATTCAATTTCCACAGAGGGCTGTGATGAAGAGGAAGCT 1905
SHA             TCATTCTCTGGGGTCTCACTCTATTCAATTTCCACAGAGGGCTGTGATGAAGAGGAAGCC 1899
OAN             TCCTTCTCTGGGGTCTCACTCTATTCCGTTTCCTTGGAGGATTGTGATGAAGAAGAAGTC 1902
GGA             GCATTAGCGGGTGTACCCGTGTCATTTCTGACATACGATGACTGCGATGAAGATGAACTC 1905
GLA             GCATTAGCGGGTGTACCCGTGTCATTTCTGACATACGATGACTGCGATGAAGATGAACTC 1905
MGA             GCATTAGCAGGTGTACCAGTGTCATTTCTGACATATGATGATTGTGATGAAGATGAACTC 1908
PCO             GCATTAGCAGGGGTACCAGTGTCACTTCTGACATATGATGATTGCGATGAAGATGAACTC 1905
NME             GCATTAGCAGGTGTACCACTATCACTTCTGGCATATGATGATTGCAGTGAAGATGAACTC 1905
TGU             GCCTTTGAAGGGGTACCCCTGTCACATATAATATATGATGGCTGTGATGAAGATGAACTC 1899
                    *     *     *  *        *       *     **    ** **

PPA             TTAAAGTCCCTAAAGTTCTCCCTTTTCATTGTATGCACTGTCACTCTGACTCTATTCCTC 1962
PTR             TTAAAGTCCCTAAAGTTCTCCCTTTTCATTGTATGCACTGTCACTCTGACTCTATTCCTC 1962
HSA             TTAAAGTCCCTAAAGTTCTCCCTTTTCATTGTATGCACTGTCACTCTGACTCTGTTCCTC 1962
GGO             TTAAAGTCCCTAAAGTTCTCCCTTTTCATTGTATGCACTGTCACTCTGACTCTGTTCCTC 1962
PPY             TTAAAGTCCCTAAAGTTCTCCCTTTTCATTGTATGCACTGTCACTCTGACTCTGTTCCTC 1962
MFA             TTAAAGTCCCTGAAGTTCTCCCTTTTCATTGTATGCACTGTCACTCTGACTCTGTTCCTC 1962
MMUL            TTAAAGTCCCTGAAGTTCTCCCTTTTCATTGTATGCACTGTCACTCTGACTCTGTTCCTC 1962
CTO             TTAAAGTCCCTAAAGTTCTCCCTTTTCGTTGTATGCACTGTCACTCTGACTCTGTTCCTC 1962
CJA             TTAAAGTCCCTCAAGTTCTCCCTTTTCATCGGATGCACTGTCACTCTGACTCTGTTCCTC 1962
TSY             TTAAAGTTCCTGACATTTTCCCTTTTCATCTTATTCACTGTCATTCTGACTCTGTTCCTC 1962
CHI             TTAGAGTCCCTGAAGTTTTCCCTTTTCATCTTGTTCACTGTCACCTTGACTCTGTTCCTC 1962
OAR             TTAGAGTCCCTGAAGTTTTCCCTTTTCATCTTATTCACTGTCACCTTGACTCTGTTCCTC 1962
RRU             TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGTTCACTTTCACCTTGACCCTGTTCCTC 1962
OGA             TTAGAGTCCCTCAGGTTTTCCCTTTTCATCTTGCTCACTGTCACCTTAACTCTGTTCCTC 1962
OLE             TTAGAGTCCCTCAGGTTTTCCCTTTTCATCTTGCTCACTGTCACCTTAACTCTGTTCCTC 1962
ODA             TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTCAGTCACTGTCACCTTGACTCTGTTCCTC 1962
BBU1            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTGTGTTCCTC 1962
BBU2            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTGTGTTCCTC 1962
BBU3            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTGTGTTCCTC 1962
BBU4            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTGTGTTCCTC 1962
BBU5            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTGTGTTCCTC 1962
BBU8            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTGTGTTCCTC 1962
BBU9            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTGTGTTCCTC 1962
BBU12           TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTGTGTTCCTC 1962
BBU14           TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTGTGTTCCTC 1962
BBU16           TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTGTGTTCCTC 1962
BBU18           TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTGTGTTCCTC 1962
BCA             TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTGTGTTCCTC 1962
BBU7            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTYACCTTGACTGTGTTCCTC 1962
BBU11           TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTYACCTTGACTGTGTTCCTC 1962
BBU13           TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTYACCTTGACTGTGTTCCTC 1962
BBU17           TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTYACCTTGACTGTGTTCCTC 1962
BBU15           TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTYACCTTGACTGTGTTCCTC 1962
BBU6            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTTACCTTGACTGTGTTCCTC 1962
BBU10           TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTYACCTTGACTGTGTTCCTC 1962
SCA1            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
SCA2            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA10           TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA16           TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
```

```
BTA7             TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA3             TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA1             TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA2             TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA4             TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA6             TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA9             TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA15            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA12            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA11            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA14            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BGR              TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA5             TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA13            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA8             TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA17            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BTA18            TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BBI              TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
BJA              TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTCAGTCACTGTCACCTTGACTCTGTTCCTC 1962
TIM              TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTCAGTCACTGTCACCTTGACTCTGTTCCTC 1962
TST              TTAGAGTTCCTAAAGTTTTCCCTTTTCATCTCAGTCACTGTCACCTTGACTCTGTTCCTC 1962
GCA              TTAGAGTCCCTGAAGTTTTCCCTTTTCATCCTGGTCACTGTCACCTTGACTCTGTTCCTC 1962
OHE              TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTAACTCTGTTCCTC 1962
OVI              TTAGAGTCCCTAAAGTTTTCCCTTTTCATCTTGGTCACTGTCACCTTAACTCTGTTCCTC 1962
SSC              TTAGAGTCCCTGAAGTTTTCCCTTTTCATCTTGTTCACTGTCACCCTGACTCTGCTTTTC 1959
PAL              CTCAAGTCCCTCAAGTTCTCCCTTTTCATCTTATTCACCGTCACGCTGGTCCTGTTCCTC 1962
AME              TTGAAGGTCATAAAGTTGTCCCTTTTCATCTCATCCACGGTCACTCTGACTCTGTTCCTC 1962
MPU              TTGAAGGCTCTACGGTTGTCTCTTTTCGTCTCCTCCACGGTGACCCTGACTCTGTTCCTC 1962
CLU              CTGCGGACCCTCACGTTCTCCCTCTTCATCTTCTCCACCGTCGGGGTCACGCTGTTCCTC 1962
ETE              TTCCAGGCCCTAAAGTGGTCCCTTTTCATCTCTGTCACCGTGATGTTGACGCTCGTCCTC 1962
OPR              CTAACGTTGCTCAAGTTCTCCCTCTTCGTTGTGTTTACTGTCACTTTGACTCTGTTCCTC 1962
MMU              ATGCGGTCCCTAAAGTTTTCCCTTTTCATCCTGTGCACGGTCACTTTGACTCTATTCCTC 1965
MDO              TTACAATTTATTCATTTCTCACTTTTTATCTTCTTCACTACCACCTTGACTGTGTTCCTC 1965
SHA              CTAAAATTTATTAATTTTACACTTTTCATCTTCTTTACCACCACCTTGACTCTGTTCCTC 1959
OAN              CTAAGGCCACTCAAGTTTTCACTTTTCCTTTTCTTTACTGTGACCTTGCTCCTGATCATA 1962
GGA              CAGCAGACACTCAGGTTCTCGGTATTCGTTTTCCTATCTGTCACCCTTCTGATGTTTCTG 1965
GLA              CAGCAGACACTCAGGTTCTCGGTATTCGTTTTCATATCTGTCACCCTTCTGATGTTTCTG 1965
MGA              CAGCAGACACTCAGGTTCTCAGTATTCATTTTCATATCTGTCACCCTTCTGATGTTTCTG 1968
PCO              CAGCAGACACTCAGGTTCTCAGTATTCATTTTCCTTTCTGTCACCCTTCTGATGTTTCTG 1965
NME              CAGCAGACACTCCGGTTCTCAGTATTCATTGTCACGTCTGTCACCCTTCTGATGTTTCTG 1965
TGU              CAGCAGACACTCAGATTCTCACTATTCGTCTTCTTCTCGGTCATTCTTCTCTTGTTTCTG 1959
                           *    *   *  * **  *        *        *     *  *  *

PPA              ATGACCATCCTCACAGTCACAAAGTTCCGGGGCTTCTGTTT---TATCTGTTATAAGACA 2019
PTR              ATGACCATCCTCACAGTCACAAAGTTCCGGGGCTTCTGTTT---TATCTGTTATAAGACA 2019
HSA              ATGACCATCCTCACAGTCACAAAGTTCCGGGGCTTCTGTTT---TATCTGTTATAAGACA 2019
GGO              ATGACCATCCTCACAGTCACAAAGTTCCGGGGCTTCTGTTT---TATCTGTTATAAGACA 2019
PPY              ATGACCATCCTCACAGTCACAAAGTGCCGGGGCTTCTGTTT---TATTTGTTATAAGACA 2019
MFA              ATGACCATCCTCATAGTCACGAAGTTCCGGGGCTTCTGTTT---TATCTGTTATAAGACA 2019
MMUL             ATGACCATCCTCATAGTCACGAAGTTCCGGGGCTTCTGTTT---TATCTGTTATAAGACA 2019
CTO              ATGACCATCCTCATAGTCACGAAGTTCCGGGGCTTCTGTTT---TATCTGTTATAAGACA 2019
CJA              ATGGCCAGCCTCATCGTCGCCAAGTTCCGGGGCTTTTGTTT---TATCTGTTATAAGACG 2019
TSY              GTGGCCATCCTTGTAGTCACGAAGTTCCGAGGCTTTTGTTT---TGTCTGTTATAAGACA 2019
CHI              GTGATCACCCTCACGGTTACAAAGTTCCGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
OAR              GTGATCATCCTCATGGTTACAAAGTTCCGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
RRU              GTGATCATCCTCATGGTTACAAAGTTCCGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
OGA              GTGGTCATCCTCACAGTTACAAAGTTCCGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
OLE              GTGGTCATCCTCACAGTTACAAAGTTCCGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
ODA              GTGGTCATCCTCACGGTTACAAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BBU1             GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU2             GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU3             GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU4             GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU5             GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU8             GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU9             GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU12            GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
```

```
BBU14           GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU16           GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU18           GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BCA             GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU7            GTGATCACCCTCACRGTTACTAAGTTCAGRGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU11           GTGATCACCCTCACRGTTACTAAGTTCAGRGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU13           GTGATCACCCTCACRGTTACTAAGTTCAGRGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU17           GTGATCACCCTCACRGTTACTAAGTTCAGRGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU15           GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU6            GTGATCACCCTCACRGTTACTAAGTTCAGRGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
BBU10           GTGATCACCCTCACGGTTACTAAGTTCAGGGGGTTTTGGTT---CATCTGTTATAAGAAA 2019
SCA1            GTGATCACCCTCACAGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
SCA2            GTGATCACCCTCACAGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA10           GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA16           GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA7            GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA3            GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA1            GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA2            GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA4            GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA6            GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA9            GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA15           GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA12           GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA11           GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA14           GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BGR             GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA5            GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA13           GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA8            GTGATCACCCTCRCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA17           GTGATCACCCTCRCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BTA18           GTGATCACCCTCRCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BBI             GTGATCACCCTCGCGGTTACTAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
BJA             GTGGTCATCCTCACGGTTACAAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
TIM             GTGGTCATCCTCACGGTTACAAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
TST             GTGGTCATCCTCACGGTTACAAAGTTCAGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
GCA             GTGGTCATCCTCACAGTTACAAAGTTCCGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
OHE             GTAGTCATCCTTATGGTTAAAAAGTTCCGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
OVI             GTAGTCATCCTTATGGTTAAAAAGTTCCGGGGGTTTTGTTT---CATCTGTTATAAGAAA 2019
SSC             GTGGCCATCCTCGTAGTCATGAAGTTCCGGGGATTTTGTTT---CATCTGTTATAAGAAA 2016
PAL             TTGACCGTCCTCACAGTCGTGAAGTTCCGGGGCTTTTGTTT---CCTCTGTTATAAGATG 2019
AME             GTGACCATCGTTGTGGTCACCAAGCTCCGGGGCCTTTGTTT---CATCTGTTACAGGGCG 2019
MPU             GTAACAGTCTTCGTGTCTACTAAGCTCCGGGGCCTTGGCTT---CATTTGCTACAGGGCG 2019
CLU             CTGGCCGTCCTCGTGGCCGCCAAGCTCCGGGGCCTTTGCTT---CCTCTGTTACAAGGCG 2019
ETE             GTGACGAGCCTCGGAGCTGCAAAGTTCCGGGGCGTTTGTTT---CATGTGTTACAAGAGG 2019
OPR             TTGACCACTCTCATGGTCACAAAATTCCGCGGCTTTTGTTT---CCTCTGTTATAAGACA 2019
MMU             GTCATCACCCTTGTAGTCATAAAGTTCCGGGGAATCTGTTT---CCTGTGCTATAAGACC 2022
MDO             ACAGCAGTTGTGACGTTCACAAGATTCCGTGGATGCTGTTTTCTCCTCTGGCGTAAGATG 2025
SHA             ACAGCAACTGTGATATTCACAAAGTTCCGTGGGCTCTGTTTTTCCCTCTGGCATAAAATG 2019
OAN             ATTAGTGTCATCGTTTACACACAGTTTCGGGGATTTTGTTT---CATTGGGATCAAAACC 2019
GGA             ATGTCAACCATTATTTTTACTCGCTGTCGGGGGATTTGTTT---TGTCTGGTATAAGACC 2022
GLA             ATGTCAACCATTATTTTTACTCGCTGTCGGGGCATTTGTTT---TGTCTGGTATAAGACC 2022
MGA             ATGTCAACCATTATTTTTACTCGCTGTCGGGGCATTTGTTT---TGTCTGGTATAAGACC 2025
PCO             ATGTCAGCCGTTGTTTTTACTCGCTGTCGGGGGATTTGTTT---TGTCTGGTATAAGACC 2022
NME             ATGTCAGCCATCATTTGTACTCGCTGTCGGGGGATTTGTTT---TGTCTGGTATAAGACC 2022
TGU             GTGGCAGTCATCATTTTTACTCGCTGCCGGGGGATTTGTTT---CATCTGGTATAAAACC 2016
                          *                 * **     * **     *  *    *

PPA             GCCCAGAGACTGGTGTTCAAGGACCATCCCCAGGGCACAGAACCTGATATGTACAAATAT 2079
PTR             GCCCAGAGACTGGTGTTCAAGGACCATCCCCAGGGCACAGAACCTGATATGTACAAATAT 2079
HSA             GCCCAGAGACTGGTGTTCAAGGACCATCCCCAGGGCACAGAACCTGATATGTACAAATAT 2079
GGO             GCCCAGAGACTGGTGTTCAAGGACCATCCCCAGGGCACAGAACCTGATATGTACAAATAT 2079
PPY             GCCCAGAGACTGGTGTTCAAGGACCATCCCCAGGGCATAGAACCTGATATGTACAAATAT 2079
MFA             GCCCAGAGACTGGTGTTCAAGTACCATCCCCAGGGCACAGAACCTGATACGTACAAATAT 2079
MMUL            GCCCAGAGACTGGTGTTCAAGTACCATCCCCAGGGCACAGAACCTGATACGTACAAATAT 2079
CTO             GCCCAGAGACTGGTGTTCAAGTACCATCCCCAGGGCACAGAACCTGATACGTACAAATAT 2079
CJA             GCCCAGAAACTGGTATTCAAGGACCATCCCCAGGG------ACCCGATACGTACAAATAT 2073
```

```
TSY               GTCCAGAGACTGGTGTTCAAGGGCCATCCGCAGGGAACAGCACCTGATACATACAAATAT 2079
CHI               GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACATACAAATAC 2079
OAR               GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACATACAAATAC 2079
RRU               GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACATACAAATAC 2079
OGA               GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
OLE               GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
ODA               GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACATACAAATAC 2079
BBU1              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU2              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU3              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU4              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU5              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU8              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU9              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU12             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU14             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU16             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU18             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BCA               GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU7              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU11             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU13             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU17             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU15             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU6              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BBU10             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
SCA1              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTATAAATAT 2079
SCA2              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATATGTATAAATAT 2079
BTA10             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA16             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA7              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA3              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA1              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA2              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA4              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA6              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA9              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA15             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA12             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA11             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA14             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BGR               GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA5              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA13             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA8              GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA17             GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BTA18             GCCCAGAGTCTGCTGTTSAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
BBI               GCCCAGAGTCTGCTGTTGAAGGACCCCATCAAGGGAAGAGAATCAGATATGTACAAATAC 2079
BJA               GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACATACAAATAC 2079
TIM               GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACATACAAATAC 2079
TST               GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACATACAAATAC 2079
GCA               GCCCAGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAT 2079
OHE               GCCCTGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
OVI               GCCCTGAGTCTGCTGTTCAAGGACCCCATCAAGGGAAGAGAATCAGATACGTACAAATAC 2079
SSC               GTCCAGAGACTGGTGTTCAAGGACCCCAGCCTGGGAAGGGAATCAGATACATACAAATAC 2076
PAL               GTCCAGAGGCTGCTCTTTGAGGACCGAACCCTGGGAAGAGACTCTGACACGTACACATAC 2079
AME               GCCCACAGACTGCTGCCCACGGTCTATGCTGAGCGCCGCGAGTCCGACACATACAAATAC 2079
MPU               GCCTGCAGACTGCTACCCACGGTCCAGGCCGAGCGCCACGAGTCCAAGCCGTACAGATAC 2079
CLU               GCCCGGCGCCTCCTGCCTGCGGGGCCCGCCGAGGACGGAGCGCCCGACGCGTACCAGTAC 2079
ETE               GCCCAGAGACTGCTCTTCGGGGTCTCCCCCCAGCGCCTGGAACTGGACAGGTACAAATAT 2079
OPR               GCCCAAAGGCTGGTGTTTGGGGACCACTCCCAGGGAACAGAGCTCCATGAATACAAATAT 2079
MMU               ATCCAGAAGCTGGTGTTCAAGGACAAGGTCTGGAGTTTGGAACCTGGTGCATATAGATAT 2082
MDO               TTCCTGACACTAGCACTTGAATACCATCCCCAGGGAGTAAAAGAGGATCAACACAAATAC 2085
SHA               GTTCAGAGACTGACGTTCAAGTACCATCGTCAGGGAGTAGAAGAGGATCAGCACAAATAC 2079
OAN               GTCACAAGATTGGTGTTAGGAGATCGTCCAAAAAGGACAGAATCAAATGCGTGTAAGTAT 2079
GGA               ATCACCAAAACTTTGATAGGAAGCCATCCACCTGCAGCAGATACAAGTGAATACATGTAC 2082
GLA               ATCACCAAAACTTTGATAGGAAGCCATCCACCTGCAGCAGATACAAGTGAATACATGTAC 2082
```

```
MGA             ATCACCAAAACTTTGATAGGAAGCCATCCACCYGCAGCAGATACAAGTGAATACATGTAT 2085
PCO             ATCACCAAAACTTTGATAGGAAGCCATCCACCAGCAGCAGATACAAGTGAATACATGTAC 2082
NME             ATCGCCAAAACTTTGGTAGGAAGCCATCCATCAGCAGTAGATACAAGTGAATACGTGTAT 2082
TGU             ACCACAAAAAGACTGATAGACAACCAACCACGAGCAGCAGATAAATGTGAATACAAATAT 2076
                                                                         **


PPA             GATGCCTATTTGTGCTTCAGCAGCAAAGACTTCACATGGGTGCAGAATGCTTTGCTCAAA 2139
PTR             GATGCCTATTTGTGCTTCAGCAGCAAAGACTTCACATGGGTGCAGAATGCTTTGCTCAAA 2139
HSA             GATGCCTATTTGTGCTTCAGCAGCAAAGACTTCACATGGGTGCAGAATGCTTTGCTCAAA 2139
GGO             GATGCCTATTTGTGCTTCAGCAGCAAAGACTTCACATGGGTGCAGAATGCTTTGCTCAAA 2139
PPY             GATGCCTATTTGTGCTTCAGCAGCAAAGATTTCACATGGGTGCAGAATGCTTTGCTCAAA 2139
MFA             GATGCCTATTTGTGCTTCAGCAGCAAAGACTTCGCATGGGTGCAGAATGCTTTGCTCAAA 2139
MMUL            GATGCCTATTTGTGCTTCAGCAGCAAAGACTTCGCATGGGTGCAGAATGCTTTGCTCAAA 2139
CTO             GATGCCTATTTGTGCTTCAGCAGCAAAGACTTCGCATGGGTGCAGAATGCTTTGCTCAAA 2139
CJA             GATGCCTATATGTGCTTCAGCAGCAAAGACTTCGAGTGGGTGCAGAATGCTTTGCTCAAA 2133
TSY             GATGCTTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTACAGAATGCTTTGCTCAAA 2139
CHI             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
OAR             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
RRU             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
OGA             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
OLE             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
ODA             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAMTGGGTGCAGAATGCTTTGCTCAAA 2139
BBU1            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU2            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU3            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU4            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU5            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU8            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU9            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU12           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU14           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU16           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU18           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BCA             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU7            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU11           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU13           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU17           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU15           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU6            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BBU10           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
SCA1            GATGCCCATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
SCA2            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
BTA10           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA16           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA7            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA3            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA1            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA2            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA4            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA6            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA9            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA15           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA12           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA11           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA14           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BGR             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA5            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA13           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA8            GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA17           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BTA18           GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BBI             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAACGCTTTGCTCAAA 2139
BJA             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAMTGGGTGCAGAATGCTTTGCTCAAA 2139
TIM             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAMTGGGTGCAGAATGCTTTGCTCAAA 2139
TST             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
GCA             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
```

```
OHE             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
OVI             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTGCAGAATGCTTTGCTCAAA 2139
SSC             GATGCCTACTTATGCTTTAGTGGTAAAGACTTTGAATGGGTGCAGGAAGCATTGCTCAAG 2136
PAL             GATGCCTATTTGTGCTTCAGTAGCAAGGACTTCGAGTGGGTGCACGATGCTTTGCTCAGA 2139
AME             GATGCCTACCTATGCTTCAGCGGCAGAGACTTCGAGTGGGTGCAGAGAGCTCTGCTCAGA 2139
MPU             GATGCATACCTCTGCTTCAGTGGCAGAGACTTTGCATGGGTGCAGCGGGCTCTGCTCAGA 2139
CLU             GACGCCTACCTGTGCTTCAGCGGCAGAGACTTCGAGTGGGTGCAGCGCGCTGCTCAGG 2139
ETE             GATGCCTATTTGTGCTTCAGCAGCAAAGACTTTGAATGGGTGCAGTCTGCGTTGCTCGTG 2139
OPR             GACGCCTACCTGTGCTTCAGCAGCAAAGACTTCGAGTGGGTGCAGACGGCTCTGCTCAAA 2139
MMU             GATGCCTACTTCTGCTTCAGCAGCAAAGACTTTGAATGGGCACAGAATGCTTTGCTCAAA 2142
MDO             GATGCCTATTTGTGCTTCAGTAGCAAAGACTTTGAATGGGTCCAGAATGCATTCCTCAAT 2145
SHA             GATGCATATTTGTGCTTCAGTAACAAGGACTTTGAATGGGTCCAGAATGCACTCCTCCAT 2139
OAN             GATGCTTATTTGTGCTTCAGTGGCAAGGACTTTGAGTGGGTCCAGAGAGCTTTTCTCATG 2139
GGA             GACGCATATTTGTGCTACAGCAAAAATGATTTCGAGTGGGTCCAGAATTCCTTGCTGAAG 2142
GLA             GACGCATATTTGTGCTACAGCAAAAATGATTTCGAGTGGGTCCAGAATTCCTTGCTGAAG 2142
MGA             GACGCATATTTGTGCTACAGCAAAAATGATTTCGAATGGGTCCAGAATTCTTTGCTGAAG 2145
PCO             GATGCATATTTGTGCTACAGCAAAAATGATTTCGAATGGGTCCAGAATTCCTTGCTGAAG 2142
NME             GATGCGTATTTGTGCTACAGCAAAAATGACTTTGAATGGGTCCAGAATTCTTTGCTGAAG 2142
TGU             GATGCTTATCTGTGCTACAGCAAAAATGACTTTGAATGGGTCCAGAATTCTTTGCTAAAG 2136
                ** **  *  * ****  **    *  ** **    ****  **     *  * **

PPA             CACCTGGACACTCAATACAGTGACGAAAACAGATTCAACCTGTGCTTTGAAGAAAGAGAC 2199
PTR             CACCTGGACACTCAATACAGTGACGAAAACAGATTCAACCTGTGCTTTGAAGAAAGAGAC 2199
HSA             CACCTGGACACTCAATACAGTGACCAAAACAGATTCAACCTGTGCTTTGAAGAAAGAGAC 2199
GGO             CACCTGGACAGTCAATACAGTGACCAAAACAGATTCAACCTGTGCTTTGAAGAAAGAGAC 2199
PPY             CACCTGGATACTCAATACAGTGACCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
MFA             CACCTGGACACTCAATACAGTGACCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
MMUL            CACCTGGACACTCAATACAGTGACCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
CTO             CACCTGGACACTCAATACAGTGACCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
CJA             CACCTGGACACTCAATACAGTGACCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2193
TSY             CACCTGGACACTCAGTATAGCACCCAAAACCAACTGAACCTGTGCTTTGAAGAAAGAGAC 2199
CHI             CACCTGGATGTCCAGTACAGCAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
OAR             CACCTGGATGTCCAGTATAGCAACCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
RRU             CACCTGGATGTCCAGTACAGCAGCCAGAACATATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
OGA             CACCTGGATGTCCAGTACAGCAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
OLE             CACCTGGATGTCCAGTACAGCAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
ODA             CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU1            CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU2            CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU3            CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU4            CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU5            CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU8            CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU9            CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU12           CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU14           CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU16           CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU18           CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BCA             CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU7            CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU11           CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU13           CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU17           CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU15           CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU6            CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBU10           CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
SCA1            CACTTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
SCA2            CACTTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA10           CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA16           CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA7            CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA3            CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA1            CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA2            CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA4            CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA6            CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA9            CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
```

```
BTA15           CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA12           CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA11           CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA14           CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BGR             CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGCC 2199
BTA5            CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA13           CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA8            CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA17           CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BTA18           CACCTGGATGTCCAGTACCACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BBI             CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
BJA             CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
TIM             CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
TST             CACCTGGATGTCCAGTACAACAGCCAAAACAGATTTAACCTGTGCTTTGAAGAAAGAGAC 2199
GCA             CACCTGGATGTCCAGTACAGCAGCCAAAACAGATTTAACTTGTGCTTTGAAGAAAGAGAC 2199
OHE             CACCTGGATGTCCAGTACAGCCCCCAAAACAGATTTAACTTGTGCTTTGAAGAAAGAGAC 2199
OVI             CACCTGGATGTCCAGTACAGCCCCCAAAACAGATTTAACTTGTGCTTTGAAGAAAGAGAC 2199
SSC             AACCTGGATGCCCAGTACAGCGACCAAAACAGATTGAACCTCTGCTTTGAAGAAAGAGAC 2196
PAL             CACCTGGACGCTCAGTACAGCGACCAAAACAGATTTCACCTGTGCTTTGAAGAGAGAGAC 2199
AME             CACCTGGATGCTCAGTACAGCGACCAGAACAGATTCAACCTGTGCTTTGAAGAAAGAGAC 2199
MPU             CACCTGGATGCTCAGTATAGTGCCCAGAACAGATTCAACCTGTGCTTTGAAGAAAGAGAC 2199
CLU             CACCTGGACGCTCAGTACAGCTCCCGAAACAGGCTGAACCTGTGCTTCGAGGAGAGGGAC 2199
ETE             CGCCTGGACACTCAGTACAGTGACCAGAACAGGTTTAGCCTGTGCTTTGAGGAAAGGGAC 2199
OPR             CATCTGGACAGACAATACAGTGACCAAAACAGATTCAACCTCTGCATTGAACAAAGAGAC 2199
MMU             CACCTGGATGCTCACTACAGTTCCCGAAACAGGCTCAGGCTATGCTTTGAAGAAAGAGAC 2202
MDO             CACTTGGACTCCCAGTACAGTCCCAAAAATAGATTTAATCTCTGTTTTGAGGAAAGAGAC 2205
SHA             CACTTAGACTCCCGGTACAATTCTGAAAATAGATTTAACCTGTGTTTCGAGGAAAGGGAC 2199
OAN             CACTTGGACTCCCAGTACAATGACAACAACAGATTTAACTTGTGCTTTGAAGAAAGAGAC 2199
GGA             CACCTGGATTCACAATATTTTGATAAAAACAGATTTACCTTGTGCTTTGAGGAACGAGAT 2202
GLA             CACCTGGATTCACAATATTTTGATAAAAACAGATTTACCTTGTGCTTTGAGGAACGAGAT 2202
MGA             CACCTGGATTCACAATATTTTGATAAAAACAGATTTACCTTGTGCTTTGAGGAACGAGAT 2205
PCO             CACCTGGATTCACAATATTTTGATAAAAACAGATTTACCCTGTGCTTTGAGGAACGAGAT 2202
NME             CACCTGGATTCACAATATTTTGATAAAAACAGATTTACTTTGTGCTTCGAGGAACGAGAT 2202
TGU             CACCTGGATTCGCAGTATTTTGATAAAAACAGATTTACTTTGTGTTTCGAAGAAAGAGAT 2196
                    * **    *  **          **     *     * **  * **  *  * *

PPA             TTTGTCCCAGGAGAAAACCGCATTGCCAATATCCAGGATGCCATCTGGAACAGTAGAAAG 2259
PTR             TTTGTCCCAGGAGAAAACCGCATTGCCAATATCCAGGATGCCATCTGGAACAGTAGAAAG 2259
HSA             TTTGTCCCAGGAGAAAACCGCATTGCCAATATCCAGGATGCCATCTGGAACAGTAGAAAG 2259
GGO             TTTGTCCCAGGAGAAAACCGCATTGCCAATATCCAGGATGCCATCTGGAACAGTAGAAAG 2259
PPY             TTTGTCCCAGGAGAAAACCGCATTGCCAATATCCAGGATGCCATCTGGAACAGTAGAAAG 2259
MFA             TTTGTCCCGGGAGAAAACCACATTGCCAATATCCAGGACGCCATCTGGAACAGTAGAAAG 2259
MMUL            TTTGTCCCGGGAGAAAACCACATTGCCAATATCCAGGACGCCATCTGGAACAGTAGAAAG 2259
CTO             TTTGTCCCGGGAGAAAACCACATTGCCAATATCCAGGACGCCATCTGGAACAGTAGAAAG 2259
CJA             TTTGTCCCAGGAGAAAACCACATTGCCAACATCCAGGACGCCATCTGGAACAGCAGAAAG 2253
TSY             TTTGTTCCAGGAGAAAACCACATCGCCAACATCCAGGATGCCATCTGCAGCAGCAGAAAG 2259
CHI             TTTATGCCTGGGGAAAACCACATCGCCAACATCCAGGATGCCGTGTGGAGCAGCAGGAAG 2259
OAR             TTTATGCCCGGGGAAAACCACATCGCCAACATCCAGGATGCCGTGTGGAGCAGCAGGAAG 2259
RRU             TTTATGCCCGGGGAAAACCACATCGCCAACATCCAGGATGCYGTGTGGAGCAGCAGGAAG 2259
OGA             TTTATGCCCGGGGAAAACCACATCGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
OLE             TTTATGCCCGGGGAAAACCACATCGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
ODA             TTTATGCCYGGGGAAAACCACATCGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU1            TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU2            TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU3            TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU4            TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU5            TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU8            TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU9            TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU12           TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU14           TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU16           TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU18           TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BCA             TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU7            TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU11           TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU13           TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
```

```
BBU17           TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU15           TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU6            TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BBU10           TTTATGCCTGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
SCA1            TTTATGCCCGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
SCA2            TTTATGCCCGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
BTA10           TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA16           TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA7            TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA3            TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA1            TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA2            TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA4            TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA6            TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA9            TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA15           TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA12           TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA11           TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA14           TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BGR             TTTATGCAGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA5            TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA13           TTTATGCCGGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA8            TTTATGCCSGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA17           TTTATGCCSGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BTA18           TTTATGCCCGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BBI             TTTATGCCCGGGGAAAACCACATTGCCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
BJA             TTTATGCCCGGGGAAAACCACATTGCCAACATCCAGGATGCYGTGTGGAGCAGCAGAAAG 2259
TIM             TTTATGCCYGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAA 2259
TST             TTTATGCCCGGGGAAAACCACATTGCCAACATCCAGGATGCCGTGTGGAGCAGCAGAAAG 2259
GCA             TTTATGCCCGGGGTAAACCATATCACCAACATCCAGGATGCTGTGTGGAGCAGCAGAAAG 2259
OHE             TTTATGCCCGGGGAAAACCACATCGCCAACATCCAAGATGCTGTGTGGAGCAGCAGGAAG 2259
OVI             TTTATGCCCGGGGAAAACCACATCGCCAACATCCAAGATGCTGTGTGGAGCAGCAGGAAG 2259
SSC             TTTGTGCCGGGGGAAGATCGCATCAGCAACATCCAGGATGCCGTGTGGAGCAGCAGGAAG 2256
PAL             TTCATGCCAGGGGAAGACCACATCGCTAACATCCACAACGCCGTGCGGAGCAGCAGGAAG 2259
AME             TTCGTCCCGGGGCGGGAGCACATCGCCAACATCCAGGATGCCGTGTGGGGCAGCAGGAAG 2259
MPU             TTTGTCCCGGGGCGGGAGCATATCGCCAACATCCAGGATGCCGTGTGGGGCAGCAGGAAG 2259
CLU             TTCGTCCCGGGGCGGGAGCACATCGCCAACATCCAGGACGCCGTGTGGAGCAGCCGCAAG 2259
ETE             TTCGTTCCTGGGGAGAACCATGTGGTCAACATCCAGGACGCCGTGTGGAGCAGCCGGAAG 2259
OPR             TTTGTCCCGGGAGAAAACCACATCACCAACATCCAGGCTGCTGTCTGGAGCAGTAGGAAG 2259
MMU             TTCATTCCAGGGGAAAACCATATCTCCAACATCCAGGCGGCTGTCTGGGGCAGCAGGAAG 2262
MDO             TTCCTTCCAGGAGAAGACCACATCAACAACATCCGGGACGCCATATGCAACAGCAAGAAA 2265
SHA             TTCCTTCCAGGAGAAGACCACATCAACAACATCCGGGATGCCATTTGGAGCAGCAGAAAG 2259
OAN             TTCCTACCAGGAGAAGATCATATTAGCAACATCCGAGATGCCATCTGGAACAGCAGAAAG 2259
GGA             TTCTTGCCTGGGGAAGAACATATCAACAATATTCGTGATGCTATTTGGAAGAGCAGGAAA 2262
GLA             TTCTTGCCTGGGGAAGAACATATCAACAATATTCGTGATGCTATTTGGAAGAGCAGGAAA 2262
MGA             TTCTTGCCTGGGGAAGAACATATCAACAATATTCGTGATGCTATTTGGAAGAGCAGGAAA 2265
PCO             TTCTTGCCTGGGGAAGAACATATCAACAATATTCGTGATGCTATTTGGAAGAGCAGGAAA 2262
NME             TTCTTGCCTGGGGAAGAACATATCAACAATATTCGTGATGCTATTTGGAAGAGCAGGAAA 2262
TGU             TTCTTGCCTGGGGAAGAACATATCAACAATATTCGTGATGCCATTTGGAGCAGCAGGAAA 2256
                **  * *  **     * *   *    ** ** *     **  *  *    **    **

PPA             ATTGTTTGTCTTGTGAGCAGACACTTCCTTAGAGATGGCTGGTGCCTTGAAGCCTTCAGT 2319
PTR             ATTGTTTGTCTTGTGAGCAGACACTTCCTTAGAGATGGCTGGTGCCTTGAAGCCTTCAGT 2319
HSA             ATCGTTTGTCTTGTGAGCAGACACTTCCTTAGAGATGGCTGGTGCCTTGAAGCCTTCAGT 2319
GGO             ATCGTTTGTCTTGTGAGCAGACACTTCCTTAGAGATGGCTGGTGCCTTGAAGCCTTCAGT 2319
PPY             ATTGTTTGTCTTGTGAGCAGACATTTCCTTAGCGATGGCTGGTGCCTTGAAGCCTTCAGT 2319
MFA             ATTGTTTGTCTTGTGAGCAGACACTTCCTTAGAGATGGTTGGTGCCTTGAAGCCTTCAGT 2319
MMUL            ATTGTTTGTCTTGTGAGCAGACACTTCCTTAGAGATGGTTGGTGCCTTGAAGCCTTCAGT 2319
CTO             ATTGTTTGTCTTGTGAGCAGACACTTCCTTAGAGATGGTTGGTGCCTTGAAGCCTTCAGT 2319
CJA             ACTGTTTGTCTTGTGAGCAGACACTTCCTTAGAGATGGCTGGTGCCTTGAAGCCTTCAGT 2313
TSY             ATTGTTTGTCTTGTGAGCAGACACTTCCTTAGAGATGGCTGGTGTCTGGAAGCCTTCAGT 2319
CHI             ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
OAR             ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
RRU             ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
OGA             ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
OLE             ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
ODA             ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
```

```
BBU1            ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU2            ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU3            ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU4            ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU5            ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU8            ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU9            ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU12           ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU14           ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU16           ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU18           ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BCA             ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU7            ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU11           ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU13           ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU17           ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU15           ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU6            ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBU10           ACTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
SCA1            ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
SCA2            ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA10           ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA16           ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA7            ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA3            ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA1            ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA2            ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA4            ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA6            ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA9            ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA15           ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA12           ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA11           ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA14           ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BGR             ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA5            ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA13           ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA8            ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA17           ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BTA18           ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BBI             ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
BJA             ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
TIM             ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
TST             ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
GCA             ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGAGACGGGTGGTGCCTCGAAGCCTTCAAT 2319
OHE             ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGGGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
OVI             ATTGTCTGTCTCGTGAGCAGACACTTCCTTAGGGACGGGTGGTGCCTCGAAGCCTTCAGT 2319
SSC             GTTGTCTGTCTGGTGAGCAGACACTTCCTTAGGGACGGCTGGTGCCTGGAAGCCTTCAGT 2316
PAL             GTCGTGTGCCTGGTGAGCAGACACTTCCTCAGAGACGGCTGGTGCCTCGAAGCCTTCAGC 2319
AME             GTGGTCTGTCTCGTGAGCAGACACTTCCTCCGAGACGGCTGGTGCCTGGAAGCCTTCACT 2319
MPU             GTGGTCTGCCTCGTGAGCCGACACTTCCTCCGGGACGGGTGGTGCCTGGAAGCCTTTGCC 2319
CLU             GTGGTCTGTCTGGTGAGCAGGCACTTCCTCCGCGACGGGTGGTGCCTGGAGGCCTTCGCG 2319
ETE             ATTGTGTGCCTTGTGAGCAGACACTTTCTCCGAGATGGGTGGTGCCTCGAAGCCTTCAGT 2319
OPR             ATAGTCTGTCTGGTGAGCAGACACTTCCTTCGGGACGGATGGTGCCTGGAAGCCTTCAGT 2319
MMU             ACGGTGTGTCTAGTGAGCAGACACTTCCTGAAGGATGGTTGGTGCCTGGAGGCCTTCAGG 2322
MDO             ACCATTTGCATTGTGACGAGGCATTTCCTTAAAGATGGCTGGTGCATTGAAGCCTTCAAT 2325
SHA             ACTATTTGCATTGTGACAAAGCATTTCCTGAAAGATGGCTGGTGCATTGAAGCCTTCAAT 2319
OAN             ACAATTTGCGTGGTCACGAGGCAGTTCCTCAAAGACGGCTGGTGTATTGAAGCCTTCAAT 2319
GGA             ACAATTTGTGTTGTGACCAGGCAGTTTCTCAAAGATGGGTGGTGTGTAGAAGCCTTTAAT 2322
GLA             ACAATTTGTGTTGTGACCAGGCAGTTTCTCAAAGATGGGTGGTGTGTAGAAGCCTTTAAT 2322
MGA             ACAATTTGTGTTGTGACCAGGCAGTTTCTCAAAGATGGGTGGTGTGTAGAAGCCTTTAAT 2325
PCO             ACAATTTGTGTTGTTACCAGGCATTTTCTCAAAGATGGATGGTGTGTAGAAGCCTTTAAT 2322
NME             ACAATTTGTGTTGTGACCAGGCAGTTTTTCAAAGATGGGTGGTGTGTAGAAGCCTTTAAT 2322
TGU             ACAATTTGCATTGTAACCAGGCATTTTCTCACAGATGGGTGGTGTGTGGAAGCCTTTAAT 2316
                    * **  * ** *     ** **  *    ** ** *****  * ** *****

PPA             TATGCCCAGGGCAGGTGCTTATCTGACCTTAACAGTGCTCTCATTATGGTGGTGGTTGGG 2379
```

PTR	TATGCCCAGGGCAGGTGCTTATCTGACCTTAACAGTGCTCTCATTATGGTGGTGGTTGGG	2379
HSA	TATGCCCAGGGCAGGTGCTTATCTGACCTTAACAGTGCTCTCATCATGGTGGTGGTTGGG	2379
GGO	TATGCCCAGGGCAGGTGCTTATCTGACCTTAACAGTGCTCTCATCATGGTGGTGGTTGGG	2379
PPY	TATGCCCAGGGCAGGTGCTTATCTGACCTTAACAGTGCTCTCATCATGGTGGTGGTTGGG	2379
MFA	TATGCCCAGGGCAGGTGCTTATCTGACCTTAACAGTGCTCTCATCATGGTGGTGGTTGGG	2379
MMUL	TATGCCCAGGGCAGGTGCTTATCTGACCTTAACAGTGCTCTCATCATGGTGGTGGTTGGG	2379
CTO	TATGCCCAGGGCAGGTGCTTATCTGACCTTAACAGTGCTCTCATCATGGTGGTGGTTGGG	2379
CJA	TATGCCCAGGGCAGGTGCTTGTCTGACCTTAACAGTGCTCTCATCATGGTGGTGGTTGGG	2373
TSY	TATGCCCACGGCAGGTGCTTGTCTGACCTTAACAGTGCCCTCATCATGGTGGTGGTTGGG	2379
CHI	TACGCCCAGAGCAGGTGCTTAGCTGACCTCAGCGGCGCCCTCATCATGGTGGTGGTGGGG	2379
OAR	TACGCCCAGAGCAGGTGCTTAGCTGACCTCAACGGCGCCCTCATCATGGTGGTGGTGGGG	2379
RRU	TACGCCCAGAGCAGGTGCTTAGCTGACCTCAACAGCGCCCTCATCATGGTGGTGGTGGGG	2379
OGA	TACGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
OLE	TACGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCACCCTCATCATGGTGGTGGTGGGG	2379
ODA	TACGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU1	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU2	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU3	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU4	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU5	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU8	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU9	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU12	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU14	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU16	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU18	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BCA	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU7	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU11	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU13	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU17	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU15	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU6	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBU10	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
SCA1	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
SCA2	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAGTGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA10	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA16	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA7	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA3	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA1	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA2	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA4	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA6	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA9	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA15	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA12	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA11	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA14	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BGR	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA5	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA13	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA8	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA17	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BTA18	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BBI	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
BJA	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
TIM	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
TST	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
GCA	TACGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTGGTGGTGGGG	2379
OHE	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTAGTGGTGGGG	2379
OVI	TATGCCCAGAGCAGGTGCTTAGCTGACCTCAATGGCGCCCTCATCATGGTAGTGGTGGGG	2379
SSC	TACGCCCAGAGCAGGTGCTTAGCAGACCTCAATGGCACCCTCATCATGGTGGTGGTTGGG	2376
PAL	TACGCCCAGAGCAGGGCCCTGGCCTACCTGAACGGCGCCCTCATCATGGTGGTGGTCGGG	2379
AME	TACGCCCAGAACAGGTGCGTGTCTGACCTGGACGGCGCCCTCATCCTGGTGATCGTCGGG	2379
MPU	TACGCCCAGAGCAGGTGTGTGTCTGATGCGGACGGTGCCCTCATCCTGGTGATCGTCGGG	2379
CLU	GCCGCGCGGAGCCGCTGCGCGTCCCACCTGGACGGCGCCCTCGTCCTGGTGGTCGTGGGC	2379

```
ETE             TACGCCCAGAGCAGGTGCCTCGCCGACCTCCGCAGTGCCCTCATCGTGGTGGTGGTTGGG 2379
OPR             TATGCCCAGAGCAGGTGTTTGTCTGATGTCAGCAGCACCCTCATCATGGTGGTAGTCGGG 2379
MMU             TATGCCCAGAGCCGGAGTCTGTCTGATCTCAAGAGCATTCTCATCGTGGTGGTGGTGGGA 2382
MDO             TTTGCTCAGAGCAGATATTTCTCTGATCTCAAAGATGTCCTCATAATGGTGGTAGCTGGA 2385
SHA             TTTGCCCAGAGCAGATACTTCTCTGATCTTAAAGATGTCCTCATCATGGTGGTAGCCGGA 2379
OAN             TTTGCCCAGAGCAGATATTTCTCTGACCTTAAGGATAGACTAATCATGGTAGTGGCAGGA 2379
GGA             TTTGCCCAGAGCAGGTACTTCAGTGATTTGAAAGAGGTTCTCATTATGGTAGTGGTTGGG 2382
GLA             TTTGCCCAGAGCAGGTACTTCAGTGATTTGAAAGAGGTTCTCATTATGGTAGTGGTTGGG 2382
MGA             TTTGCCCAGAGCAGGTACTTCAGTGATTTGAAAGAGGTTCTCATTATGGTAGTAGTTGGG 2385
PCO             TTTGCCCAGAGCAGATACTTCAGTGATTTGAAAGAGGTTCTCATTATGGTAGTAGTTGGG 2382
NME             TTTGCCCAGAGCAGGTACTTCAGTGATTTGAAAGAGGTTCTCATTATGGTAGTAGTTGGG 2382
TGU             TTTGCCCAGAGCAGGTACTTCTGTGATCTGAAGGATGTCCTTATTATGGTAGTGGTTGGG 2376
                   ** *    * *           *             **  *  ****  * *  **

PPA             TCCTTGTCCCAGTACCAGTTGATGAAACATCAATCCATCAGAGGCTTTGTACAGAAACAG 2439
PTR             TCCTTGTCCCAGTACCAGTTGATGAAACATCAATCCATCAGAGGCTTTGTACAGAAACAG 2439
HSA             TCCTTGTCCCAGTACCAGTTGATGAAACATCAATCCATCAGAGGCTTTGTACAGAAACAG 2439
GGO             TCCTTGTCCCAGTACCAGTTGATGAAACATCAATCCATCAGAGGCTTTGTACAGAAACAG 2439
PPY             TCCTTGTCCCAGTACCAGCTGATGAAACATCAGTCCATCAGAGGCTTTGTACAGAAACAG 2439
MFA             TCCTTGTCCCAGTACCAGTTGATGAAACATCAATCCATTAGAGGCTTTGTACAGAAACAG 2439
MMUL            TCCTTGTCCCAGTACCAGTTGATGAAACATCAATCCATTAGAGGCTTTGTACAGAAACAG 2439
CTO             TCCTTGTCCCAGTACCAGTTGATGAAACATCAATCCATTAGAGGCTTTGTACAGAAACAG 2439
CJA             TCCTTGTCCCCGTACCAGTTGATGAAACATCAATCCATCAGAGGCTTTGTACAGAATCAG 2433
TSY             TCCCTGTCCCAGTACCAGTTGATGAAACATCAACCCATTAGGGGCTTCATACATAAAAAG 2439
CHI             TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
OAR             TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
RRU             TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
OGA             TCCCTGTCCCAGTTCCATTTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
OLE             TCCCTGTCCCAGTTCCATTTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
ODA             TCCCTGTCCCAGTTCCATTTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU1            TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU2            TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU3            TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU4            TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU5            TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU8            TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU9            TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU12           TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU14           TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU16           TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU18           TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BCA             TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU7            TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU11           TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU13           TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU17           TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU15           TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU6            TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBU10           TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
SCA1            TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
SCA2            TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTYGTCCAGGAACGG 2439
BTA10           TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA16           TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA7            TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA3            TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA1            TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA2            TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA4            TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA6            TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA9            TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA15           TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA12           TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA11           TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA14           TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BGR             TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA5            TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA13           TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
```

```
BTA8            TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA17           TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BTA18           TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BBI             TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
BJA             TCCCTGTCCCAGTTCCATCTGATGAGGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
TIM             TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
TST             TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
GCA             TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGTCCATCAGAGGGTTCGTCCAGAAACGG 2439
OHE             TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGCCCATCAGAGGGTTCGTCCAGAAACAG 2439
OVI             TCCCTGTCCCAGTTCCATCTGATGAAGCATCAGCCCATCAGAGGGTTCGTCCAGAAACAG 2439
SSC             TCCCTGCCTCAGTATCAACTGATGAAGCATCAGTCCATCAGAGGATTTGTCCGGAAACAG 2436
PAL             TCCTTGTCCCAGTACCAGCTCATGAAACACGAGGCCGTCAGGGCCTTTGTACAGAAACGG 2439
AME             TCCCTATCCCAGTATGACCTGAGGAAGCATCAGTGTATCAGAGGGTTTGTGCGGAAGCGA 2439
MPU             TCCCTGTCCCGGTTCCAGCTGATGAAGCACCGGGGCATTGCAGGGTTTGTGCGGAAACGG 2439
CLU             TCCCTGTCGCAGTACCAGCTGAGGAGGCACCCGGCCATCGGGGGCTTCGTGCGGCAGCGC 2439
ETE             TCCCTGTCCCAGTACCAGCTGATGAAGCACCGGCCCCTCCAAGGGTTCATCCAGAAGCAG 2439
OPR             ACTCTGAGTCAATATCAGCTGATGAAGCATCAATACCTCCGAGGCTTTGTGCAGAAGCAG 2439
MMU             TCGCTGTCCCAGTATCAGCTGATGAGACATGAGACCATCAGAGGGTTTCTGCAAAAGCAA 2442
MDO             TCCCTCTCCCAGTATCAGCTAATGAAATACCCACCTATCCGAGTCTTTGTACAGAGGCAA 2445
SHA             TCACTCTCCCAGTATCAACTGATGAAATACCCACCAATCCGAGTCTTTGTGCAGAGGCAA 2439
OAN             TCACTCTCTCAGTATCAGCTGATGAAGTACCAACCCATTAGGGTCTTTATCCAGAGGCAA 2439
GGA             TCACTTTCTCAATATCAACTGATGAAACACAAACCAATTCGAATTTTTTTACAAAGGAGT 2442
GLA             TCACTTTCTCAATATCAACTGATGAAACACAAACCAATTCGAATTTTTTTACAAAGGAGT 2442
MGA             TCACTTTCTCAATATCAACTGATGAAACACAAACCAATTCGAATTTTTTTACAAAGGAGT 2445
PCO             TCACTTTCTCAATATCAGCTGATGAAACACAAGCCAATTCGAATTTTTTTACAAAGAAGT 2442
NME             TCACTCTCTCAATATCAACTGATGAAACACAAACCAATTCGAATCTTTTTACAAAGGAGT 2442
TGU             TCACTTTCTCAGTATCAACTGAAGAAACACAAACCAATTCGAAACTTCTTACAAAGGAGT 2436
                 *  *    *  *   *  * * **    *        *      **  * *

PPA             CAGTATTTGAGATGGCCTGAGGATCTCCAGGATGTTGGCTGGTTTCTTCATAAACTCTCT 2499
PTR             CAGTATTTGAGGTGGCCTGAGGATCTCCAGGATGTTGGCTGGTTTCTTCATAAACTCTCT 2499
HSA             CAGTATTTGAGGTGGCCTGAGGATCTCCAGGATGTTGGCTGGTTTCTTCATAAACTCTCT 2499
GGO             CAGTATTTGAGGTGGCCTGAGGATCTCCAGGATGTTGGCTGGTTTCTTCATAAACTCTCT 2499
PPY             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGGCTGGTTTCTTCATAAACTCTCT 2499
MFA             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGGCTGGTTTCTTCATAAACTCTCT 2499
MMUL            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGGCTGGTTTCTTCATAAACTCTCT 2499
CTO             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGGCTGGTTTCTTCATAAACTCTCT 2499
CJA             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATATTGGCTGGTTTCTTCATAAACTCTCT 2493
TSY             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGGCTGGTTTCTTAATAAACTGTCT 2499
CHI             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
OAR             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
RRU             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAGTAAACTCTCT 2499
OGA             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
OLE             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
ODA             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU1            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU2            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU3            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU4            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU5            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU8            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU9            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU12           CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU14           CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU16           CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU18           CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BCA             CAGTACTTGAGGTGGCCTGAGGATYTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU7            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU11           CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU13           CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU17           CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU15           CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU6            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBU10           CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
SCA1            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
SCA2            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA10           CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
```

```
BTA16           CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA7            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA3            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA1            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA2            CAGTACTTGAGGTGGCCTGARGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA4            CAGTACTTGAGGTGGCCTGARGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA6            CAGTACTTGAGGTGGCCTGARGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA9            CAGTACTTGAGGTGGCCTGARGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA15           CAGTACTTGAGGTGGCCTGARGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA12           CAGTACTTGAGGTGGCCTGARGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA11           CAGTACTTGAGGTGGCCTGAAGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA14           CAGTACTTGAGGTGGCCTGAAGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BGR             CAGTACTTGAGGTGGCCTGAAGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA5            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA13           CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA8            CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA17           CAGTACTTGAGGTGGCCTGARGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BTA18           CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BBI             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
BJA             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
TIM             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
TST             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
GCA             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGATGTTGACTGGTTTCTCAATAAACTCTCT 2499
OHE             CARTACTTGAGGTGGCCTGAGGATCTCCAGGATGTCGACTGGTTTCTCAATAAACTCTCT 2499
OVI             CAATACTTGAGGTGGCCTGAGGATCTCCAGGATGTCGACTGGTTTCTCAATAAACTCTCT 2499
SSC             CAGTACTTGAGGTGGCCTGAGGATCTCCAGGACGTCAGCTGGTTTCTCAACAAGCTCTCT 2496
PAL             CAGTACCTGAGGTGGCCGGAGGATCTCCAGGACGTCGGCCGGTTTCTCGATAAACTCTCT 2499
AME             CAGTACTTGAGGTGGCCCGAGGATCTCCAGGACGTTGGCTGGTTCCTTCACACACTCTCT 2499
MPU             CACTACCTGAGGTGGCCCGAGGACCTCCAGGACGTGGGCTGGTTCCTTCACACACTCTCC 2499
CLU             CGGTACTTGAGGTGGCCCGAGGATCTGCAGGACGTGGGCTGGTTCCTGGACACGCTCTCC 2499
ETE             CAGTACTTGAGGTGGCCTGAGGACATGCAGGACGTGGAATGGTTTCTCAATAAACTCTCT 2499
OPR             CTGTACTTGAGGTGGCCTGAGGATCTCCAAGATGTCCACTGGTTCCTCAATAGACTGTCT 2499
MMU             CAGTACTTGAGGTGGCCTGAAGACCTCCAGGATGTTGGCTGGTTTCTCGATAAACTCTCC 2502
MDO             CCATACCTGAAGTGGCCTGAGGACCTTCAGGATGTTGGCTGGTTCTTAAATAAACTCTCC 2505
SHA             CCATACCTGAAGTGGCCAGAGGACCTTCAGGATGTTGGCTGGTTCTTAAATAAACTCTCT 2499
OAN             CACTACTTGAAGTGGCCTGAGAATCTTCAGGACATTGGGTGGTTTCTAGATAAACTCTCC 2499
GGA             CGATATCTGCGTTGGCCTGAAGATTATCAAGATATAGGCTGGTTTTTGGATAACCTTTCT 2502
GLA             CGATATCTGCGTTGGCCTGAAGATTATCAAGATATAGGCTGGTTTTTGGATAATCTTTCT 2502
MGA             CGATATCTGCGTTGGCCTGAAGATTATCAAGATATAGACTGGTTTTTAGATAGCCTTGCT 2505
PCO             CGATATCTGCGTTGGCCTGAAGATTATCAAGATATAGACTGGTTTTTAGATAACCTTTCT 2502
NME             CGGTATTTGCGTTGGCCTGAAGATTATCAAGATATAGACTGGTTTCTAGATAACCTTTCT 2502
TGU             CAGTATTTGCGGTGGCCTGAAGATTATCAAGATGTAGACTGGTTTTTAGATAACCTTTCT 2496
                *  **  **   ***** **  *    ** **  *     ****  *    *  **  *

PPA             CAACAGATACTAAAGAAAGAAAAAGAAAAGAAGAAAGACAATAA---CATTCCGTTGCAA 2556
PTR             CAACAGATACTAAAGAAAGAAAAAGAAAAGAAGAAAGACAATAA---CATTCCGTTGCAA 2556
HSA             CAACAGATACTAAAGAAAGAAAAAGAAAAGAAGAAAGACAATAA---CATTCCGTTGCAA 2556
GGO             CAACAGATACTAAAGAAAGAAAAAGAAAAGAAGAAAGACAATAA---CATTCCGTTGCAA 2556
PPY             CAACAGATACTAAAGAAAGAAAAAGAAAAGAAGAAAGACAATAA---CATTCCGTTGCAA 2556
MFA             CAACAGATACTAAAGAAAGAAAAAGAAAAGAAGAAAGACAGTAA---CATTCCGTTGCGA 2556
MMUL            CAACAGATACTAAAGAAAGAAAAAGAAAAGAAGAAAGACAGTAA---CATTCCGTTGCGA 2556
CTO             AAACAGATACTAAAGAAAGAAAAAGAAAAGAAGAAAGACAGTAA---CATTCCGTTGCGA 2556
CJA             CAACAGATACTAAAGAAAGAAAAAGAAAAGAAGAAAGACAGTAA---CATTCCTTTGCAA 2550
TSY             CAACAGATACTAAAGAAAGAAAAAGAAAAGAAGAAAGACAATAATAACATTCAGTTGCAA 2559
CHI             CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
OAR             CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
RRU             CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
OGA             CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
OLE             CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
ODA             CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BBU1            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU2            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU3            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU4            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU5            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU8            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU9            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
```

```
BBU12           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU14           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU16           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU18           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BCA             CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU7            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU11           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU13           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU17           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU15           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU6            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BBU10           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
SCA1            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
SCA2            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BTA10           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA16           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA7            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA3            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA1            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA2            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA4            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA6            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA9            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA15           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA12           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA11           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA14           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BGR             CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA5            CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA13           CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA8            CAATGCATTCTAAAGAAAGAAAAGRAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA17           CAATGCATTCTAAAGAAAGAAAAGRAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BTA18           CAATGCATTCTAAAGAAAGAAAAGRAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
BBI             CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTAC---TATTCAGCTGCAA 2556
BJA             CAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTRC---TATTCAGCTGCAA 2556
TIM             CAATGCATTCTAAAGAAAGAAAAGGAAAAGAAGAAAGACAGTGC---TATTGAGTTGCAA 2556
TST             CAATGCATTCTAAAGAAAGAAAAGGAAAAGAAGAAAGACAGTGC---TATTGAGTTGCAA 2556
GCA             GAATGCATTCTAAAGAAAGAAAAGGAAAGGAAGAAAGACAGTGC---TGTTCAGCTGCAA 2556
OHE             CAATGCATTCTAAAGGAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
OVI             CAATGCATTCTAAAGGAAGAAAAGGAAAGGAAGAAAGACAGTGC---TATTCAGCTGCAA 2556
SSC             CAATACATTCTAAAGAAAGTCAAGGAAAAGAAGAAAGACAGCGA---CATTCAGTTGCAA 2553
PAL             CAGCACCTACTACGGAAGGAAAAGGAAAAGAAGAAAGACGACAG---CATTCAGCTGCAA 2556
AME             CAGCACATTCTGAAGAAAGGGAAGGACGCCAAGAGGGACGGTAG---CATCCCACTGCAA 2556
MPU             CAGCACATTCTGAAGAGAGAGAAGGACACCATCAGGGATGGGAG---CATCCAGCTGCAG 2556
CLU             CGACACATCCTGCAGGAGCAGAGGGGCGCGCGCGGGGATGGCGG---CATCCCGCTGCGC 2556
ETE             CGGGAAATACTCAAGAAAGAGAAGAAACAGAAGAGAGGAAGTAG---CATCCCACTGCAA 2556
OPR             CAATGCATAGTGAAGAAGGAGAGACCAAAGAAGAGAGGTGAAAG---CATTATGCTGCAA 2556
MMU             GGATGCATTCTAAAGGAAGAAAAAGGAAAGAAAAGAAGCAGTTC---CATCCAGTTGCGA 2559
MDO             CAACGCATATTAAACAAAAAAGAAGAAAAGAAGAAATCCAATAA---CATCCCCTTGCAA 2562
SHA             CAAAGCATACTTACCAAAAAAGAAGAAAAGAAGAAATCCAACAA---CATCGCCTTACAA 2556
OAN             CAATCTGTGCTAAAGGAAAAGGATGTGAAAAAGAAAGCCAACCA---GATAGAGCTGCAA 2556
GGA             TCCCAAATTCTGAAGGAAAAAAAAGTGCAAAGGAACGTCAGTGG---TATAGAGCTGCAA 2559
GLA             TCCCAAATTCTGAAGGAAAAAAAAGTGCAAAGGAATGTCAGTGG---TATAGAGCTGCAA 2559
MGA             TCCCAAATTCTGAAGGAAAAAAAAGTGCAAAGGGATGTCAGTGG---TACAGAGCTGCAA 2562
PCO             TCCCAAATTCTGAAGGAAAAAAAAGTGCAAAGGAATGTCAGTGG---TATAGAGCTGCAA 2559
NME             TGCCAAATTCTGAAGGAAAAAAAAGTGCAAAGGAACGTCAGTGG---TATAGAGCTGCAA 2559
TGU             TGCCAAATTCTGAAGGAAAAAAAAGTGCAAAGGAAAACCAGTGG---TATAGAGCTGCAG 2553
                       *  *                                            * *

PPA             ACTGTAGCAACCATCTC---CTAA 2577
PTR             ACTGTAGCAACCATCTC---CTAA 2577
HSA             ACTGTAGCAACCATCTC---CTAA 2577
GGO             ACTGTAGCAACCATCTC---CTAA 2577
PPY             ACTGTAGCAACCATCTC---CTAA 2577
MFA             ACTGTAGCAACCATCTC---CTAA 2577
MMUL            ACTGTAGCAACCATCTC---CTAA 2577
CTO             ACTGTAGCAACCATCTC---CTAA 2577
```

```
CJA             ACCGTGGCAACCATCTC---CTAA 2571
TSY             AGTGTTGCAACTATCTC---CTAA 2580
CHI             AGTGTAACCACCATCTC---CTAG 2577
OAR             AGTGTAACCACCATCTC---CTAG 2577
RRU             AGTGTAACCACCGTCTC---CTAG 2577
OGA             AGTGTAACCACCATCTC---CTAG 2577
OLE             AGTGTAACCACCATCTC---CTAG 2577
ODA             AGTGTAACCACCATCTC---CTAG 2577
BBU1            AATGTAACCACCATCTC---CTAG 2577
BBU2            AATGTAACCACCATCTC---CTAG 2577
BBU3            AATGTAACCACCATCTC---CTAG 2577
BBU4            AATGTAACCACCATCTC---CTAG 2577
BBU5            AATGTAACCACCATCTC---CTAG 2577
BBU8            AATGTAACCACCATCTC---CTAG 2577
BBU9            AATGTAACCACCATCTC---CTAG 2577
BBU12           AATGTAACCACCATCTC---CTAG 2577
BBU14           AATGTAACCACCATCTC---CTAG 2577
BBU16           AATGTAACCACCATCTC---CTAG 2577
BBU18           AATGTAACCACCATCTC---CTAG 2577
BCA             AATGTAACCACCATCTC---CTAG 2577
BBU7            AATGTAACCACCATSTC---CTAG 2577
BBU11           AATGTAACCACCATSTC---CTAG 2577
BBU13           AATGTAACCACCATSTC---CTAG 2577
BBU17           AATGTAACCACCATSTC---CTAG 2577
BBU15           AATGTAACCACCATSTC---CTAG 2577
BBU6            AATGTAACCACCATSTC---CTAG 2577
BBU10           AATGTAACCACCATCTC---CTAG 2577
SCA1            AATGTAACCACCATCTC---CTAG 2577
SCA2            AATGTAACCACCATCTC---CTAG 2577
BTA10           AATGTAACCACCATCTC---CTAG 2577
BTA16           AATGTAACCACCATCTC---CTAG 2577
BTA7            AATGTAACCACCATCTC---CTAG 2577
BTA3            AATGTAACCACCATCTC---CTAG 2577
BTA1            AATGTAACCACCATCTC---CTAG 2577
BTA2            AATGTAACCACCATCTC---CTAG 2577
BTA4            AATGTAACCACCATCTC---CTAG 2577
BTA6            AATGTAACCACCATCTC---CTAG 2577
BTA9            AATGTAACCACCATCTC---CTAG 2577
BTA15           AATGTAACCACCATCTC---CTAG 2577
BTA12           AATGTAACCACCATCTC---CTAG 2577
BTA11           AATGTAACCACCATCTC---CTAG 2577
BTA14           AATGTAACCACCATCTC---CTAG 2577
BGR             AATGTAACCACCATCTC---CTAG 2577
BTA5            AATGTAACCACCATCTC---CTAG 2577
BTA13           AATGTAACCACCATCTC---CTAG 2577
BTA8            AATGTAACCACCATCTC---CTAG 2577
BTA17           AATGTAACCACCATCTC---CTAG 2577
BTA18           AATGTAACCACCATCTC---CTAG 2577
BBI             AATGTAACCACCATCTC---CTAG 2577
BJA             AATGTAACCACCATCTC---CTAG 2577
TIM             AATGTAACCACCATCTC---CTAG 2577
TST             AATGTAACCACCATCTC---CTAG 2577
GCA             AATGTAACCACAATCTC---CTAG 2577
OHE             AGTGTAACCACCATCTC---CTAG 2577
OVI             AGCGTAACCACCATCTC---CTAG 2577
SSC             AGCGTGACCA---TCTC---CTAG 2571
PAL             ACTATAGCAACCATCTC---CTAG 2577
AME             ACTGTGGCGGCCGTCTC---CTAG 2577
MPU             GCTGTGGTGACCGTCTC---CTAG 2577
CLU             ACCGTGGCGGCCGTCGC---CTAG 2577
ETE             ACGGTAGCAACCATCTC---CTAG 2577
OPR             ACTGTGGCCACCATCTC---CTAG 2577
MMU             ACCATAGCAACCATTTC---CTAG 2580
MDO             ACTGTAGCAACCATATC---CTAA 2583
SHA             ACCGTAGCAACTGTATC---CTAG 2577
OAN             ACTATTAGAATGACATC---TTAG 2577
GGA             ACTATAGCGACAGTCTCACACTGA 2583
```

```
GLA             ACTATAGCGACAGTCTCACACTGA 2583
MGA             ACTATAGCGACAGTCTCACGCTGA 2586
PCO             ACTATAGCGACAGTCTCACACTGA 2583
NME             ACTATAGCGACAGTCTCACACTGA 2583
TGU             CCTGTAGCAACTGTCTCACATTGA 2577
                    *           *    *
```