

Intraspecific and intragenomic variation as measured from the dual control  
regions of the Western Cottonmouth, *Agkistrodon piscivorus leucostoma*  
mitochondrial genome

Dallas Lee Flickinger

Major Professor Dr. A Bruce Cahoon

Professor, Department of Biology

Thesis Committee:

Dr. Ashley Morris and Dr. Brian Miller

Middle Tennessee State University

Murfreesboro, Tennessee

December 2013

*Dedicated to Dr. Dallas Alston and Denny Guritza, who told me to take a step  
outside the box.*

### **Acknowledgements**

I thank Dr. Bruce Cahoon for mentoring me through my years in graduate school as he has helped me through the most adverse moments, he has shown patience somehow, and has been a great influence on my work ethic. I thank my committee, Dr. Ashley Morris and Dr. Brian Miller for their knowledge and their input. I thank Chris Davis and Dr. Matthew Elrod-Erickson for their invaluable input during the process of my revisions. I would also like to thank my parents, Michael and Sandi Flickinger for their advice and support throughout my academic career. I would finally like to thank my two brothers, Chris and Will, my many friends back home in Kansas and Illinois, my friends here in Tennessee, and friends and family in Brazil.

## Abstract

Snake mitochondrial genomes have the unusual feature of dual control regions. Control regions are intergenic areas that are responsible for DNA replication and transcription initiation. Although they are functional, they do not code for protein, and it is hypothesized that these regions can sustain greater rates of mutation than other parts of the genome. Despite this assumption, there are no published studies that compare control regions from multiple individuals from a population. In this study, I successfully sequenced both control regions from individual cottonmouth snakes (*Agkistrodon piscivorus leucostoma*) collected from a single, large, interbreeding population living within a 20-mile radius near Caddo Lake, Texas. The dual control regions within this population showed three polymorphisms at paralogous bases within the two control regions. There were also two indels found only in control region 2. These polymorphisms could be grouped into eight haplogroups, suggesting the control regions may sustain a high level of mutation and would be an appropriate marker for future biogeography or population genetic studies. When the two control regions from individuals were compared, several instances were found where a polymorphism in one control region disagreed with the paralogous base in the other control region. These results suggest homologous recombination may be a slow or random process or that the two regions are beginning the process of divergence.

## **Table of Contents:**

<b>Contents</b>	<b>Page #</b>
List of Tables	<b>vi</b>
List of Figures	<b>vii</b>
Chapter I: Introduction	<b>1</b>
The Mitochondrial Genome	<b>2</b>
mtDNA Control Regions	<b>3</b>
Snake Mitochondrial Control Regions	<b>4</b>
Origin of Dual Control Regions	<b>5</b>
Purpose of This Study	<b>8</b>
Chapter II: Materials and Methods	<b>9</b>
Study Site	<b>10</b>

DNA Extraction	<b>11</b>
PCR Amplification of CR Regions	<b>12</b>
DNA Sequencing	<b>13</b>
Alignments	<b>13</b>
Chapter III: Results	<b>15</b>
mtDNA Sequencing and Polymorphism Confirmation	<b>16</b>
Control Region Haplotypes	<b>17</b>
Chapter IV: Discussion	<b>22</b>
Snake Mitochondrial Control Regions CR1 and CR2 Polymorphisms	<b>24</b>
Haplotypes	<b>25</b>
The Two Control Regions are Dissimilar	<b>26</b>
Conclusions	<b>28</b>
Literature Cited	<b>30</b>
Appendices	<b>34</b>

### List of Tables

<b>Table 3.1.</b>	SNPs identified in the <i>Agkistrodon piscivorus</i> mitogenome control region 1. Yellow highlights indicate the reference control region, a blank box represents no polymorphism, red highlights indicate a polymorphism. Blue indicates a polymorphism in a control region that does not occur in the equivalent position in the other control region. An asterisk denotes samples where both control regions were successfully sequenced.....	<b>19</b>
<b>Table 3.2.</b>	SNPs identified in the <i>Agkistrodon piscivorus</i> mitogenome control region 2. Yellow highlights indicate the reference control region, a blank box represents no polymorphism, red highlights indicate a polymorphism. Blue indicates a polymorphism in a control region that does not occur in the equivalent position in the other control region. An asterisk denotes samples where both control regions were successfully sequenced.....	<b>20</b>
<b>Table App. 1.</b>	Primers Used. Primers in Yellow were used for sequencing.....	<b>35</b>

## List of Figures

<b>Figure 1.1.</b>	Gene content and order for <i>A. piscivorus</i> and typical snake mitogenomes. Control regions are denoted by left facing arrows. Figure modified from Hall et al. 2012.....	<b>5</b>
<b>Figure 2.1.</b>	Map of Caddo Lake (Bailey et al. 2009).....	<b>10</b>
<b>Figure 2.2.</b>	Map of the three sample sites near Caddo Lake, TX.....	<b>11</b>
<b>Figure 2.3.</b>	Two sequence runs showed a disagreement in the Poly-A sequence at the 3' end of the control region 2.....	<b>14</b>
<b>Figure 3.1.</b>	Haplotype Network for Control Region 1. This figure shows how the different haplotypes are related to each other.....	<b>18</b>
<b>Figure 3.2.</b>	Haplotype Network for Control Region 2. This figure shows how the different haplotypes are related to each other.....	<b>18</b>
<b>Figure App.1.</b>	Alignment of all <i>A. piscivorus</i> Control Region 1's produced for this project...	<b>36</b>
<b>Figure App.2.</b>	Alignment of all <i>A. piscivorus</i> Control Region 2's produced for this project...	<b>46</b>
<b>Figure App.3.</b>	Alignment of CR1 and CR2 regions in specimens where available.....	<b>56</b>
<b>Figure App.4.</b>	Alignment of <i>A. piscivorus</i> Control Regions with polymorphism locations indicated by vertical maroon bar below pictorial.....	<b>58</b>
<b>Figure App.5.</b>	Alignments of <i>A. piscivorus</i> Control Regions divided into haplogroups according to shared polymorphisms.....	<b>79</b>
<b>Figure App.6.</b>	Haplotype network of concatemers for specimens which contained both control regions.....	<b>81</b>
<b>Figure App.7.</b>	Alignment of all <i>A. piscivorous</i> CR1 and CR2 concatemers successfully produced for this project.....	<b>82</b>



**CHAPTER I**  
**INTRODUCTION**

### **The Mitochondrial Genome**

The vertebrate mitochondrial (mt) genome is commonly used to measure evolutionary divergence and variation among and within species, and to study genomic structure and function using protein-coding genes. Conservation of genome size, consistent gene content, and a lack of introns or intergenic spacers in vertebrate mitochondrial genomes are generally interpreted as evidence that these genomes are under selection for small size (Schirtzinger et al. 2012). From a technical standpoint, mtDNA is an attractive sequencing target for vertebrates because it is ubiquitously distributed among most cells, is easy to isolate and assay, and has a simple genetic structure of 15-20 kb lacking complicated components such as long tracts of repetitive DNA, transposable elements, pseudogenes, and introns.

There is a strong selective pressure to maintain gene function in the mitochondria, so mtDNA has a highly conserved gene order (synteny) and gene composition among vertebrates. Even so, it is a useful indicator of variation if changes in nucleotide sequences of protein-coding genes or intergenic regions are compared (Rokas et al. 2003). It can also be used as an indicator of intra-specific variation by comparing nucleotide sequences from individuals and defining single base changes, aka single nucleotide polymorphisms (SNPs).

SNPs have been used to measure divergence within a population, define differences between alleles, and to identify DNA-linked diseases (Finger et al. 2009; Fridjonsson et al. 2011). They are detected by sequencing a single locus from multiple individuals of a species

or population and identifying groups of individuals with a single base change at a specific site (Williams et al. 1990). The term SNP has been used to define single base length differences in population studies (Eberhard et al. 2001). These SNPs are known as insertions/deletions (in/dels) and are thought to occur frequently at single nucleotide tandem repeats (Eberhard et al. 2001).

In spite of the conservation of gene function necessary for mitochondria, mtDNA mutations can arise and disseminate at a relatively rapid rate due to asexual fission. For instance, a new heritable mutation within a mitochondrial genome can arise within the lifespan of an individual and be passed to offspring without meiotic recombination (Lodish 2013; Douglas and Gower 2010). Mutation rates across the mitochondrial genome are not uniform; SNPs can occur at variable rates at different regions within the mitochondrial genome.

### **mtDNA Control Regions**

The control region is a functional but noncoding segment of the mitochondrial genome that is responsible for the initiation of transcription and replication (Morris-Pocock et al. 2010; Alter and Palumbi 2009). It is highly variable in many vertebrate species and it is hypothesized that the mitochondrial control region is the most rapidly evolving portion of vertebrate mitochondrial genomes (Alter and Palumbi 2009).

Most vertebrate mitochondrial genomes have a single control region, but some groups of animals, including snakes, have two. The first mitochondrial genome with dual

control regions to be sequenced was *Dinodon semicarinatus* (Japanese colubrid snake) (Kumazawa et al. 1998). Since then, dual control regions have been found in birds (Bensch and Haerlid 2000; Eberhard et al. 2001; Abbott et al. 2005), arthropods (Black and Roehrdanz 1998), ticks (Campbell and Barker 1999), fish (Lee et al. 2001), and ostracods (Ogoh and Ohmiya 2007), which suggest duplications of the control region have occurred in many organisms, including vertebrates, and are more common than previously thought (Kumaza et al. 1998; Schirtzinger et al. 2012).

### **Snake Mitogenomes and Control Regions**

Compared to other vertebrate groups listed above, the mitochondrial genomes of snakes have short protein coding genes, highly conserved gene order, short tRNAs, a high mutation rate, and two control regions (Jiang et al. 2007). To date, most sequenced snake mitogenomes have dual control regions; exceptionally, the scolecophidian snakes *Leptotyphlops dulcis*, *Ramphotyphlops australis*, and *Typhlops murius* have a single control region

One control region (CR1) is positioned adjacent to the 5' end of the 12s rRNA as it is in other vertebrates, while the second control region (CR2) is positioned between the NADH dehydrogenase subunits (ND1 and ND2) (Figure 1.1, Hall et al. 2012). Each control region has a length of approximately one thousand bases. Snake control regions are flanked by tRNAs. As an example for the purpose of tRNAs serving as flanks, tRNA "Leucine" flanks CR2

and can potentially slow the rate of transcription of rRNA and mRNA by acting as a terminator of heavy strand transcripts.

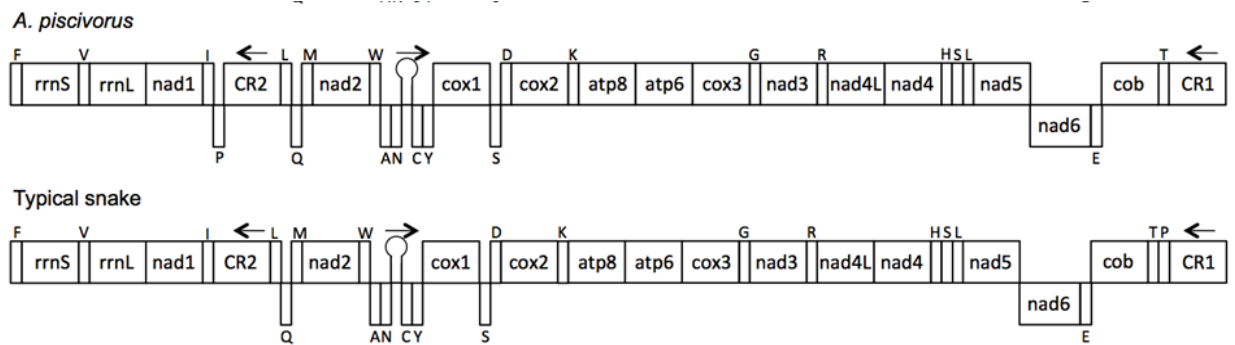


Figure 1.1: Gene content and order for *A. piscivorus* and typical snake mitogenomes. Control regions are denoted by left facing arrows. Figure modified from Hall et al. 2012.

### Origin of Dual Control Regions

Understanding the underlying mechanisms, evolutionary dynamics, and fitness consequences of duplicated control regions remains an ongoing challenge in the field of molecular evolution, because it defies the traditional view that vertebrate mitochondrial genomes have evolved to be compact (Kumazawa et al. 1998; Schirtzinger et al. 2012). There are two processes which have been proposed to explain the presence and maintenance of dual control regions. The first process is explained by loss of a duplicated

DNA segment over time, which is that control regions may have been present in the mitochondrial proto-bacterial ancestor, then lost in some organisms while maintained in others. Alternatively for the second process, a second control region may have arisen from a duplication event (Morris-Pocock et al. 2010; Schirtzinger et al. 2012). Duplication events have had several mechanisms proposed as to how they occur, but have been difficult to demonstrate (Kumazawa et al. 1998; Morris-Pocock et al. 2010; Schirtzinger et al. 2012). Schirtzinger et al. (2012) describes four possibilities for the outcome of a duplicated gene after a duplication event, which can also be applied to a duplicated control region:

1. One of the duplicates becomes nonfunctional and then slowly degrades from the genome over several generations.
2. Duplicates of the same gene retain different functions from the original gene, which may have had multiple functions.
3. The duplicate gene acquires mutations and potentially new functions.
4. Duplicate copies maintain the same function and are maintained through gene conversions.

Dual control regions have been studied extensively in birds (Schirtzinger et al. 2012), squamate reptiles (Castoe et al. 2009), and fish (Cui et al. 2009), but large scale intermolecular comparisons of dual control regions in vertebrate genomes have not been completed, so it is currently difficult to reject any of the hypotheses proposed by the Kumazawa et al. 1998 and Jiang et al. 2007. Comparison studies have been limited to one

or two genomes, and those have shown no differences between the control regions within a genome (Kumazawa et al. 1998; Jiang et al. 2007). This suggests the fourth possible outcome outlined above is in effect. Alternatively, it could also be an indication of a relatively recent duplication where there has not been enough time for them to diverge. There are no studies, to date, testing differences in the functionality of these regions, but their identical sequences suggests they would both be active.

Snake mitochondrial control regions may be a better model system for these types of studies because they lack large discordant genetic sequences, which are present in birds, and the positions of the two control regions in the mitochondrial genomes of snakes are more consistent. Previous studies have conducted interspecific analysis of the two snake mitochondrial control regions in *Dinodon semicarinatus*, *Pantherophis slowinskii*, *Ovaphis okinavensis*, *Boa constrictor*, *Acrochordus granulatus*, *Xenopeltis unicolor*, *Python regius*, *Cylindrophis ruffus*, and *Agkistrodon piscivorus* (Jiang et al. 2007), along with a selection of scolecophidian snakes compared to some alethinophidian snakes (Douglas and Gower 2010). Intraspecific analysis of *Dinodon semicarcinatus* (Kumazawa et al. 1998) and *Agkistrodon piscivorus* (Jiang et al. 2007) have been conducted using a sample size of four and two specimens respectively. Thus, a larger sample size of dual control regions in snakes may provide more robust conclusions regarding variations and evolutionary mechanisms maintaining this unique attribute.

### **Purpose of This Study:**

The purpose of my study was to sequence the mitochondrial control regions from a high sample size of specimens in the western cottonmouth subspecies, *Agkistrodon piscivorus leucostoma* and characterize single nucleotide polymorphisms. I hypothesized that control regions do not encode proteins and could potentially sustain a relatively high rate of mutation, compared to other regions of the mitogenome. These mutations could potentially define a large number of haplogroups that would be useful for future population or biogeography studies. Previous studies have reported no intramolecular or intermolecular differences between control regions but their sample sizes were very low (n=2) (Eberhard et al. 2001; Jiang et al. 2007; Fridjonsson et al. 2011). I surmised that a comparison of control regions from a larger group of individuals would yield polymorphisms.



**CHAPTER II**  
**MATERIALS AND METHODS**

### Study Site

Tissue and blood samples were collected from snakes found in the Caddo Lake National Wildlife Refuge (CLNWR) for an unrelated project. CLNWR consists of 3,437 ha of mostly bottomland hardwood forest and scattered wetlands bordering the western portion of Caddo Lake. The *A. piscivorus* samples used for this project were collected from three of the four creeks that pass through the refuge and drain into the lake (Figure 2.1). These sites will be referred to collectively as CL. Samples were also collected at two privately owned sites off of the refuge owned by Bob Sanders and Ray Blevins, referred to as CB and RB respectively (Figure 2.2). CB is located 15 miles from Caddo Lake, while RB is located about 5 miles away. The samples were collected during 2005, 2009, and 2011. These wetlands are presumed to have remained intact for centuries with adequate resources to sustain a large, stable, and interbreeding population of *A. piscivorus*.

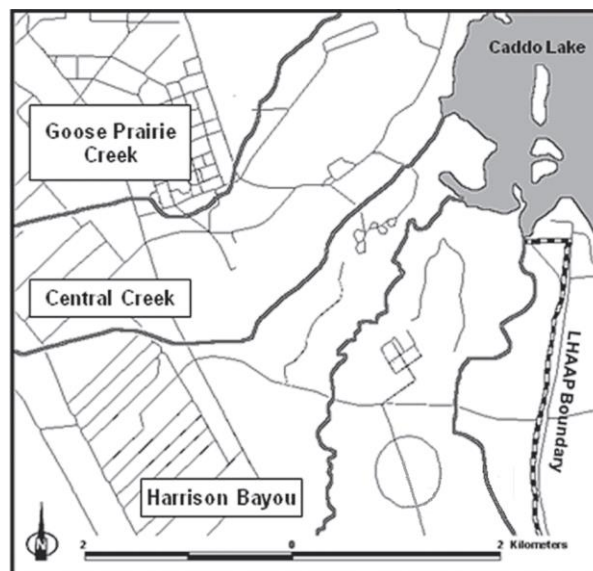


Figure 2.1: Map of Caddo Lake (Bailey et al. 2009).

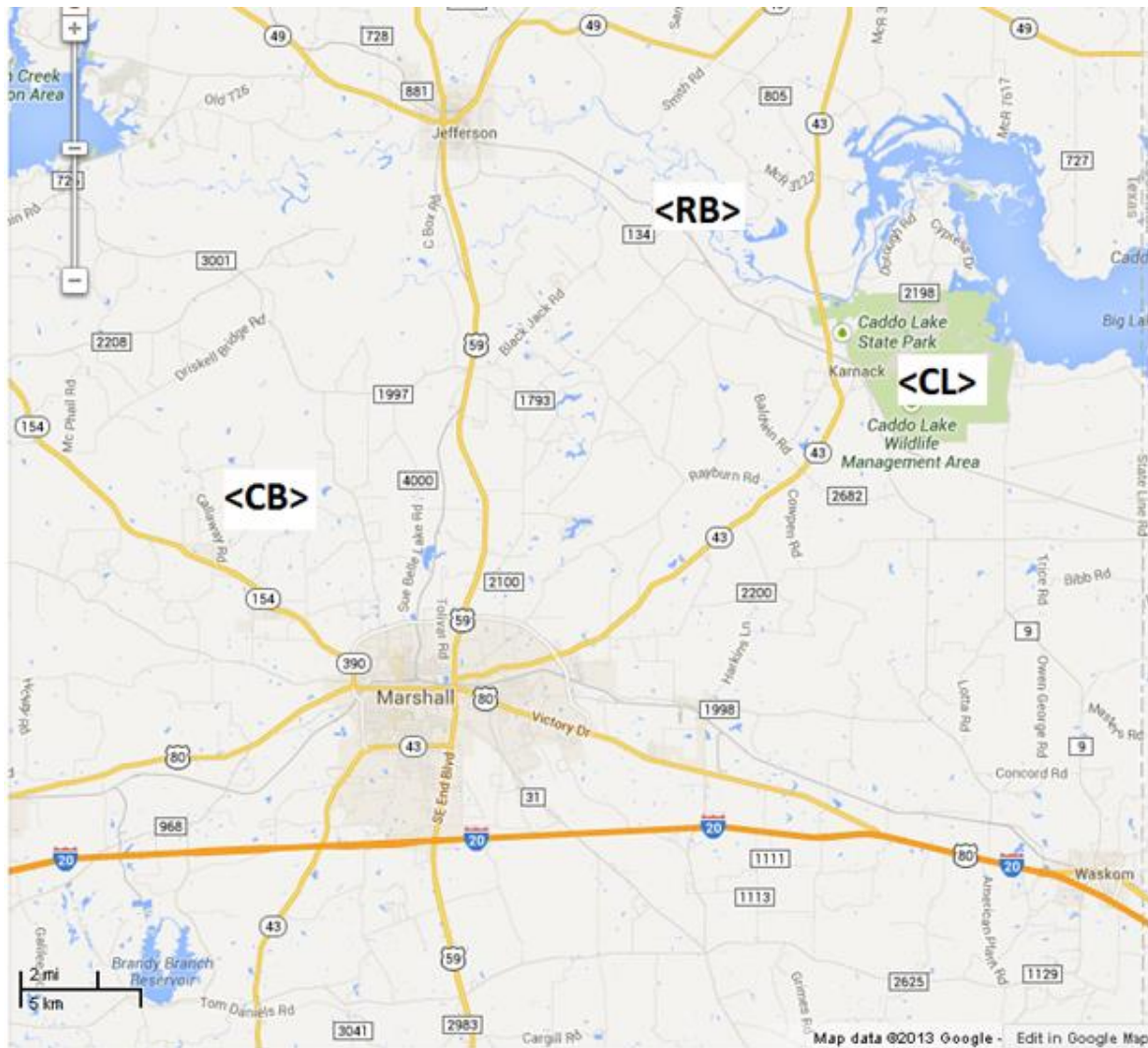


Figure 2.2: Map of the three sample sites near Caddo Lake, TX.

### DNA Extraction

Total DNA was purified from either muscle tissue or whole blood frozen at the times of collection. Purification was achieved following the protocol in Hall et al. (2012). For snake muscle, 1 mL of urea lysis buffer was added to a small piece of snake muscle tissue and

ground with a mortar and pestle to form a slurry. An organic extraction was performed with phenol:chloroform:isoamyl alcohol (25:24:1), and the aqueous layer with DNA was transferred to a new tube. DNA was precipitated with 2-propanol, washed with 70% ethanol, air dried, and resuspended in 50 µL of TE buffer (10 mM Tris HCl pH 8.0; 1 mM EDTA pH 8.0). DNA was stored at –20°C. A nanodrop spectrophotometer (Thermo Scientific) was used to measure the total amount of DNA for whole blood samples and for tissue samples.

### **PCR Amplification of CR Regions**

DNA samples were used as templates for PCR with specific primers for amplification of control regions. All amplification products were visualized by separation in 0.8 % agarose gel electrophoresis, stained with 2 µLs ethidium bromide from a 1ng/ml etbr working stock, and compared to a DNA standard marker (1Kb Plus Ladder– Gibco. Brl). Primers “R14” and “L11” were used to amplify Control Region 1 and “R19” and “L17” to amplify Control Region 2 (Appendix Table 1). I made a 100 pmol stock dilution of the combined primers utilized for each region. Two µLs of the stock primer dilutions were combined with ExTaq used at a concentration of 1U with the dNTPs and Buffer provided by the manufacturer per their directions (TaKaRa). The thermal cycler profile was as follows: initial denaturation at 95°C for 5 minutes, followed by 35 cycles of 95 °C 30 seconds, 50 °C 30 seconds, and 68 °C for 4 minutes, with a final 68 °C extension for 10 minutes. After PCR, amplification success was confirmed on X% agarose gel post-stained with EtBr (with concentration). The successful

samples were treated with Exonuclease 1 and Shrimp alkaline (ExoSAP) phosphatase to remove unused primers and nucleotides.

### **DNA Sequencing**

Samples were sequenced using Applied Biosystems (Applied Biosystems, Grand Island, NY) BigDye chemistry and run on an ABI 3130xl Genetic Analyzer at Middle Tennessee State University. Sequencing of CR1 was accomplished with the primers “CR1L” at an annealing temperature of 58 °C, “CR1R” at an annealing temperature of 55 C, and “L12” at an annealing temperature of 58 °C. CR2 was sequenced using “CR2L” at an annealing temperature of 58 °C and “L18” at an annealing temperature of 55 °C to sequence Control Region 2 (Appendix Table 1).

### **Alignments**

Control regions were aligned into two separate files for each control region using Sequencher 4.9 (GeneCodes Corp., Ann Arbor, MI). All samples were checked by eye for quality, and poor sequences without well-defined electropherogram peaks were discarded. Control regions were sequenced with multiple primers and each base had a sequencing coverage of at least two successful PCR amplicons. Initially, all sequences were aligned to the *A. piscivorus* mitogenome deposited in GenBank (DQ523161), which was collected in Louisiana. All CR1 control region consensus sequences were aligned (Appendix, Figure 3A) and the same was done for CR2 (Appendix, Figure 3B). Single nucleotide polymorphisms were identified by eye as base disagreements (Figure 2.3). For CR1 – CR2 comparisons, the

regions were aligned and compared from each snake for which these two regions were successfully sequenced (Appendix, Figure 4)

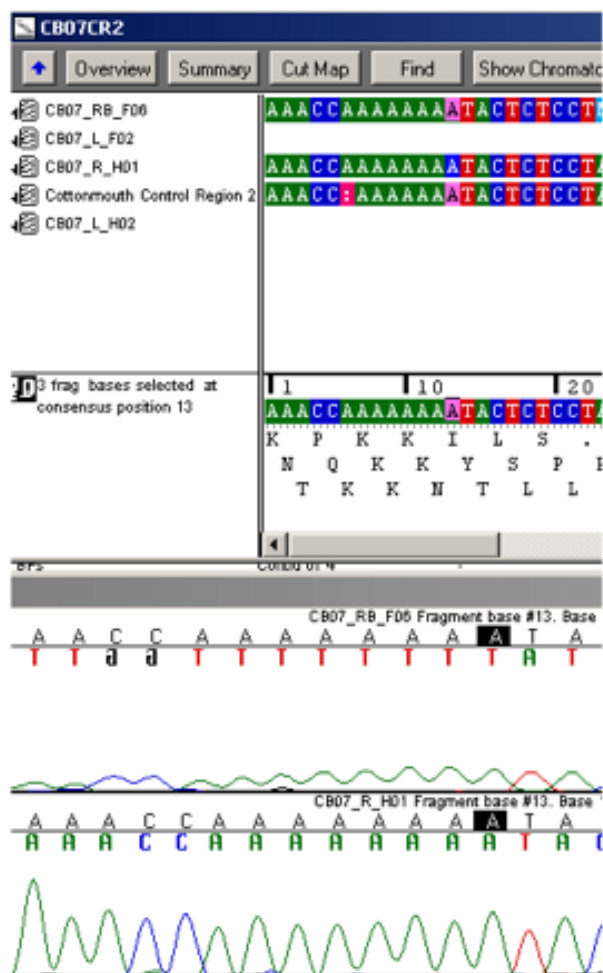


Figure 2.3: Two sequence runs showed a disagreement in the Poly-A sequence at the 3' end of the Control Region 2.

## **CHAPTER III**

### **RESULTS**

### **mtDNA Sequencing and Polymorphism Confirmation**

Polymerase chain reaction (PCR) amplification and sequencing of CR1 and CR2 resulted in 1023 base pairs and 1019 base pairs respectively, with at least 2x coverage for each completed sequence. Sequencing was attempted from 96 snake samples. Of those, 32 CR1s were successfully sequenced and 37 CR2s. CR1 & CR2 were successfully sequenced from the same snake in 21 samples.

Alignment of the 32 CR1s revealed 3 SNPs (Table 3.1, Appendix Figure 1). All CR1s sequenced in this study differed from the reference sequence at base 16377. Five specimens also had a polymorphism at base 16397. One specimen showed a polymorphism at 16846. All polymorphisms in the CR1s occurred as a C →T substitution.

When the 37 CR2s were aligned (Appendix Figure 2), 2 individuals did not differ from the reference sequence. Twenty-nine had a deleted C at base 4278 within a poly-C stretch, and two of those had an insertion at base 3635 within a poly-A stretch (Table 3.2). Three C →T SNPs were identified at bases 3809, 3829, and 4278. Twenty-five individuals differed from the reference sequence at base 3809, 4 at 3829, and 2 at 4278.

All CR1s were aligned together to show locations of polymorphisms as were the CR2s (Appendix Figure 3). In cases where both CRs were sequenced from the same snake, CR1 was aligned to CR2 to identify intra-genomic differences (Tables 3.1 and 3.2, and Appendix Figure 4). Of the 21 alignments, 9 had at least one difference between the CR1 and the CR2.



### Control Region Haplotypes

Haplotypes were created based on the newly identified polymorphisms (Tables 3.1 and 3.2, Appendix Figure 5). Haplotype A for CR1 and CR2 is from the reference sequence (GenBank DQ523161), the first sequenced mitogenome of the *Agkistrodon piscivorus leucostoma*. Subsequent haplotypes were defined based on the presence of polymorphisms with respect to Haplotype A. The approach I used to define haplotypes was to consider each CR independently. If the CR1 SNPs are considered, independent of the CR2, there are four definable haplotypes. Of these four, the reference sequence was unique and assigned haplotype CR1A. One other unique haplotype, CR1C, also had a single specimen. CR1D, had 5 representatives. The largest group was CR1B, with 26 individuals. When considering the CR2 SNPs, 7 haplotypes can be assigned. One haplotype (CR2F) contained one specimen, CR2B had 2 specimens, CR2A and CR2D had 3 specimens each, CR2G had 5 specimens, CR2C had 10, and CR2E had 12. These haplotypes were then used in a TCS analysis to visualize their relations to each other (Figure 3.1 and Figure 3.2). CR1 and CR2 were then combined into concatemers and haplotype groups (Appendix Figure 6) were determined from a Clustal W analysis (Appendix Figure 7).

Although all the samples came from a single interbreeding population and sample sizes are relatively small, some differences between sample sites were observed. For example, CR2 haplotype F and CR1 haplotype C were not found at the CL sampling site. CR2 haplotype B was only seen at the CB sampling site and the CR2 haplotype D was not found

at the RB site. All sites contained the CR1 B and CR2 E haplotypes. No site contained the CR1A haplotype, but two specimens at the CL site contained the CR2A haplotype.

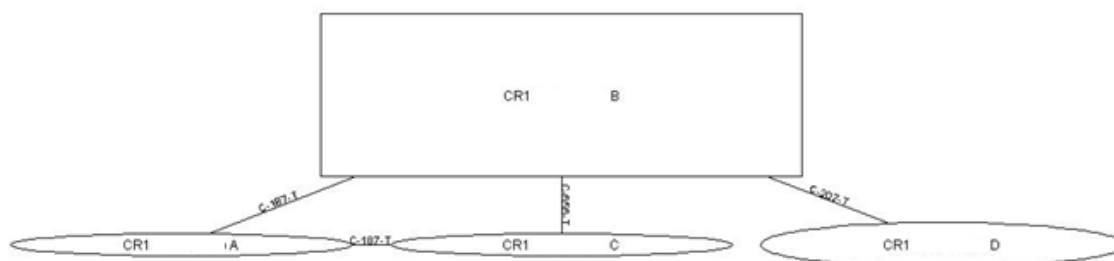


Figure 3.1: Haplotype Network for Control Region 1. This figure shows how the different haplotypes are related to each other.

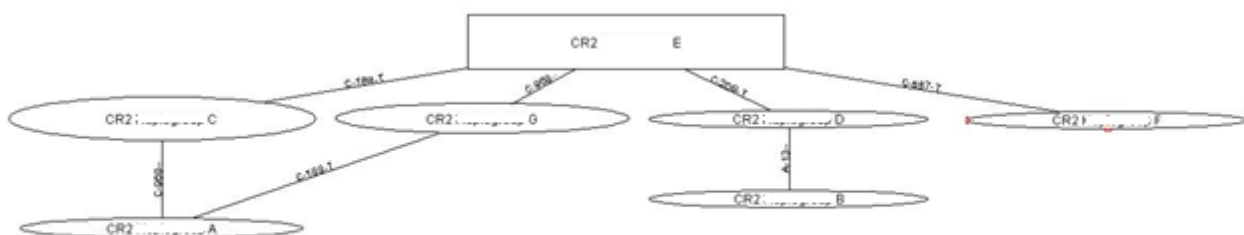


Figure 3.2: Haplotype Network for Control Region 2. This figure shows how the different haplotypes are related to each other.

Table 3.1: SNPs identified in the *Agkistrodon piscivorus* mitogenome Control Region 1. Yellow highlights indicate the reference control region, a blank box represents no polymorphism, red highlights indicate a polymorphism. Blue indicates a polymorphism in a control region that does not occur in the equivalent position in the other control region. An asterisk denotes samples where both control regions were successfully sequenced.

Single Nucleotide Polymorphism CR1				
CR1 Specimens	SNP16377	SNP16397	SNP16846	Haplogroup
Control	C	C	C	CR1A
BL02*	T			CR1B
BL03	T			CR1B
BL04*	T			CR1B
BL05*	T			CR1B
BL07*	T			CR1B
BL09	T			CR1B
BL10	T			CR1B
BL11	T			CR1B
BL13	T			CR1B
BL14	T			CR1B
BL15	T			CR1B
BL16	T			CR1B
BL17	T			CR1B
BL20*	T			CR1B
BL29*	T	T		CR1D
BL34*	T			CR1B
BL38*	T			CR1B
CB03*	T			CR1B
CB05*	T	T		CR1D
CB06*	T			CR1B
CB07*	T	T		CR1D
CB09*	T	T		CR1D
CB12*	T			CR1B
CB13*	T			CR1B
CB14*	T			CR1B
CB16*	T			CR1B
GPC02	T			CR1B
GPC05*	T			CR1B
GPC10*	T			CR1B
RB03*	T		T	CR1C
RB06*	T			CR1B
RB08*	T	T		CR1D

Table 3.2: SNPs identified in the *Agkistrodon piscivorus* mitogenome Control Region 2. Yellow highlights indicate the reference control region, a blank box represents no polymorphism, red highlights indicate a polymorphism. Blue indicates a polymorphism in a control region that does not occur in the equivalent position in the other control region. An asterisk denotes samples where both control regions were successfully sequenced.

Single Nucleotide Polymorphism CR2						
CR2 Specimens	In3635	SNP3809	SNP3829	SNP4278	Del4589	Haplogroup
Control	N/A	C	C	C	C	CR2A
BL02*						CR2A
BL04*						CR2A
BL05*					DEL: C	CR2C
BL07*		T				CR2G
BL20*					DEL: C	CR2C
BL21					DEL: C	CR2C
BL22		T			DEL: C	CR2E
BL23					DEL: C	CR2C
BL24		T			DEL: C	CR2E
BL28		T				CR2G
BL29*		T	T		DEL: C	CR2D
BL33					DEL: C	CR2C
BL34*		T			DEL: C	CR2E
BL38*					DEL: C	CR2C
BL46		T			DEL: C	CR2E
BL47		T			DEL: C	CR2E
BL48		T			DEL: C	CR2E
CB02		T				CR2G
CB03*					DEL: C	CR2C
CB05*		T	T		DEL: C	CR2D
CB06*		T				CR2G
CB07*	INS: A	T	T		DEL: C	CR2B
CB08		T			DEL: C	CR2E
CB09*	INS: A	T	T		DEL: C	CR2B
CB12*		T			DEL: C	CR2E
CB13*					DEL: C	CR2C
CB14*		T		T	DEL: C	CR2F
CB16*		T			DEL: C	CR2E
GPC01		T			DEL: C	CR2E
GPC04					DEL: C	CR2C
GPC05*		T				CR2G
GPC07					DEL: C	CR2C
GPC08		T				CR2G
GPC10*		T			DEL: C	CR2E
RB03*		T		T	DEL: C	CR2F
RB06*		T			DEL: C	CR2E
RB08*		T			DEL: C	CR2D

The single nucleotide polymorphisms were C → T transitions and were found at bases 16377, 16397, and 16846 of the CR1 and bases 3809, 3829, and 4278 of CR2. Bases 16377, 16397, and 16846 on CR1 are the equivalent (paralogous) bases of 3809, 3829, and 4278 of CR2 when the two control regions are aligned, so 3809/16377, 3829/16397, and 4278/16846 can be considered paralogous bases and are essentially the same SNPs. Of the three, SNP 3809/16377 was the most common polymorphism, occurring in all the CR1s and 25/37 of the CR2s. Seven occurrences of this SNP in CR2 did not have an equivalent base change in the CR1 (samples BL02, BL04, BL05, BL20, BL38, CB03, and CB13). SNP 3829/16397 occurred in 4 CR2s and 5 CR1s with one instance of disagreement (sample RB08). The least common SNP, 4589/16846, occurred in two CR2s and one CR1, with one instance of disagreement (sample CB14).

The second group of characteristics involves insertion/deletion (Indel) type polymorphisms, which were only found in the CR2. These insertions/deletions occurred within tandem repeats of single nucleotides. The most common one was a deletion of a cytosine at base 4589 in 29/37 CR2s. Insertion of a single adenine occurred at base 3635 for two specimens (CB07 & CB09). Both instances of this insertion coincided with polymorphisms at bases 3809 and 3829.

**CHAPTER IV**

**DISCUSSION**

This study describes the intramolecular variation and intraspecific variation of the two mitochondrial control regions of *A. piscivorus leucostoma*. Previous studies concluded CR1 and CR2 from any single individual would be identical (Kumazawa et al. 1998; Jiang et al. 2007). That conclusion was based on sequences from only two individuals, making this observation easy to challenge simply by increasing the sample size. Intra-specific variation within snake control regions is unpublished but necessary if these regions are to be considered for phylogenetic or biogeography studies. For example, comparison of control regions from two sub-species of cottonmouth (*A. piscivorus conanti* and *A. piscivorus leucostoma*) have 19 differences for the CR1 and 18 substitutions for the CR2 (Jiang et al. 2007; Douglas et al. 2009). An estimate of intraspecific variation of the two control regions is missing from those studies.

I sequenced control regions from individual snakes from a single interbreeding population. They were collected from three sample areas within 20 miles of each other (Douglas et al. 2009). Of the 32 CR1s and the 37 CR2s, 1 insertion, 1 deletion, and 3 single nucleotide polymorphisms were identified.

### **Snake Mitochondrial Control Regions CR1 and CR2 polymorphisms**

The data in this study revealed the presence of intra and intermolecular differences between the control regions of a single species. These differences can be put into two groups, single nucleotide polymorphisms and insertion/deletions.

Kumazawa et al. (1998) were the first to discover that snakes had two control regions, and most other sequenced snake mtDNAs, to date, also have two control regions (Kumazawa et al. 1998; Jiang et al. 2007). Since then, dual control regions have been found in other squamates as well as amphibians, crocodylians, turtles, birds, and fish (Schirtzinger et al 2012). Of all the vertebrates found to have two mitochondrial control regions, snakes are considered unique because of their adaptively remodeled proteins thought to have evolved in parallel with the duplication of the control region. In addition, their ubiquitous existence suggests snake mitochondrial genomes evolved very early in their divergence from other squamates (Douglas and Gower 2010). My results are difficult to compare with other control region studies because very few comparable studies have been published and there are no published accounts of intra-specific or intra-molecular variation of control regions from any species. One interspecific set of comparisons for 63 birds showed enough homology to align and compare the regions with the exception of a 50 bp area that did not align (Morris-Pocock et al. 2010). No attempts have been made to align control regions from other snake species.



### Haplotypes

The control region is the site where replication and transcription occur for vertebrate mitochondrial genomes and are noncoding, thus, under less selective pressure. The reduction of selective pressure can cause high amounts of variation among all classifications of organisms down to the intraspecific level (Alter and Palumbi 2009). Previous studies have conducted broad interspecific analysis using the 12S, 16S, and ND4 of the cottonmouth mitochondrial genome (using two separate sub species, 1 specimen of each) compared to the *Agkistrodon bilineatus* and *Agkistrodon contortrix* (Parkinson et al. 2000), and interspecific and broad (covering the entire range of the species) intraspecific analysis using the cytochrome b (Guiher and Burbrink 2008) of the cottonmouth genome (82 samples) to compare to the *Agkistrodon contortrix*. Prior to my study, one intraspecific cottonmouth study used protein-coding genes ATP6 and ATP8 to establish haplotypes based on the sequenced concatamers of these two genes (Douglas et al. 2009). The ATP8 and ATP6 sequences of *A. p. leucostoma*, combined for a total of 849 base pairs and showed enough polymorphisms in 27 specimens to create 8 haplotypes from specimens sampled from 15 sites that spanned 5 states. The control regions used in this study had 4-7 definable haplotypes which rivals ATP8 and ATP6. If one also considers these samples were taken from a single population it is conceivable that even more diversity would exist if a larger sampling had been conducted. Furthermore, the control regions serve as a unique marker because there are no other gene duplications in the snake mitochondrial genomes.

### **The Two Control Regions are Dissimilar**

Intra-molecular comparison of the two control regions revealed 9/21 individuals had at least one SNP between CR1 and CR2. Interestingly, these discrepancies all occurred at the three identified paralogous SNPs. The occurrence of the polymorphism in one CR but not the other suggests a mutation occurred in one of the CRs but has not been transferred to the other via homologous recombination.

I hypothesize the dissimilar polymorphisms that occur at paralogous bases 3809/16377, 3829/16397 and 4278/16846 are due to a delayed homologous recombination event. Recombination can begin when the replication of the heavy strand pauses at the origin of replication for the light strand. While the replication is paused, three strands of DNA remain within the boundaries of the "D-loop". Any one of several events could allow the polymerase to detach from replicating the heavy strand, allowing a region of the nascent heavy strand to become unattached and then recombine with the second control region of the parental strand.

There are two possible fates for nascent DNA strands that allow them to recombine with one another. The first fate would be crossing over. Because there are no known mechanisms involved with replication regulation, perhaps mtDNA replicates in near unison within a mitochondria during a cell's interphase. Mitochondria contain many copies of the circular genome, where crowding within the mitochondria could be a common occurrence.

When this concept of crowding is coupled with disassociated H strands at varied time points during the replications of all the genomes intramolecularly, opportunity exists for the free floating H strand to randomly crossover at a nicked site where the polymerase could replicate the unintended control region. For example, a free-floating nascent CR1 crosses a neighboring parental H strand CR2 before the replication of the light strand begins (on that neighboring Parental H strand) (Kumazawa et al. 1998; Lodish et al. 2012).

The second fate of unattached DNA would be for the nascent strand to completely detach from the parental strand and form a circular genomic intermediate. Kumazawa et al. (1998) were the first researchers to suggest the existence of free-floating intermediates. The unique discordant polymorphism in my study was that the string of C's at the end of the Control Region 2 showed an inconsistent deletion of one C. This inconsistent occurrence suggests that an excision repair mechanism is used at random to homogenize the control regions when they recombine (Lodish et al. 2012).

The random nature of these proposed mechanisms fits our data. The absence of complete identity between the two CRs suggests that homologous recombination may occur infrequently. Alternatively, Morris-Pocock et al. (2010) suggest that duplicated copies of genes allow for gene rearrangements and degradation. After a region of DNA is duplicated, one of the two can degrade or change significantly from the original (Douglas

and Gower 2010; Morris-Pocock 2010). Perhaps the differences I observed between the two CRs are small steps towards what will one day be very different stretches of DNA.

### **Conclusions**

To my knowledge, this is the first study to use a moderately large sample set to explore the dual noncoding control regions of the mitochondrial control regions in any snakes species in order to compare sequences intra-specifically (between individuals) and intra-molecularly (the two CRs within an individual). I established that the two control regions were not always identical, neither within a population nor within an individual. The number of haplotypes found within a large interbreeding population suggests there may be many others in a larger population or outside of this one in Texas.

Also to my knowledge, this is the first study to suggest that an SNP could originate in either of the regions and be maintained for an unspecified period of time, suggesting recombination is a relatively slow or random process. This research may establish the dual control region as a useful marker for future phylogenetic or biogeographical studies and may offer unique opportunities for future study of the molecular mechanism of recombination in metazoans.

Snakes are considered to show accelerated rates of mtDNA evolution compared to other vertebrates yet their coding regions of their mitochondria are under the same selective pressure to encode multimeric proteins associated with cellular energy production

(Schirtzinger et al. 2012). Thus, hypothetically, an organism with two control regions would eventually lose one to gain a more compact genome structure. Factors that may have contributed to the duplication and maintenance of the control regions in snakes could be the shift to non-burrowing lifestyle, increased body size, increased skull kinesis, development of special venom proteins, and the ability of individuals to dramatically remodel their organs and physiology (Douglas and Gower 2010).

**LITERATURE CITED**

- Abbot CL, Double MC, Trueman JWH, Robinson A, Cockburn A. 2005. An unusual source of apparent mitochondrial heteroplasmy: duplicate mitochondrial control regions in *Thalassarche albatrosses*. *Molecular Ecology*. 14: 3605-3613.
- Alter SE and Palumbi SR. 2009. Comparing Evolutionary Patterns and Variability in the Mitochondrial Control Region and Cytochrome b in three Species of Baleen Whales. *Journal of Molecular Evolution*. 68: 97-111.
- Bailey FC, Cobb VA, Rainwater TR, Worrall T, Klukowski M. 2009. Adrenocortical Effects of Human Encounters on Free-Ranging Cottonmouths (*Agkistrodon piscivorus*). *Journal of Herpetology*. 43(2): 260-266.
- Bensch S and Haerlid A. 2000. Mitochondrial genomic rearrangements in songbirds. *Molecular Biology and Evolution*. 17: 107-113.
- Black WC and Roehrdanz RL. 1998. Mitochondrial gene order is not conserved in arthropods: prostriate and metastriate tick mitochondrial genomes. *Molecular Biology and Evolution*. 15: 1772-1785.
- Campbell NJH and Barker SC. 1999. The novel mitochondrial gene rearrangement of the cattle tick, *Boophilus microplus*: fivefold tandem repetition of a coding region. *Molecular Biology and Evolution*. 16: 732- 740.
- Castoe TA, Gu W, de Koning APJ, Daza JM, Jiang ZJ, Parkinson CL, Pollock DD. 2009. Dynamic Nucleotide Mutation Gradients and Control Region usage in Squamate Reptile Mitochondrial Genomes. *Cytogenetics and Genome Research*. 127: 112-127.
- Castoe TA and Parkinson CL. (2006). Bayesian mixed models and the phylogeny of pitvipers (Viperidae: Serpentes). *Molecular phylogenetics and evolution*. 39(1), 91-110.
- Cui Z, Liu Y, Li CP, You F, Chu KH. 2009. The complete mitochondrial genome of the large yellow croaker, *Larimichthys crocea* (Perciformes, Sciaenidae): Unusual features of its control region and the phylogenetic position of the Sciaenidae. *Gene*. 432: 33-43.
- Douglas DA and Gower DJ. 2010. Snake mitochondrial genomes: phylogenetic relationships and implications of extended taxon sampling for interpretation of mitogenomic evolution. *BMC Genomics*. 11(14): 1-16.

Douglas ME, Douglas MR, Schuett GW, Porras LW. 2009. Climate change and evolution of the New World pitviper genus *Agkistrodon* (Viperidae). *Journal of Biogeography*. 36: 1164-1180.

Eberhard JR, Wright TF, Bermingham E. 2001. Duplication and concerted evolution of the mitochondrial control region in the parrot genus *Amazona*. *Molecular Biology and Evolution*. 18(7):1330-1342.

Finger AJ, Stephens MR, Clipperton NW, May B. 2009. Six diagnostic single nucleotide polymorphism markers for detecting introgression between cutthroat and rainbow trouts. *Molecular Ecology Resources*. 9: 759-763.

Fridjonsson O, Olafsson, K, Tompsett S, Bjornsdottir S, Consuegra S, Knox D, de Leaniz CG, Magnusdottir S, Olafsdottir G, Verspoor E, Hjorleifsdottir S. 2011. Detection and mapping of mtDNA SNPs in Atlantic salmon using high throughput DNA sequencing. *BMC Genomics*. 12: 179-188.

Guiher TJ and Burbrink FT. 2008. Demographic and phylogeographic histories of two venomous North American snakes of the genus *Agkistrodon*. *Molecular Phylogenetics and Evolution*. 48: 543-553.

Hall JB, Cobb VA, Cahoon AB. 2012. The complete mitochondrial DNA sequence of *Crotalus horridus* (timber rattlesnake). *Mitochondrial DNA*, in press

Jiang ZJ, Castoe TA, Austin CC, Burbrink FT, Herron MD, McGuire JA, Parkinson CL, Pollock DD. 2007. Comparative mitochondrial genomics of snakes: extraordinary substitution rate dynamics and functionality of the duplicate control region. *BMC Evolutionary Biology*. 7: 123.

Kumazawa Y, Ota H, Nishida M, Ozawa T. 1998. The Complete Nucleotide Sequence of a Snake (*Dinodon semicarinatus*) Mitochondrial Genome With Two Identical Control Regions. *Genetics*. 150: 313-329.

Lee JS, Miya M, Lee YS, Kim CG, Park EH, Aoki Y, Nishida M. 2001. The complete DNA sequence of the mitochondrial genome of the self fertilizing fish *Rivulus marmoratus* (Cyprinodontiformes, Rivulidae) and the first description of duplication of a control region in fish. *Gene*. 280: 1-7.



Lodish H., Berk A., Kaiser CA, Krieger M, Scott MP, Bretscher A, . . . Matsudaira P. (2012). *Molecular Cell Biology* (Vol. 7). New York, NY: W.H. Freeman and Company.

Morris-Pocock JA, Taylor SA, Birt TP, Friesen VL. 2010. Concerted evolution of duplicated mitochondrial control regions in three related seabird species. *BMC Evolutionary Biology*. 10(14): 1-10.

Ogoh K and Ohmiya Y. 2007. Concerted evolution of duplicated control regions within an ostracod mitochondrial genome. *Molecular Biology and Evolution*. 24: 74-78.

Parkinson CL, Zamudio KR, Greene HW. 2000. Phylogeography of the pitviper clade *Agkistrodon*: historical ecology, species status, and conservation of cantils. *Molecular Ecology*. 9: 411-420.

Rokas A, Ladoukakis E, Zouros E. 2003. Animal mitochondrial DNA recombination revisited. *Trends in Ecology and Evolution*. 18(8): 411-417.

Schirtzinger EE, Tavares ES, Gonzales LA, Eberhard JR, Miyaki CY, Sanchez JJ, Hernandez A, Mueller H, Graves GR, Fleischer RC, Wright TF. 2012. Multiple independent origins of mitochondrial control region duplications in the order Psittaciformes. *Molecular Phylogenetics and Evolution*. 64: 342-356.

Williams JGK, Kubelik AR, Livak KJ, Rafalski JA, Tingey SV. 1990. DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. *Nucleic Acids Research*. 18(22): 6531-6535.

**APPENDICES**

Appendix Table 1: Primers used. Primers in yellow were used for sequencing

Gene	Left Primer	Left Primer	Right Primer	Right Primer
mtCR1	CrotL11	AAACCAGTAGAACCACCATTTACA	CrotR14	TTTTGTGGTCTGTTAATTGCTAGT
mtCR2	CrotL17	CCCGATTTTCGATATGACCA	CrotR19	ATTTTATTGAGAATTAGTCATTTTGGT
mtCR1	CrotL_12	CATGTTCTTATCACGTATGCCTGT	CrotR13	GTACACTTACCATGTTACGACTTGC
mtCR2	CrotL18	TTCACCTCATGTTTCTTATCAGG	CrotR19	ATTTTATTGAGAATTAGTCATTTTGGT
mtCR1	ApCR1_L	ACCAAAGCCGGATATTCCTT	ApCR1_R	TTTGTTGGAGGGTCATACCA
mtCR2	ApCR2_L	GCCCCCAAAGCCAGTATT	ApCR2_R	GTTGAGGTTTTAAGCCTTTTGC
Gene	Right Alternate Seq Primer	Right Alternate Seq Primer		
mtCR1	CR1_seqR_B	TCACGGAAGGGTTAAATCA		
mtCR2	CR2_seqR_B	GGAGAAAGTGCTAGACCAAGAA		

Appendix Figure 1: Alignment of all *A. piscivorus* Control Region 1's produced for this project.

```

GPC05_CR1      AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
GPC10_CR1      AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
GPC02_CR1      AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
CB16_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
CB14_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
CB13_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
CB12_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
CB06_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
CB03_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL9_CR1        AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL7_CR1        AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL5_CR1        AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL4_CR1        AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL3_CR1        AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL38_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL34_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL2_CR1        AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL20_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL17_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL16_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL15_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL14_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL13_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL11_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL10_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
RB06_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
RB03_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
BL29_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
CB05_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
CB07_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
CB09_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
RB08_CR1       AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
DQ523161_CR1  AAACCAAAAAAAAAACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 16250
*****

```



















GPC05_CR1	TTG 17213
GPC10_CR1	TTG 17213
GPC02_CR1	TTG 17213
CB16_CR1	TTG 17213
CB14_CR1	TTG 17213
CB13_CR1	TTG 17213
CB12_CR1	TTG 17213
CB06_CR1	TTG 17213
CB03_CR1	TTG 17213
BL9_CR1	TTG 17213
BL7_CR1	TTG 17213
BL5_CR1	TTG 17213
BL4_CR1	TTG 17213
BL3_CR1	TTG 17213
BL38_CR1	TTG 17213
BL34_CR1	TTG 17213
BL2_CR1	TTG 17213
BL20_CR1	TTG 17213
BL17_CR1	TTG 17213
BL16_CR1	TTG 17213
BL15_CR1	TTG 17213
BL14_CR1	TTG 17213
BL13_CR1	TTG 17213
BL11_CR1	TTG 17213
BL10_CR1	TTG 17213
RB06_CR1	TTG 17213
RB03_CR1	TTG 17213
BL29_CR1	TTG 17213
CB05_CR1	TTG 17213
CB07_CR1	TTG 17213
CB09_CR1	TTG 17213
RB08_CR1	TTG 17213
DQ523161_CR1	TTG 17213
	***

Appendix Figure 2 – Alignment of all *A. piscivorous* Control Region 2's produced for this project.

```

CB07CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3682
CB09CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3682
BL29CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
CB05CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL22CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL24CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL34CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL46CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL48CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
CB08CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
CB12CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
CB16CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
GPC01CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
GPC10CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
RB06CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
RB08CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL47CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
GPC08CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
GPC05CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
CB06CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
CB02CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL7CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL28CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
CB14CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
RB03CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL2CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
CB13CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL4CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL20CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL21CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL23CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL33CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL38CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
BL5CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
CB03CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
GPC04CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
GPC07CR2 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
CR2 DQ523161 AAACCAAAAAAAAAA TACTCTCCTAGGACCCCCCCCCTACCCCCCCCCTAGCTGGGTCCCGA 3681
*****

```















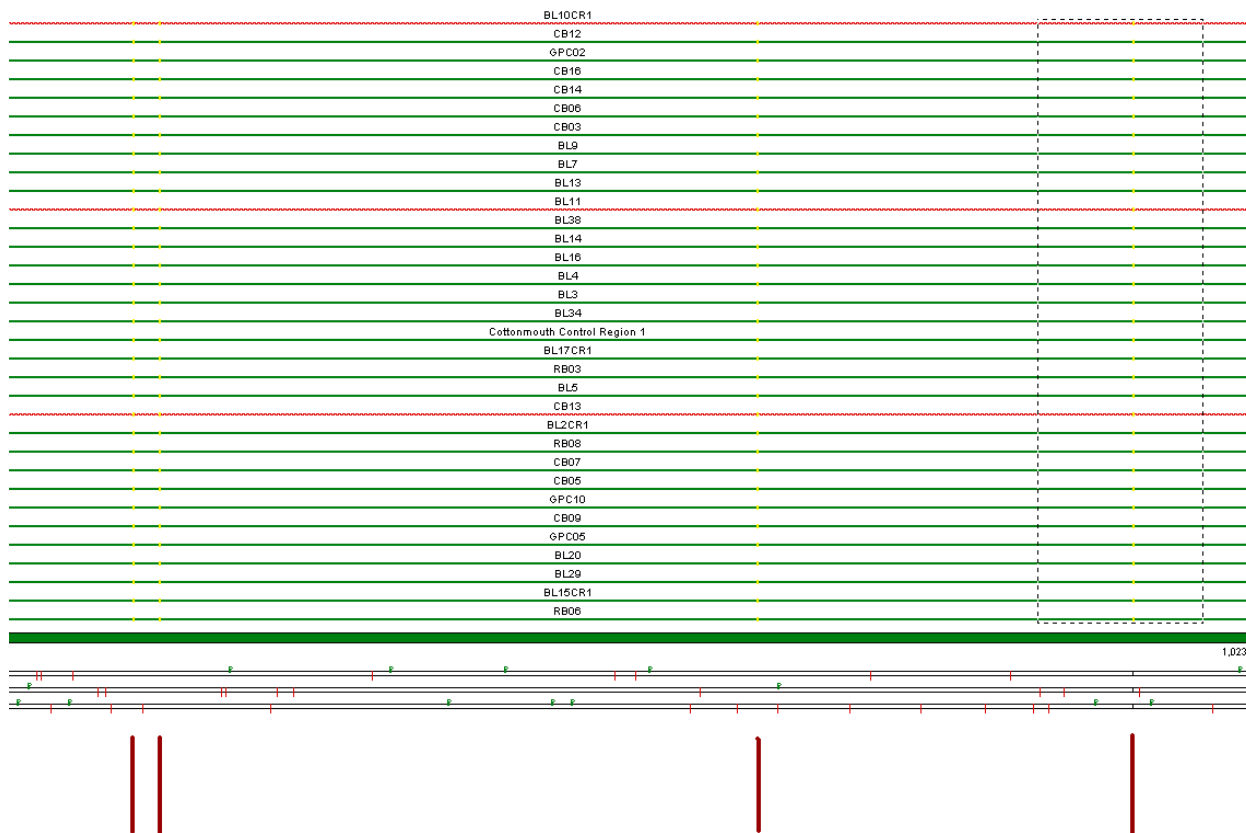




CB07CR2	T 4642
CB09CR2	T 4642
BL29CR2	T 4641
CB05CR2	T 4641
BL22CR2	T 4641
BL24CR2	T 4641
BL34CR2	T 4641
BL46CR2	T 4641
BL48CR2	T 4641
CB08CR2	T 4641
CB12CR2	T 4641
CB16CR2	T 4641
GPC01CR2	T 4641
GPC10CR2	T 4641
RB06CR2	T 4641
RB08CR2	T 4641
BL47CR2	T 4641
GPC08CR2	T 4642
GPC05CR2	T 4642
CB06CR2	T 4642
CB02CR2	T 4642
BL7CR2	T 4642
BL28CR2	T 4642
CB14CR2	T 4641
RB03CR2	T 4641
BL2CR2	T 4642
CB13CR2	T 4641
BL4CR2	T 4642
BL20CR2	T 4641
BL21CR2	T 4641
BL23CR2	T 4641
BL33CR2	T 4641
BL38CR2	T 4641
BL5CR2	T 4641
CB03CR2	T 4641
GPC04CR2	T 4641
GPC07CR2	T 4641
CR2_DQ523161	T 4642
	*

Appendix Figure 3 – Alignment of *A. piscivorus* Control Regions with polymorphism locations indicated by vertical maroon bar below pictorial.

Appendix Figure 3A – Control Region 1





Appendix Figure 3B: Control Region 2



## Appendix Figure 4 – Alignment of CR1 and CR2 regions in specimens where available

```

BL20_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCTAGCTGGGTCCCGAA 16250
BL20_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCTAGCTGGGTCCCGAA 3682
*****

BL20_CR1 ATTTGGCCTTATATGTACTCTTTACATATAGGGTCCCTCATGTGCTATGTATAATAATAC 16310
BL20_CR2 ATTTGGCCTTATATGTACTCTTTACATATAGGGTCCCTCATGTGCTATGTATAATAATAC 3742
*****

BL20_CR1 ATTAATCGTTTTGCCCATGACTATCAAACGGGAATTAACCTTAATTAATTATATACAA 16370
BL20_CR2 ATTAATCGTTTTGCCCATGACTATCAAACGGGAATTAACCTTAATTAATTATATACAA 3802
*****

BL20_CR1 AACTGGTTCATTAAACATATTTTCCCTCCCTCATTTTCTGGTCTGTTCTATTTCAGCAGAGGT 16430
BL20_CR2 AACTGGTTCATTAAACATATTTTCCCTCCCTCATTTTCTGGTCTGTTCTATTTCAGCAGAGGT 3862
*****

BL20_CR1 TGTCGGTTATTAGTAACCATGGCTATCCACTTCAAACGGGTGCCCGTGATTTAACCCCTT 16490
BL20_CR2 TGTCGGTTATTAGTAACCATGGCTATCCACTTCAAACGGGTGCCCGTGATTTAACCCCTT 3922
*****

BL20_CR1 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGCTTTTCACGTCCATATA 16550
BL20_CR2 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGCTTTTCACGTCCATATA 3982
*****

BL20_CR1 TTGTAACCTCCCGTTTATGTCCTTTCCAAGGCCGCTGGTTACACCTTCAAGGGCATCT 16610
BL20_CR2 TTGTAACCTCCCGTTTATGTCCTTTCCAAGGCCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

BL20_CR1 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGGCCTATGGTCGCACCCTTT 16670
BL20_CR2 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGGCCTATGGTCGCACCCTTT 4102
*****

BL20_CR1 ATATTGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 16730
BL20_CR2 ATATTGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 4162
*****

BL20_CR1 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 16790
BL20_CR2 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 4222
*****

BL20_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTCTTGGTCTAGCACTTTCTCCTATACGGAT 16850
BL20_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTCTTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

BL20_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910
BL20_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342
*****

BL20_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCAGATTTTCAAATTTTACCTAAA 16970
BL20_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCAGATTTTCAAATTTTACCTAAA 4402
*****

BL20_CR1 CCCATCCCCTTTTCTATACCAAAATTTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
BL20_CR2 CCCATCCCCTTTTCTATACCAAAATTTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

BL20_CR1 TTTTAAATATTTATTTTTTTTAAAGTGAATAAAGATTTATAAAAAACGCCGATCCA 17090
BL20_CR2 TTTTAAATATTTATTTTTTTTAAAGTGAATAAAGATTTATAAAAAACGCCGATCCA 4522
*****

BL20_CR1 TTTTCAAGATGCGAAATATCACTACTTCTCCAGGGCTGACTCACCGATGCAAACCC 17150
BL20_CR2 TTTTCAAGATGCGAAATATCACTACTTCTCCAGGGCTGACTCACCGATGCAAACCC 4582
*****

BL20_CR1 CCCCCACAGACAAGCCATTTTTGCTTTATTTTTTAATTACGTCAGATTTTTATATG 17210
BL20_CR2 CCCCCACAGACAAGCCATTTTTGCTTTATTTTTTAATTACGTCAGATTTTTATATG- 4641
*****

BL20_CR1 TTG 17213
BL20_CR2 ---

```

```

RB08_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
RB08_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

RB08_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
RB08_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

RB08_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 16370
RB08_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 3802
*****

RB08_CR1 AACTGGTTCATTAACATATTTCCCTTCCCTCATTTCTGGTCTTCTATTCAGCAGAGGT 16430
RB08_CR2 AACTGGTTCATTAACATATTTCCCTTCCCTCATTTCTGGTCTTCTATTCAGCAGAGGT 3862
*****

RB08_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCCCGTATTTAACCCCT 16490
RB08_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCCCGTATTTAACCCCT 3922
*****

RB08_CR1 CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGTTTTACGTCATATA 16550
RB08_CR2 CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGTTTTACGTCATATA 3982
*****

RB08_CR1 TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 16610
RB08_CR2 TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

RB08_CR1 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGGCCTATGGTCGCACCCTTT 16670
RB08_CR2 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGGCCTATGGTCGCACCCTTT 4102
*****

RB08_CR1 ATATGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTCCACCCCTGGTTGGCT 16730
RB08_CR2 ATATGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTCCACCCCTGGTTGGCT 4162
*****

RB08_CR1 TTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 16790
RB08_CR2 TTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 4222
*****

RB08_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
RB08_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

RB08_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910
RB08_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342
*****

RB08_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
RB08_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

RB08_CR1 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
RB08_CR2 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

RB08_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 17090
RB08_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 4522
*****

RB08_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTACCGATGCAAACCC 17150
RB08_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTACCGATGCAAACCC 4582
*****

RB08_CR1 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG 17210
RB08_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG- 4641
*****

RB08_CR1 TTG 17213
RB08_CR2 ---

```

```

RB06_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
RB06_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

RB06_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
RB06_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

RB06_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAAA 16370
RB06_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAAA 3802
*****

RB06_CR1 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCTTCTATTCAGCAGAGGT 16430
RB06_CR2 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCTTCTATTCAGCAGAGGT 3862
*****

RB06_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCCCGTATTTAACCCCT 16490
RB06_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCCCGTATTTAACCCCT 3922
*****

RB06_CR1 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGCTTTTACGTCATATA 16550
RB06_CR2 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGCTTTTACGTCATATA 3982
*****

RB06_CR1 TTGTAACCTCCCGTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 16610
RB06_CR2 TTGTAACCTCCCGTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

RB06_CR1 CAATGGTCCGGAACACCCCGCTTACTTGCTCTTTCCAAGCCCTATGGTCCGACCCCTT 16670
RB06_CR2 CAATGGTCCGGAACACCCCGCTTACTTGCTCTTTCCAAGCCCTATGGTCCGACCCCTT 4102
*****

RB06_CR1 ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTCCACCCCTGGTTGGCT 16730
RB06_CR2 ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTCCACCCCTGGTTGGCT 4162
*****

RB06_CR1 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 16790
RB06_CR2 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 4222
*****

RB06_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
RB06_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

RB06_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910
RB06_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342
*****

RB06_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
RB06_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

RB06_CR1 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
RB06_CR2 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

RB06_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 17090
RB06_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 4522
*****

RB06_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCATCTGACTACCGATGCAAACCC 17150
RB06_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCATCTGACTACCGATGCAAACCC 4582
*****

RB06_CR1 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG 17210
RB06_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG- 4641
*****

RB06_CR1 TTG 17213
RB06_CR2 ---

```

```

RB03_CR1      AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
RB03_CR2      AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

RB03_CR1      ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
RB03_CR2      ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

RB03_CR1      ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAACAA 16370
RB03_CR2      ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAACAA 3802
*****

RB03_CR1      AACTGGTTCATTAAACATATTTCCCTCCCTCATTTTCTGGTCTTCTATTTCAGCAGAGGT 16430
RB03_CR2      AACTGGTTCATTAAACATATTTCCCTCCCTCATTTTCTGGTCTTCTATTTCAGCAGAGGT 3862
*****

RB03_CR1      TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 16490
RB03_CR2      TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 3922
*****

RB03_CR1      CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 16550
RB03_CR2      CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 3982
*****

RB03_CR1      TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 16610
RB03_CR2      TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

RB03_CR1      CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 16670
RB03_CR2      CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 4102
*****

RB03_CR1      ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTTCCACCCCTGGTTGGCT 16730
RB03_CR2      ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTTCCACCCCTGGTTGGCT 4162
*****

RB03_CR1      TTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 16790
RB03_CR2      TTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 4222
*****

RB03_CR1      GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATATGGAT 16850
RB03_CR2      GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATATGGAT 4282
*****

RB03_CR1      ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910
RB03_CR2      ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342
*****

RB03_CR1      ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
RB03_CR2      ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

RB03_CR1      CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
RB03_CR2      CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

RB03_CR1      TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACGCCGATCCA 17090
RB03_CR2      TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACGCCGATCCA 4522
*****

RB03_CR1      TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTACCGATGCAAACCC 17150
RB03_CR2      TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTACCGATGCAAACCC 4582
*****

RB03_CR1      CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG 17210
RB03_CR2      CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG- 4641
*****

RB03_CR1      TTG 17213
RB03_CR2      ---

```

GPC10\_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250  
 GPC10\_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682  
 \*\*\*\*\*

GPC10\_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310  
 GPC10\_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742  
 \*\*\*\*\*

GPC10\_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 16370  
 GPC10\_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 3802  
 \*\*\*\*\*

GPC10\_CR1 AACTGGTTCATTAACATATTTCCCTCCCTCATTTTCTGGTCTTCTATTTCAGCAGAGGT 16430  
 GPC10\_CR2 AACTGGTTCATTAACATATTTCCCTCCCTCATTTTCTGGTCTTCTATTTCAGCAGAGGT 3862  
 \*\*\*\*\*

GPC10\_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 16490  
 GPC10\_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 3922  
 \*\*\*\*\*

GPC10\_CR1 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 16550  
 GPC10\_CR2 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 3982  
 \*\*\*\*\*

GPC10\_CR1 TTGTAACCTCCCGTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 16610  
 GPC10\_CR2 TTGTAACCTCCCGTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 4042  
 \*\*\*\*\*

GPC10\_CR1 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 16670  
 GPC10\_CR2 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 4102  
 \*\*\*\*\*

GPC10\_CR1 ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTTCCACCCCTGGTTGGCT 16730  
 GPC10\_CR2 ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTTCCACCCCTGGTTGGCT 4162  
 \*\*\*\*\*

GPC10\_CR1 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 16790  
 GPC10\_CR2 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 4222  
 \*\*\*\*\*

GPC10\_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850  
 GPC10\_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282  
 \*\*\*\*\*

GPC10\_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910  
 GPC10\_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342  
 \*\*\*\*\*

GPC10\_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970  
 GPC10\_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402  
 \*\*\*\*\*

GPC10\_CR1 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030  
 GPC10\_CR2 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462  
 \*\*\*\*\*

GPC10\_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 17090  
 GPC10\_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 4522  
 \*\*\*\*\*

GPC10\_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 17150  
 GPC10\_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 4582  
 \*\*\*\*\*

GPC10\_CR1 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG 17210  
 GPC10\_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG- 4641  
 \*\*\*\*\*

GPC10\_CR1 TTG 17213  
 GPC10\_CR2 ---

```

CB16_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
CB16_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

CB16_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
CB16_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

CB16_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 16370
CB16_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 3802
*****

CB16_CR1 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCGTTCTATTCAGCAGAGGT 16430
CB16_CR2 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCGTTCTATTCAGCAGAGGT 3862
*****

CB16_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 16490
CB16_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 3922
*****

CB16_CR1 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTACGTCATATA 16550
CB16_CR2 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTACGTCATATA 3982
*****

CB16_CR1 TTGTAACCTCCCGTTTTATGTCCTTTCAAGGCGCTGGTTACACCTTCAAGGGCATCT 16610
CB16_CR2 TTGTAACCTCCCGTTTTATGTCCTTTCAAGGCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

CB16_CR1 CAATGGTCCGGAACACCCCGCTTACTTGCTCTTTCAAGGCCTATGGTCGCACCCTTT 16670
CB16_CR2 CAATGGTCCGGAACACCCCGCTTACTTGCTCTTTCAAGGCCTATGGTCGCACCCTTT 4102
*****

CB16_CR1 ATATGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTCCACCCCTGGTTGGCT 16730
CB16_CR2 ATATGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTCCACCCCTGGTTGGCT 4162
*****

CB16_CR1 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 16790
CB16_CR2 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 4222
*****

CB16_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
CB16_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

CB16_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTTATTTTT 16910
CB16_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTTATTTTT 4342
*****

CB16_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
CB16_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

CB16_CR1 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
CB16_CR2 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

CB16_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACGGCATCCA 17090
CB16_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACGGCATCCA 4522
*****

CB16_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGCGCTGACTCACCGATGCAAACCC 17150
CB16_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGCGCTGACTCACCGATGCAAACCC 4582
*****

CB16_CR1 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATACGTCCGAGATTTTATATG 17210
CB16_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATACGTCCGAGATTTTATATG- 4641
*****

CB16_CR1 TTG 17213
CB16_CR2 ---

```

```

CB14_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
CB14_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

CB14_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCTCATGTCGCTATGTATAATAATAC 16310
CB14_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCTCATGTCGCTATGTATAATAATAC 3742
*****

CB14_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAAA 16370
CB14_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAAA 3802
*****

CB14_CR1 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCGTTCTATTTCAGCAGAGGT 16430
CB14_CR2 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCGTTCTATTTCAGCAGAGGT 3862
*****

CB14_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAAACCTT 16490
CB14_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAAACCTT 3922
*****

CB14_CR1 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTACGTCATATA 16550
CB14_CR2 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTACGTCATATA 3982
*****

CB14_CR1 TTGTAACCTCCCGTTTTATGTCCTTTCAAGGCGCTGGTTACACCTTCAAGGGCATCT 16610
CB14_CR2 TTGTAACCTCCCGTTTTATGTCCTTTCAAGGCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

CB14_CR1 CAATGGTCCGGAACCCCGCCTTACTTGCTCTTTCAAGGCCTATGGTCGCACCCTTT 16670
CB14_CR2 CAATGGTCCGGAACCCCGCCTTACTTGCTCTTTCAAGGCCTATGGTCGCACCCTTT 4102
*****

CB14_CR1 ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTTCCACCCCTGGTTGGCT 16730
CB14_CR2 ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTTCCACCCCTGGTTGGCT 4162
*****

CB14_CR1 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 16790
CB14_CR2 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 4222
*****

CB14_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
CB14_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

CB14_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910
CB14_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342
*****

CB14_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
CB14_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

CB14_CR1 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
CB14_CR2 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

CB14_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 17090
CB14_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 4522
*****

CB14_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGCGCTGACTACCGATGCAAACCC 17150
CB14_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGCGCTGACTACCGATGCAAACCC 4582
*****

CB14_CR1 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG 17210
CB14_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG- 4641
*****

CB14_CR1 TTG 17213
CB14_CR2 ---

```



```

CB13_CR1      AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
CB13_CR2      AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

CB13_CR1      ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
CB13_CR2      ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

CB13_CR1      ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 16370
CB13_CR2      ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 3802
*****

CB13_CR1      AACTGGTTCATTAACATATTTCCCTCCCTCATTTTCTGGTCTTCTATTCAGCAGAGGT 16430
CB13_CR2      AACTGGTTCATTAACATATTTCCCTCCCTCATTTTCTGGTCTTCTATTCAGCAGAGGT 3862
*****

CB13_CR1      TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 16490
CB13_CR2      TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 3922
*****

CB13_CR1      CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTTACGTCATATA 16550
CB13_CR2      CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTTACGTCATATA 3982
*****

CB13_CR1      TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 16610
CB13_CR2      TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

CB13_CR1      CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 16670
CB13_CR2      CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 4102
*****

CB13_CR1      ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTTCCACCCCTGGTTGGCT 16730
CB13_CR2      ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTTCCACCCCTGGTTGGCT 4162
*****

CB13_CR1      TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 16790
CB13_CR2      TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 4222
*****

CB13_CR1      GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
CB13_CR2      GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

CB13_CR1      ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910
CB13_CR2      ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342
*****

CB13_CR1      ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
CB13_CR2      ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

CB13_CR1      CCCATCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
CB13_CR2      CCCATCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

CB13_CR1      TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 17090
CB13_CR2      TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 4522
*****

CB13_CR1      TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 17150
CB13_CR2      TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 4582
*****

CB13_CR1      CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG 17210
CB13_CR2      CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG- 4641
*****

CB13_CR1      TTG 17213
CB13_CR2      ---

```

```

CB09_CR1 -AAACCAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGA 16249
CB09_CR2 AAACCAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGA 3682
**.*.*****

CB09_CR1 AATTTGGCCTTATATGTACTCTTACATATAGGGTCCTCATGTCGCTATGTATAATAATA 16309
CB09_CR2 AATTTGGCCTTATATGTACTCTTACATATAGGGTCCTCATGTCGCTATGTATAATAATA 3742
*****

CB09_CR1 CATTAAATCGTTTTGCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACA 16369
CB09_CR2 CATTAAATCGTTTTGCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACA 3802
*****

CB09_CR1 AAACGGTTCATTAACATATTTCCCTTCCCTCATTTCTGGTCGTTCTATTACGACAGAG 16429
CB09_CR2 AAACGGTTCATTAACATATTTCCCTTCCCTCATTTCTGGTCGTTCTATTACGACAGAG 3862
*****

CB09_CR1 TTGTCGCTTATTAGTAACCATGGCTATCCACTTCAAACCGGTGTCCCGTGATTTAACCT 16489
CB09_CR2 TTGTCGCTTATTAGTAACCATGGCTATCCACTTCAAACCGGTGTCCCGTGATTTAACCT 3922
*****

CB09_CR1 TCCCGTGAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGCTTTTCAGTCCATAT 16549
CB09_CR2 TCCCGTGAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGCTTTTCAGTCCATAT 3982
*****

CB09_CR1 ATTGTAACCTCCCGTTTATGTCTTTCCAAGGCCGTGGTTACACCTTCAAGGGCATC 16609
CB09_CR2 ATTGTAACCTCCCGTTTATGTCTTTCCAAGGCCGTGGTTACACCTTCAAGGGCATC 4042
*****

CB09_CR1 TCAATGGTCCGGAACCCCGCCTTACTTGCTCTTTCCAAGGCCTATGGTCGCACCCCT 16669
CB09_CR2 TCAATGGTCCGGAACCCCGCCTTACTTGCTCTTTCCAAGGCCTATGGTCGCACCCCT 4102
*****

CB09_CR1 TATATTGGTACATTTACCTCATGTCTTATCAGTATGCCTGTCCACCCCTGGTTGGC 16729
CB09_CR2 TATATTGGTACATTTACCTCATGTCTTATCAGTATGCCTGTCCACCCCTGGTTGGC 4162
*****

CB09_CR1 TTTTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCG 16789
CB09_CR2 TTTTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCG 4222
*****

CB09_CR1 GGGTAGACCATTAGTCCAGGTGGAGCTATATCTTGGTCTAGCACTTCTCCTATACGGA 16849
CB09_CR2 GGGTAGACCATTAGTCCAGGTGGAGCTATATCTTGGTCTAGCACTTCTCCTATACGGA 4282
*****

CB09_CR1 TACATCTCTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTT 16909
CB09_CR2 TACATCTCTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTT 4342
*****

CB09_CR1 TATTAAGAAATCCCGTTGTAATAACATTTTTTTACCCGATTTTCAAATTTTACCTAA 16969
CB09_CR2 TATTAAGAAATCCCGTTGTAATAACATTTTTTTACCCGATTTTCAAATTTTACCTAA 4402
*****

CB09_CR1 ACCCATCCCACCTTTCTATACCAAAATTTCAAACCCGAATTCCTATAAGAAATTTTTTTA 17029
CB09_CR2 ACCCATCCCACCTTTCTATACCAAAATTTCAAACCCGAATTCCTATAAGAAATTTTTTTA 4462
*****

CB09_CR1 TTTTTAAATATTTATTTTTTTAACGTGAAAAATAAAAAGATTATAAAAAACGCCGATCC 17089
CB09_CR2 TTTTTAAATATTTATTTTTTTAACGTGAAAAATAAAAAGATTATAAAAAACGCCGATCC 4522
*****

CB09_CR1 ATTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAAC 17149
CB09_CR2 ATTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAAC 4582
*****

CB09_CR1 CCCCCCAGACAAAGCCATTTTGTCTTATTTTAATTACGTCGAGATTTTATAT 17209
CB09_CR2 CCCCCCAGACAAAGCCATTTTGTCTTATTTTAATTACGTCGAGATTTTATAT 4642
*****

CB09_CR1 GTTG 17213
CB09_CR2 ----

```

CB12\_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250  
 CB12\_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682  
 \*\*\*\*\*

CB12\_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310  
 CB12\_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742  
 \*\*\*\*\*

CB12\_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAACAA 16370  
 CB12\_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAACAA 3802  
 \*\*\*\*\*

CB12\_CR1 AACTGGTTCATTAACATATTTCCCTCCCTCATTTTCTGGTCTTCTATTTCAGCAGAGGT 16430  
 CB12\_CR2 AACTGGTTCATTAACATATTTCCCTCCCTCATTTTCTGGTCTTCTATTTCAGCAGAGGT 3862  
 \*\*\*\*\*

CB12\_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 16490  
 CB12\_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 3922  
 \*\*\*\*\*

CB12\_CR1 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 16550  
 CB12\_CR2 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 3982  
 \*\*\*\*\*

CB12\_CR1 TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 16610  
 CB12\_CR2 TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 4042  
 \*\*\*\*\*

CB12\_CR1 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 16670  
 CB12\_CR2 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 4102  
 \*\*\*\*\*

CB12\_CR1 ATATGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 16730  
 CB12\_CR2 ATATGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 4162  
 \*\*\*\*\*

CB12\_CR1 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 16790  
 CB12\_CR2 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 4222  
 \*\*\*\*\*

CB12\_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850  
 CB12\_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282  
 \*\*\*\*\*

CB12\_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910  
 CB12\_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342  
 \*\*\*\*\*

CB12\_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970  
 CB12\_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402  
 \*\*\*\*\*

CB12\_CR1 CCCATCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030  
 CB12\_CR2 CCCATCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462  
 \*\*\*\*\*

CB12\_CR1 TTTTAAATATTTATTTTTTTAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 17090  
 CB12\_CR2 TTTTAAATATTTATTTTTTTAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 4522  
 \*\*\*\*\*

CB12\_CR1 TTTTCAAGATGCGAAATATCACTACTTCTCCAGGCGCTGACTCACCGATGCAAACCC 17150  
 CB12\_CR2 TTTTCAAGATGCGAAATATCACTACTTCTCCAGGCGCTGACTCACCGATGCAAACCC 4582  
 \*\*\*\*\*

CB12\_CR1 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG 17210  
 CB12\_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG- 4641  
 \*\*\*\*\*

CB12\_CR1 TTG 17213  
 CB12\_CR2 ---

```

CB07_CR1 -AAACCAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGA 16249
CB07_CR2 AAACCAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGA 3682
**.*.*****

CB07_CR1 AATTTGGCCTTATATGTACTCTTACATATAGGGTCCTCATGTCGCTATGTATAATAATA 16309
CB07_CR2 AATTTGGCCTTATATGTACTCTTACATATAGGGTCCTCATGTCGCTATGTATAATAATA 3742
*****

CB07_CR1 CATTAAATCGTTTTGCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACA 16369
CB07_CR2 CATTAAATCGTTTTGCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACA 3802
*****

CB07_CR1 AAACGGTTCATTAACATATTTCCCTTCCCTCATTTCTGGTCGTTCTATTACGACAGAG 16429
CB07_CR2 AAACGGTTCATTAACATATTTCCCTTCCCTCATTTCTGGTCGTTCTATTACGACAGAG 3862
*****

CB07_CR1 TTGTCGCTTATTAGTAACCATGGCTATCCACTTCAAACCGGTGTCCCGTGATTTAACCC 16489
CB07_CR2 TTGTCGCTTATTAGTAACCATGGCTATCCACTTCAAACCGGTGTCCCGTGATTTAACCC 3922
*****

CB07_CR1 TCCCGTGAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGCTTTTCACGTCCATAT 16549
CB07_CR2 TCCCGTGAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGCTTTTCACGTCCATAT 3982
*****

CB07_CR1 ATTGTAACCTCCCGTTTATGTCCCTTCCAAGGCCGTGGTTACACCTTCAAGGGCATC 16609
CB07_CR2 ATTGTAACCTCCCGTTTATGTCCCTTCCAAGGCCGTGGTTACACCTTCAAGGGCATC 4042
*****

CB07_CR1 TCAATGGTCCGGAACCCCGCCTTACTTGCTCTTCCAAGGCCATGGTCGCACCCCTT 16669
CB07_CR2 TCAATGGTCCGGAACCCCGCCTTACTTGCTCTTCCAAGGCCATGGTCGCACCCCTT 4102
*****

CB07_CR1 TATATTGGTACATTTACCTCATGTCTTATCAGTATGCCTGTCCACCCCTGGTTGGC 16729
CB07_CR2 TATATTGGTACATTTACCTCATGTCTTATCAGTATGCCTGTCCACCCCTGGTTGGC 4162
*****

CB07_CR1 TTTTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCG 16789
CB07_CR2 TTTTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCG 4222
*****

CB07_CR1 GGGTAGACCATTAGTCCAGGTGGAGCTATATCTTGGTCTAGCACTTTCTCCTATACGGA 16849
CB07_CR2 GGGTAGACCATTAGTCCAGGTGGAGCTATATCTTGGTCTAGCACTTTCTCCTATACGGA 4282
*****

CB07_CR1 TACATCTCTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTT 16909
CB07_CR2 TACATCTCTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTT 4342
*****

CB07_CR1 TATTAAGAAATCCCGTTGTAATAACATTTTTTTACCCGATTTTCAAATTTTACCTAA 16969
CB07_CR2 TATTAAGAAATCCCGTTGTAATAACATTTTTTTACCCGATTTTCAAATTTTACCTAA 4402
*****

CB07_CR1 ACCCATCCCACCTTTCTATACCAAAATTTCAAACCCGAATTCCTATAAGAAATTTTTTTA 17029
CB07_CR2 ACCCATCCCACCTTTCTATACCAAAATTTCAAACCCGAATTCCTATAAGAAATTTTTTTA 4462
*****

CB07_CR1 TTTTTAAATATTTATTTTTTTTAACTGAAAAATAAAAAGATTATAAAAAACGCCGATCC 17089
CB07_CR2 TTTTTAAATATTTATTTTTTTTAACTGAAAAATAAAAAGATTATAAAAAACGCCGATCC 4522
*****

CB07_CR1 ATTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAAC 17149
CB07_CR2 ATTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAAC 4582
*****

CB07_CR1 CCCCCACAGACAAAGCCATTTTGTCTTATTTTAAATACGTCGAGATTTTATAT 17209
CB07_CR2 CCCCCACAGACAAAGCCATTTTGTCTTATTTTAAATACGTCGAGATTTTATAT 4642
*****

CB07_CR1 GTTG 17213
CB07_CR2 ----

```

```

CB06_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
CB06_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

CB06_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
CB06_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

CB06_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 16370
CB06_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 3802
*****

CB06_CR1 AACTGGTTCATTAACATATTTCCCTCCCTCATTTTCTGGTCGTTCTATTTCAGCAGAGGT 16430
CB06_CR2 AACTGGTTCATTAACATATTTCCCTCCCTCATTTTCTGGTCGTTCTATTTCAGCAGAGGT 3862
*****

CB06_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 16490
CB06_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 3922
*****

CB06_CR1 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 16550
CB06_CR2 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 3982
*****

CB06_CR1 TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 16610
CB06_CR2 TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

CB06_CR1 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGGCCTATGGTCGCACCCTTT 16670
CB06_CR2 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGGCCTATGGTCGCACCCTTT 4102
*****

CB06_CR1 ATATGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTTCCACCCCTGGTTGGCT 16730
CB06_CR2 ATATGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTTCCACCCCTGGTTGGCT 4162
*****

CB06_CR1 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 16790
CB06_CR2 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 4222
*****

CB06_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
CB06_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

CB06_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATATATTTTT 16910
CB06_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATATATTTTT 4342
*****

CB06_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
CB06_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

CB06_CR1 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
CB06_CR2 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

CB06_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 17090
CB06_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 4522
*****

CB06_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 17150
CB06_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 4582
*****

CB06_CR1 CCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAATTACGTCGAGATTTTATAT 17209
CB06_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAATTACGTCGAGATTTTATAT 4642
*****

CB06_CR1 GTTG 17213
CB06_CR2 ----

```

```

CB05_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
CB05_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

CB05_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
CB05_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

CB05_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAACAA 16370
CB05_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAACAA 3802
*****

CB05_CR1 AACTGGTTCATTAACATATTTCCCTTCCCTCATTTCTGGTCTTCTATTCAGCAGAGGT 16430
CB05_CR2 AACTGGTTCATTAACATATTTCCCTTCCCTCATTTCTGGTCTTCTATTCAGCAGAGGT 3862
*****

CB05_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 16490
CB05_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 3922
*****

CB05_CR1 CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGCTTTTACGTCATATA 16550
CB05_CR2 CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGCTTTTACGTCATATA 3982
*****

CB05_CR1 TTGTAACCTCCCGTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 16610
CB05_CR2 TTGTAACCTCCCGTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

CB05_CR1 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 16670
CB05_CR2 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 4102
*****

CB05_CR1 ATATGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 16730
CB05_CR2 ATATGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 4162
*****

CB05_CR1 TTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 16790
CB05_CR2 TTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 4222
*****

CB05_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
CB05_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

CB05_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910
CB05_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342
*****

CB05_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
CB05_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

CB05_CR1 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
CB05_CR2 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

CB05_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 17090
CB05_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 4522
*****

CB05_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGCGCTGACTCACCGATGCAAACCC 17150
CB05_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGCGCTGACTCACCGATGCAAACCC 4582
*****

CB05_CR1 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG 17210
CB05_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG- 4641
*****

CB05_CR1 TTG 17213
CB05_CR2 ---

```

```

CB03_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
CB03_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

CB03_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
CB03_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

CB03_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 16370
CB03_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 3802
*****

CB03_CR1 AACTGGTTCATTAACATATTTCCCTCCCTCATTTTCTGGTCGTTCTATTTCAGCAGAGGT 16430
CB03_CR2 AACTGGTTCATTAACATATTTCCCTCCCTCATTTTCTGGTCGTTCTATTTCAGCAGAGGT 3862
*****

CB03_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 16490
CB03_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 3922
*****

CB03_CR1 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGCTTTTACGTCATATA 16550
CB03_CR2 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGCTTTTACGTCATATA 3982
*****

CB03_CR1 TTGTAACCTCCCGTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 16610
CB03_CR2 TTGTAACCTCCCGTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

CB03_CR1 CAATGGTCCGGAACACCCCGCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 16670
CB03_CR2 CAATGGTCCGGAACACCCCGCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 4102
*****

CB03_CR1 ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTTCCACCCCTGGTTGGCT 16730
CB03_CR2 ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTTCCACCCCTGGTTGGCT 4162
*****

CB03_CR1 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 16790
CB03_CR2 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 4222
*****

CB03_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
CB03_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

CB03_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910
CB03_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342
*****

CB03_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
CB03_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

CB03_CR1 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
CB03_CR2 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

CB03_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 17090
CB03_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 4522
*****

CB03_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 17150
CB03_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 4582
*****

CB03_CR1 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG 17210
CB03_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG- 4641
*****

CB03_CR1 TTG 17213
CB03_CR2 ---

```

BL7\_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250  
 BL7\_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682  
 \*\*\*\*\*

BL7\_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310  
 BL7\_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742  
 \*\*\*\*\*

BL7\_CR1 ATTAATCGTTTTGCCCATGACTATCAACGGGAATTTAACTTTAATTAATATATATAACAA 16370  
 BL7\_CR2 ATTAATCGTTTTGCCCATGACTATCAACGGGAATTTAACTTTAATTAATATATATAACAA 3802  
 \*\*\*\*\*

BL7\_CR1 AACTGGTTCATTAACATATTTCCCTCCCTCATTTTCTGGTCTTCTATTTCAGCAGAGGT 16430  
 BL7\_CR2 AACTGGTTCATTAACATATTTCCCTCCCTCATTTTCTGGTCTTCTATTTCAGCAGAGGT 3862  
 \*\*\*\*\*

BL7\_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCCGGTGTCCCGTGATTTAACCCCTT 16490  
 BL7\_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCCGGTGTCCCGTGATTTAACCCCTT 3922  
 \*\*\*\*\*

BL7\_CR1 CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 16550  
 BL7\_CR2 CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 3982  
 \*\*\*\*\*

BL7\_CR1 TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 16610  
 BL7\_CR2 TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 4042  
 \*\*\*\*\*

BL7\_CR1 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGGCCTATGGTCGCACCCTTT 16670  
 BL7\_CR2 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGGCCTATGGTCGCACCCTTT 4102  
 \*\*\*\*\*

BL7\_CR1 ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTCCACCCCTGGTTGGCT 16730  
 BL7\_CR2 ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTCCACCCCTGGTTGGCT 4162  
 \*\*\*\*\*

BL7\_CR1 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 16790  
 BL7\_CR2 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 4222  
 \*\*\*\*\*

BL7\_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850  
 BL7\_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282  
 \*\*\*\*\*

BL7\_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910  
 BL7\_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342  
 \*\*\*\*\*

BL7\_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970  
 BL7\_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402  
 \*\*\*\*\*

BL7\_CR1 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030  
 BL7\_CR2 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462  
 \*\*\*\*\*

BL7\_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 17090  
 BL7\_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 4522  
 \*\*\*\*\*

BL7\_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCAGATGCAAACCC 17150  
 BL7\_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCAGATGCAAACCC 4582  
 \*\*\*\*\*

BL7\_CR1 CCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATACGTCGAGATTTTATAT 1019  
 BL7\_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATACGTCGAGATTTTATAT 4642  
 \*\*\*\*\*

BL7\_CR1 GTTG 17213  
 BL7\_CR2 ----



```

BL5_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
BL5_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

BL5_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
BL5_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

BL5_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAAA 16370
BL5_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAAA 3802
*****

BL5_CR1 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCTTCTATTCAGCAGAGGT 16430
BL5_CR2 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCTTCTATTCAGCAGAGGT 3862
*****

BL5_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCCCGTGATTTAACCCCT 16490
BL5_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCCCGTGATTTAACCCCT 3922
*****

BL5_CR1 CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGCTTTTACGTCATATA 16550
BL5_CR2 CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGCTTTTACGTCATATA 3982
*****

BL5_CR1 TTGTAACCTCCCGTTTATGTCCTTTCAAGGCCGCTGGTTACACCTTCAAGGGCATCT 16610
BL5_CR2 TTGTAACCTCCCGTTTATGTCCTTTCAAGGCCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

BL5_CR1 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCAAGGCCTATGGTCGCACCCTTT 16670
BL5_CR2 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCAAGGCCTATGGTCGCACCCTTT 4102
*****

BL5_CR1 ATATTGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTCCACCCCTGGTTGGCT 16730
BL5_CR2 ATATTGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTCCACCCCTGGTTGGCT 4162
*****

BL5_CR1 TTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 16790
BL5_CR2 TTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 4222
*****

BL5_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
BL5_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

BL5_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTTATTTTT 16910
BL5_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTTATTTTT 4342
*****

BL5_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
BL5_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

BL5_CR1 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
BL5_CR2 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

BL5_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 17090
BL5_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 4522
*****

BL5_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 17150
BL5_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 4582
*****

BL5_CR1 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG 17210
BL5_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG- 4641
*****

BL5_CR1 TTG 17213
BL5_CR2 ---

```

```

BL4_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
BL4_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

BL4_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
BL4_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

BL4_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAAA 16370
BL4_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAAA 3802
*****

BL4_CR1 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCTTCTATTTCAGCAGAGGT 16430
BL4_CR2 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCTTCTATTTCAGCAGAGGT 3862
*****

BL4_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTATTTAACCCCTT 16490
BL4_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTATTTAACCCCTT 3922
*****

BL4_CR1 CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGCTTTTCACGTCCATATA 16550
BL4_CR2 CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGCTTTTCACGTCCATATA 3982
*****

BL4_CR1 TTGTAACCTCCCGTTTATGTCCTTTCAAGGCGCTGGTTACACCTTCAAGGGCATCT 16610
BL4_CR2 TTGTAACCTCCCGTTTATGTCCTTTCAAGGCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

BL4_CR1 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCAAGGCCTATGGTCCGACCCCTT 16670
BL4_CR2 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCAAGGCCTATGGTCCGACCCCTT 4102
*****

BL4_CR1 ATATTGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 16730
BL4_CR2 ATATTGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 4162
*****

BL4_CR1 TTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 16790
BL4_CR2 TTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 4222
*****

BL4_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
BL4_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

BL4_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910
BL4_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342
*****

BL4_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
BL4_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

BL4_CR1 CCCATCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
BL4_CR2 CCCATCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

BL4_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACGCCGATCCA 17090
BL4_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACGCCGATCCA 4522
*****

BL4_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGCGCTGACTACCGATGCAAACCC 17150
BL4_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGCGCTGACTACCGATGCAAACCC 4582
*****

BL4_CR1 CCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAATTACGTCGAGATTTTTATAT 1019
BL4_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAATTACGTCGAGATTTTTATAT 4642
*****

BL4_CR1 GTTG 17213
BL4_CR2 ----

```

```

BL38_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
BL38_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

BL38_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
BL38_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

BL38_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAAA 16370
BL38_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAAA 3802
*****

BL38_CR1 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCTTCTATTCAGCAGAGGT 16430
BL38_CR2 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCTTCTATTCAGCAGAGGT 3862
*****

BL38_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTATTTAACCCCT 16490
BL38_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTATTTAACCCCT 3922
*****

BL38_CR1 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTACGTCATATA 16550
BL38_CR2 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGTTTTACGTCATATA 3982
*****

BL38_CR1 TTGTAACCTCCCGTTTTATGTCCTTTCAAGCCGCTGGTTACACCTCAAGGGCATCT 16610
BL38_CR2 TTGTAACCTCCCGTTTTATGTCCTTTCAAGCCGCTGGTTACACCTCAAGGGCATCT 4042
*****

BL38_CR1 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCAAGGCCTATGGTCGCACCCTTT 16670
BL38_CR2 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCAAGGCCTATGGTCGCACCCTTT 4102
*****

BL38_CR1 ATATTGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 16730
BL38_CR2 ATATTGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 4162
*****

BL38_CR1 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 16790
BL38_CR2 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 4222
*****

BL38_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
BL38_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

BL38_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910
BL38_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342
*****

BL38_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
BL38_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

BL38_CR1 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
BL38_CR2 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

BL38_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 17090
BL38_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 4522
*****

BL38_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 17150
BL38_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 4582
*****

BL38_CR1 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG 17210
BL38_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG- 4641
*****

BL38_CR1 TTG 17213
BL38_CR2 ---

```

```

BL34_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
BL34_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

BL34_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
BL34_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

BL34_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 16370
BL34_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATACAA 3802
*****

BL34_CR1 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCTGTTCTATTCAGCAGAGGT 16430
BL34_CR2 AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCTGTTCTATTCAGCAGAGGT 3862
*****

BL34_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 16490
BL34_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 3922
*****

BL34_CR1 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGCTTTTACGTCATATA 16550
BL34_CR2 CCCGTGAAATCCTCTATCCTTTACCTCAGGCATACAGTCCCGCTTTTACGTCATATA 3982
*****

BL34_CR1 TTGTAACCTCCCGTTTATGTCCTTTCAAGGCCGCTGGTTACACCTTCAAGGGCATCT 16610
BL34_CR2 TTGTAACCTCCCGTTTATGTCCTTTCAAGGCCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

BL34_CR1 CAATGGTCCGGAACCCCGCCTTACTTGCTCTTTCAAGGCCTATGGTCGCACCCTTT 16670
BL34_CR2 CAATGGTCCGGAACCCCGCCTTACTTGCTCTTTCAAGGCCTATGGTCGCACCCTTT 4102
*****

BL34_CR1 ATATTGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 16730
BL34_CR2 ATATTGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 4162
*****

BL34_CR1 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 16790
BL34_CR2 TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTCACCCCTCTCCGG 4222
*****

BL34_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
BL34_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

BL34_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTTATTTTT 16910
BL34_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTTATTTTT 4342
*****

BL34_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
BL34_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

BL34_CR1 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
BL34_CR2 CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

BL34_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 17090
BL34_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACCGCATCCA 4522
*****

BL34_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCAGATGCAAACCC 17150
BL34_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCAGATGCAAACCC 4582
*****

BL34_CR1 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG 17210
BL34_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG- 4641
*****

BL34_CR1 TTG 17213
BL34_CR2 ---

```

```

BL2_CR1      AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
BL2_CR2      AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

BL2_CR1      ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
BL2_CR2      ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

BL2_CR1      ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAACAA 16370
BL2_CR2      ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAACAA 3802
*****

BL2_CR1      AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCTGTTCTATTCAGCAGAGGT 16430
BL2_CR2      AACTGGTTCATTAACATATTTCCCTCCCTCATTTCTGGTCTGTTCTATTCAGCAGAGGT 3862
*****

BL2_CR1      TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 16490
BL2_CR2      TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCTT 3922
*****

BL2_CR1      CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 16550
BL2_CR2      CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 3982
*****

BL2_CR1      TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 16610
BL2_CR2      TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

BL2_CR1      CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGGCCTATGGTCCGACCCCTT 16670
BL2_CR2      CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGGCCTATGGTCCGACCCCTT 4102
*****

BL2_CR1      ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTCCACCCCTGGTTGGCT 16730
BL2_CR2      ATATTGGTACATTTACCTCATGTTCTTATCACGTATGCCTGTCCACCCCTGGTTGGCT 4162
*****

BL2_CR1      TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 16790
BL2_CR2      TTTTATAGGTACCTTTACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 4222
*****

BL2_CR1      GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
BL2_CR2      GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

BL2_CR1      ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 16910
BL2_CR2      ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTATTTTTT 4342
*****

BL2_CR1      ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
BL2_CR2      ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

BL2_CR1      CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
BL2_CR2      CCCATCCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

BL2_CR1      TTTTAAATATTTATTTTTTTAACGTGAAAAATAAAAAGATTATAAAAAACGCCGATCCA 17090
BL2_CR2      TTTTAAATATTTATTTTTTTAACGTGAAAAATAAAAAGATTATAAAAAACGCCGATCCA 4522
*****

BL2_CR1      TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 17150
BL2_CR2      TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTCACCGATGCAAACCC 4582
*****

BL2_CR1      CCCCC-ACAGACAAAGCCATTTTTGTCTTTATTTTAATTACGTCGAGATTTTTATAT 1019
BL2_CR2      CCCCCACAGACAAAGCCATTTTTGTCTTTATTTTAATTACGTCGAGATTTTTATAT 4642
*****

BL2_CR1      GTTG 17213
BL2_CR2      ----

```

```

BL29_CR1 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 16250
BL29_CR2 AAACCAAAAAAATACTCTCCTAGGACCCCCCTACCCCCCACTAGCTGGGTCCCGAA 3682
*****

BL29_CR1 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 16310
BL29_CR2 ATTTGGCCTTATATGTAAGTCTTTACATATAGGGTCCCTCATGTCGCTATGTATAATAATAC 3742
*****

BL29_CR1 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAAA 16370
BL29_CR2 ATTAATCGTTTTGCCCATGACTATCAACCGGAATTTAACTTTAATTAATATATATAAA 3802
*****

BL29_CR1 AACTGGTTCATTAACATATTTCCCTTCCCTCATTTCTGGTCTTCTATTTCAGCAGAGGT 16430
BL29_CR2 AACTGGTTCATTAACATATTTCCCTTCCCTCATTTCTGGTCTTCTATTTCAGCAGAGGT 3862
*****

BL29_CR1 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCT 16490
BL29_CR2 TGTCGGTTATAGTAACCATGGCTATCCACTTCAACCGGTGTCGGTGTATTAACCCCT 3922
*****

BL29_CR1 CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 16550
BL29_CR2 CCCGTGAAATCCTCTATCCTTTCACCTCAGGCATACAGTCCCGTTTTTCACGTCCATATA 3982
*****

BL29_CR1 TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 16610
BL29_CR2 TTGTAACCTCCCGTTTTATGTCCTTTCCAAGCCGCTGGTTACACCTTCAAGGGCATCT 4042
*****

BL29_CR1 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 16670
BL29_CR2 CAATGGTCCGGAACACCCCGCCTTACTTGCTCTTTCCAAGCCCTATGGTCGCACCCTTT 4102
*****

BL29_CR1 ATATTGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 16730
BL29_CR2 ATATTGGTACATTTACCTCATGTTCTTATCAGTATGCCTGTTCCACCCCTGGTTGGCT 4162
*****

BL29_CR1 TTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 16790
BL29_CR2 TTTTATAGGTACCTTTCACCTGACACCCATATATGCCCGTTACCGTACCCCTCTCCGG 4222
*****

BL29_CR1 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 16850
BL29_CR2 GGTAGACCATTAGTCCAGGTGGAGCTATATTTCTGGTCTAGCACTTTCTCCTATACGGAT 4282
*****

BL29_CR1 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTTATTTTT 16910
BL29_CR2 ACATCTCTTAATGCTCGTTATACATACTTTTCTCTACTACCGAAAATTCATTTATTTTT 4342
*****

BL29_CR1 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 16970
BL29_CR2 ATTAAGAAATCCCGTTGTAATAACATTTTTTACCCGATTTTCAAATTTTACCTAAA 4402
*****

BL29_CR1 CCCATCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 17030
BL29_CR2 CCCATCCACTTTTCTATACCAAAAATTCAAACCCGAATTCCTATAAGAAATTTTTTAT 4462
*****

BL29_CR1 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACGCCGATCCA 17090
BL29_CR2 TTTTAAATATTTATTTTTTTTAAACGTGAAAAATAAAAAGATTATAAAAAACGCCGATCCA 4522
*****

BL29_CR1 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTACCGATGCAAACCC 17150
BL29_CR2 TTTTCAAGATGCGAAATATCACTACTTCTTCCAGGGCGTCTGACTACCGATGCAAACCC 4582
*****

BL29_CR1 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG 17210
BL29_CR2 CCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTTATATG- 4641
*****

BL29_CR1 TTG 17213
BL29_CR2 ---

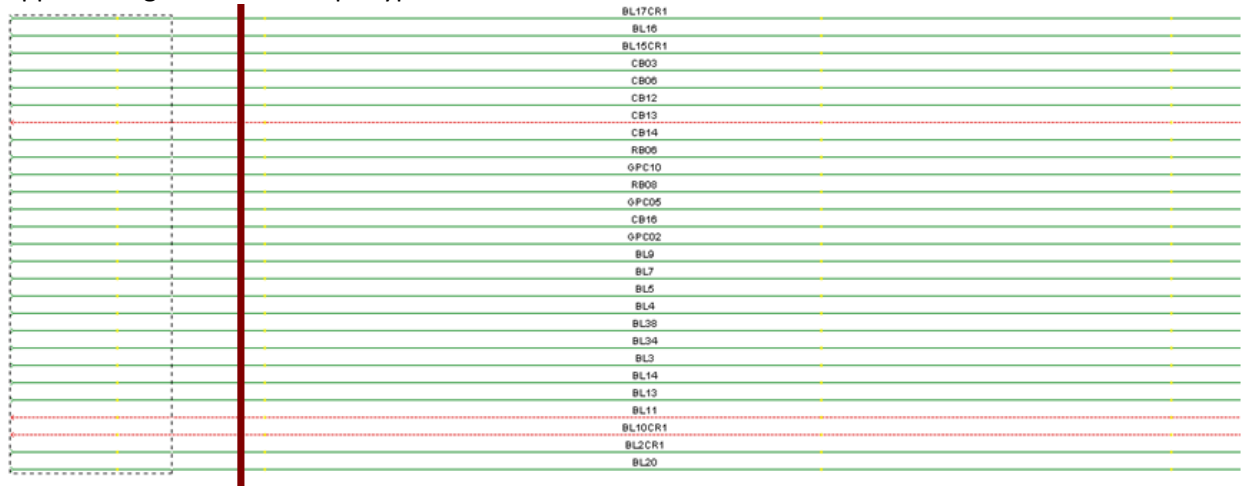
```

Appendix Figure 5 – Alignments of *A. piscivorous* Control Regions divided into haplogroups according to shared polymorphisms.

Appendix Figure 5A: Reference CR1



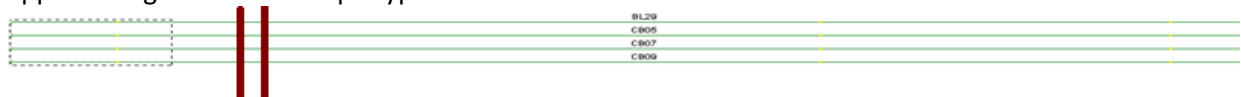
Appendix Figure 5B: CR1 Haplotype B



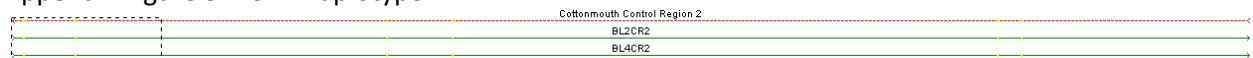
Appendix Figure 5C: CR1 Haplotype C



Appendix Figure 5D: CR1 Haplotype D



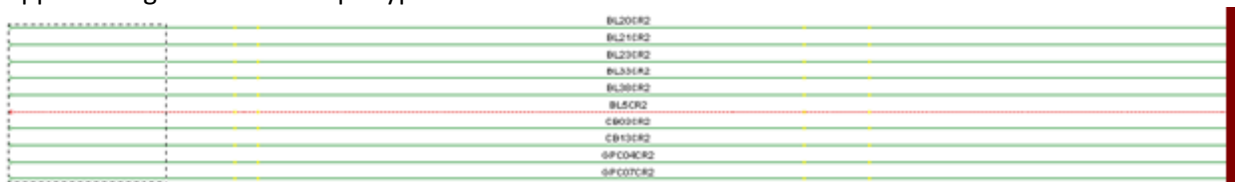
Appendix Figure 5E: CR2 Haplotype A



Appendix Figure 5F: CR2 Haplotype B



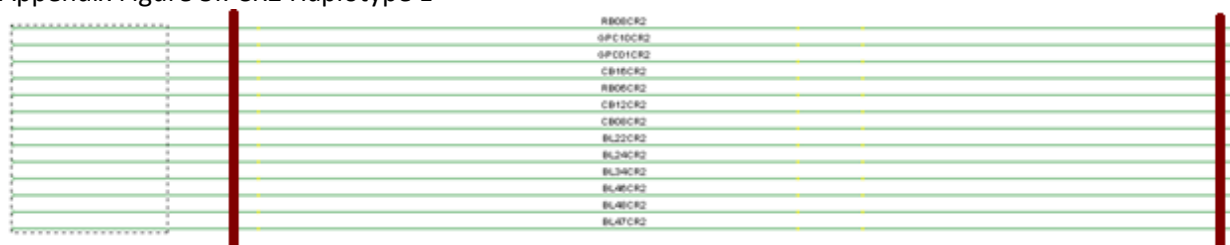
Appendix Figure 5G: CR2 Haplotype C



Appendix Figure 5H: CR2 Haplotype D



Appendix Figure 5I: CR2 Haplotype E

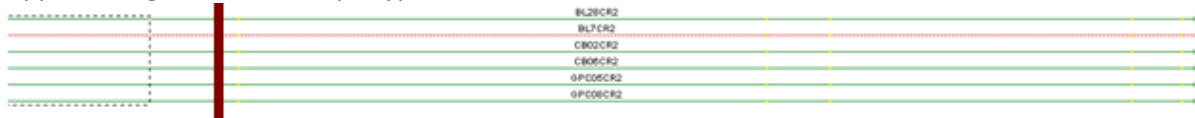


Appendix Figure 5J: CR2 Haplotype F





Appendix Figure 5K: CR2 Haplotype G



Appendix Figure 6: Haplotype network of concatemers for specimens which contained both control regions.

Haplotype A: Control specimen DQ523161

Haplotype B: CB07, CB09

Haplotype C: BL34, BL07, CB06, CB12, CB16, GPC10 RB06

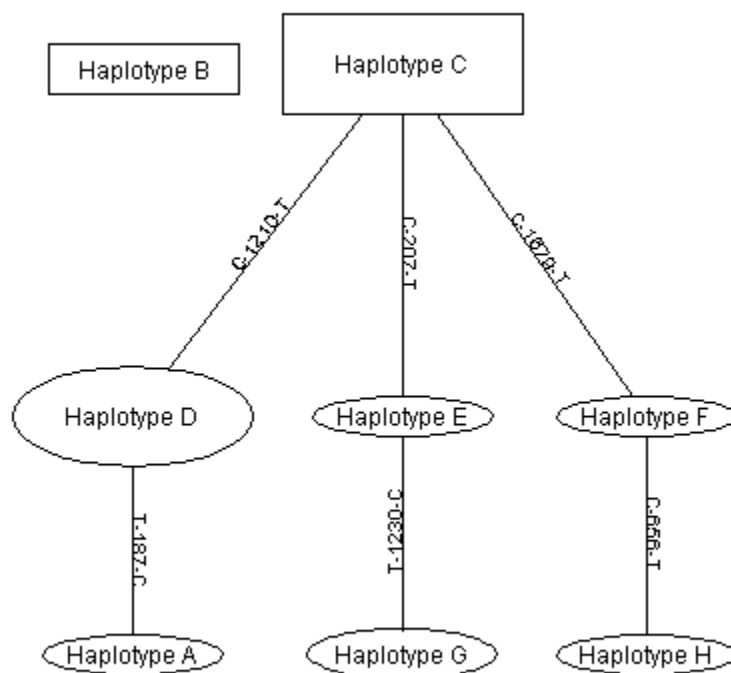
Haplotype D: BL20, BL2, BL38, BL04, BL05, CB03, CB13

Haplotype E: RB08

Haplotype F: CB14

Haplotype G: BL29, CB05

Haplotype H: RB03



Appendix Figure 7 – Alignment of all *A. piscivorus* CR1 and CR2 concatemers successfully produced for this project

```

BL2_1_2      AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
CB13_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
BL4_1_2      AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
BL20_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
BL38_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
BL5_1_2      AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
CB03_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
BL7_1_2      AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
CB06_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
CB07_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
CB09_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
BL29_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
CB05_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
RB08_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
RB06_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
BL34_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
CB12_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
CB16_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
GPC10_1_2    AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
CB14_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
RB03_1_2     AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
Control_1_2  AAACCAAAAAAATACTCTCCTAGGACCCCCCCTACCCCCCCCCTAGCTGGGTCCCGAA 60
*****

BL2_1_2      ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
CB13_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
BL4_1_2      ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
BL20_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
BL38_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
BL5_1_2      ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
CB03_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
BL7_1_2      ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
CB06_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
CB07_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
CB09_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
BL29_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
CB05_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
RB08_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
RB06_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
BL34_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
CB12_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
CB16_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
GPC10_1_2    ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
CB14_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
RB03_1_2     ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
Control_1_2  ATTTGGCCCTTATATGTACTCTTTACATATAGGGTCCTCATGTGCGTATGTATAATAATAC 120
*****

BL2_1_2      ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
CB13_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
BL4_1_2      ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
BL20_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
BL38_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
BL5_1_2      ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
CB03_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
BL7_1_2      ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
CB06_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
CB07_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
CB09_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
BL29_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
CB05_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
RB08_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
RB06_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
BL34_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
CB12_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
CB16_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
GPC10_1_2    ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
CB14_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
RB03_1_2     ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
Control_1_2  ATTAATCGTTTTGCCCCATGACTATCAAACGGGAATTTAACTTTAATTAATTATATACAA 180
*****

```























```

BL2 1 2      ACCCCCCCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2039
CB13 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
BL4 1 2      ACCCCCCCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2039
BL20 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
BL38 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
BL5 1 2      ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
CB03 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
BL7 1 2      ACCCCCCCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2039
CB06 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2039
CB07 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2039
CB09 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2039
BL29 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
CB05 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
RB08 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
RB06 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
BL34 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
CB12 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
CB16 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
GPC10 1 2   ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
CB14 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
RB03 1 2     ACCCCCCCCC-ACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2038
Control_1_2 ACCCCCCCCCCACAGACAAAGCCATTTTGTCTTTATTTTAAATTACGTCCGAGATTTT 2039
*****

```

```

BL2 1 2      ATAT 2043
CB13 1 2     ATAT 2042
BL4 1 2      ATAT 2043
BL20 1 2     ATAT 2042
BL38 1 2     ATAT 2042
BL5 1 2      ATAT 2042
CB03 1 2     ATAT 2042
BL7 1 2      ATAT 2043
CB06 1 2     ATAT 2043
CB07 1 2     ATAT 2043
CB09 1 2     ATAT 2043
BL29 1 2     ATAT 2042
CB05 1 2     ATAT 2042
RB08 1 2     ATAT 2042
RB06 1 2     ATAT 2042
BL34 1 2     ATAT 2042
CB12 1 2     ATAT 2042
CB16 1 2     ATAT 2042
GPC10 1 2   ATAT 2042
CB14 1 2     ATAT 2042
RB03 1 2     ATAT 2042
Control_1_2 ATAT 2043
****

```