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Identification of chicken repeat 1 (CR1) elements in forensically important carrion fly species and characterization of one such element within *Sarcophaga bullata*

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Identification of Chicken Repeat 1 (CR1) elements in forensically important carrion fly species and characterization of one such element within *Sarcophaga bullata*.

Michelle Lee Thompson

**Thesis submitted to the
Eberly College of Arts and Sciences
at West Virginia University
in partial fulfillment of the requirements
for the degree of**

**Master of Science
in
Genetics and Genome Biology/
Forensic Biology**

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**Morgantown, West Virginia
2009**

Keywords: Mobile Elements, CR1, Carrion flies, Forensic Identification

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Abstract

Identification of Chicken Repeat 1 (CR1) elements in forensically important carrion fly species and characterization of one such element within *Sarcophaga bullata*.

Michelle Lee Thompson

Retrotransposons including CR1 (Chicken Repeat 1) elements mobilize in a genome in a way that makes them useful for phylogenetic analysis and species identification. This study was designed to identify lineages of CR1 elements in the genomes of forensically important carrion fly species and to further characterize the one element, *Sarcophaga bullata* CR1B, through genome walk techniques.

Using conserved oligonucleotide primers, CR1 fragments from several carrion fly taxa were amplified, cloned and sequenced, and the recovered sequences were analyzed to identify different lineages of elements. A variety of retrotransposon families were recovered that exhibit similarity to known retrotransposon families from other dipterans (e.g. mosquitoes, *Drosophila*). We also provide evidence that several of these lineages may have given rise to taxon-specific subfamilies that have been recently active in carrion fly genomes.

The final reconstructed sequence from the *S. bullata* CR1B genome walk is presumed to be the complete Open Reading Frame 2 (ORF2) portion of the element containing both the reverse transcriptase (RT) and endonuclease (EN) domains. These domains were used to identify conserved amino acid regions in the recovered consensus via comparison to known non-LTR retrotransposons. A phylogenetic analysis of the RT domain revealed the recovered ORF in *S. bullata* compares favorably with previously documented CR1-like elements.

This work will serve as the basis for additional analyses targeted at developing a simple, efficient marker system for the identification of forensically important carrion flies. The fast turnaround time possible for this system will also help to make it an extremely useful tool. Though much work will be needed to completely develop the method, the data presented here lays the groundwork for future efforts.

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Chapter 1: Introduction

Any genetic unit that possesses the capability of moving or copying itself throughout the genome is described by the basic term transposable element (TE). Also known as “jumping genes”, first described by Barbra McClintock in her work with maize, TE insertion events can change gene expression patterns and structural features of genomes thereby serving as a driving force of evolution (McClintock 1956). This ability to change the landscape of the genome is precisely why transposable elements have become a hot research topic (Kidwell and Lisch 1997). We now know high proportions of eukaryotic genomes consist of transposable elements. For example about 40% of the human genome is made up of TEs (Lander, Linton et al. 2001).

Transposable elements are classified into two categories based on their method of movement (Figure 1.1). Class 1 elements utilize a “copy and paste” method involving an RNA intermediate where as Class 2 elements typically mobilize via a “cut and paste” mechanism (Mizuuchi 1992; Deininger and Batzer 2002; Wessler 2006). Within Class 1, elements can be classified into Long Terminal Repeat (LTR) retrotransposons and non-LTR retrotransposons.

Non-LTR retrotransposons can be further subdivided into two families: Long Interspersed Elements (LINEs), and their non-autonomous counterparts, the Short Interspersed Elements (SINEs). Our current understanding suggests that SINEs mobilize by ‘hijacking’ the machinery encoded within their autonomous partners. Briefly, SINEs utilize their A and B boxes as promoter sequences to recruit RNA Polymerase III, which will then produce an RNA transcript of the element. The transcripts are then reverse transcribed and incorporated into the genome using enzymes encoded by LINEs (Bushman 2002; Kajikawa and Okada 2002; Dewannieux, Esnault et al. 2003).

Figure 1.1 Schematic representation describing the general structure of transposable element types. Class 1 elements consist of LTR retrotransposons and non-LTR elements such as the LINE and SINE elements. These have Target site duplications (TSDs), long terminal repeats (LTRs) and or untranslated regions (UTRs) surrounding their open reading frames (ORFs) and or AB promoter sequences. Class 2 elements flanking regions have inverted terminal regions (ITRs) and direct repeats (DRs).

Class I TEs have been shown to be very reliable for species identification and for resolving species phylogeny questions (Murata, Takasaki et al. 1993; Nishihara, Satta et al. 2005; Ray, Xing et al. 2005; Kaiser, van Tuinen et al. 2007). Because of their ability to insert essentially anywhere in the genome, it is very unlikely that any two elements would insert randomly at the same site in two different genomes. This virtually eliminates the chance of identity-by-state homoplasy (Batzer and Deininger 2002; Salem, Ray et al. 2005). Simple PCR reactions with specific primers have been used to produce species-specific banding patterns and thereby establish species identity in unknown samples (Figure 1.2) (Herke, Xing et al. 2007).

The idea of using such a simple system to identify species would be especially useful in dipteran insects where it is difficult for a non-expert to identify taxa. The order Diptera is one of the largest insect orders and representatives can be found in almost

every habitat (Byrd and Castner 2001). A major family within Diptera is Calliphoridae, members of which are collectively known as blow flies. The blow flies (1,000 species), along with the sarcophagid (2,000 species) and muscid flies (700 species), are extremely important in forensic investigations where PMI (post mortem interval) is estimated (Byrd and Castner 2001). Their importance is because they are often the first flies that come to carrion for a food source and breeding medium, and they have a life cycle that is extremely predictable (Rodriguez 1983).

Figure 1.2: Schematic representation of agarose electrophoresis illustrating species-specific banding pattern differences due to a transposable element insertion. The larger band corresponding to species A has a transposable element (TE) insertion at the specific portion of the DNA where as Species B does not and shows a shorter product that migrates farther.

An investigator is often able to establish the PMI by determining three pieces of information 1) the species retrieved from the corpse 2) the developmental stage observed, and 3) the temperatures to which the specimen was exposed.

The first piece of information, taxon identity, is extremely important to ascertaining an accurate PMI as there can be substantial differences in developmental patterns among taxa. For example, there are species such as *Calliphora vicina* and

Calliphora vomitoria that display drastically different mean cumulative development times (538.4 and 572.6 hours respectively) at 20 °C (Ames and Turner 2003).

Unfortunately, distinguishing closely related taxa such as these two, especially when they are not well preserved, can be a difficult process.

When the egg or larval stage is collected from carrion it is often even more difficult to distinguish the species morphologically (Greenberg and Singh 1995). Dichotomous keys are often used to identify specimens and, though this method is generally accepted, accurate results are not guaranteed due to the substantial difficulty a non-expert may encounter during the identification process. Other problems such as specimen death can arise when the immature stage is found because it is often necessary to incubate a portion of the larva collected in order to have the opportunity of observing the adult fly. DNA-based methods, on the other hand, should better allow accurate species identification because it would be useful for both adult and larval stages of the live or dead specimens.

Identifying forensically important carrion fly species using molecular markers has been previously investigated. A study using ribosomal RNA (rRNA) has already been published; however it claims to only lay the groundwork of a marker system (Stevens and Wall 2001). Though it provides the possibility of a superior marker system, it will require high quality DNA and a turnaround of at least 48 hrs to obtain results (Stevens and Wall 2001). A method using the predicted gel banding patterns of restriction endonuclease cleaved DNA has also been developed (Sperling, Anderson et al. 1994). This method is problematic due to the possibility of mutations at the restriction site, therefore fixed or nearly fixed restriction sites are needed for each given species (Benecke and Wells 2001).

Much work has also gone into developing mitochondrial DNA (mt-DNA) based identification methods (Sperling, Anderson et al. 1994; Wallman and Donnellan 2001; Wells, Pape et al. 2001; Wells and Sperling 2001; Otranto and Stevens 2002; Harvey, Dadour et al. 2003). As with any other method problems have been identified. It is still unknown to the investigators if the phylogenetic analysis of COI sequence method will hold up after further investigation due to paraphyly (Wells and Stevens 2008).

Primary assessment of a TE- based marker system is the focus of this thesis. Chapter 2 is a survey of TE activity in forensically important carrion flies. Retrotransposons are present in a variety of taxa and these elements may have been recently active. Chapter 3 describes a consensus of the complete Open Reading Frame (ORF) of a CRI-like retrotransposon found in *Sarcophaga bullata*. This was characterized and compared to known CR1-like retrotransposons. The element compares favorably with known CR1-like elements from a variety of taxa. It harbors many of the major functional domains typical of this family of elements. Chapter 4 details general conclusions derived from this thesis and additional applications for these findings.

Chapter 2: Identification of Chicken Repeat 1 (CR1) elements in carrion fly genomes

Abstract

Retrotransposons including CR1 (Chicken Repeat 1) elements mobilize in the genome in a way that makes them useful for phylogenetic analysis and species identification. This study was designed to identify lineages of CR1 elements in the genomes of forensically important carrion fly species. Using conserved oligonucleotide primers, CR1 fragments were amplified and sequenced from several carrion fly taxa and the sequences recovered were analyzed to identify different clades of elements. A variety of retrotransposon families were recovered that exhibit similarity to known retrotransposon families from other dipterans (e.g. mosquitoes, *Drosophila*). We also provide evidence that several of these lineages may have given rise to taxon-specific subfamilies that have been recently active in carrion fly genomes.

Introduction

LINEs (Long INterspersed Elements) are Class 1 transposable elements (TEs) (i.e. retrotransposons). As such, they utilize a “copy and paste” method of movement involving an RNA intermediate (Figure 2.1) (Deininger and Batzer 2002). Briefly, this process involves transcription into messenger RNA (mRNA) by RNA polymerase II, and then reverse transcription and reincorporation into the genome via a process termed Target Primed Reverse Transcription (TPRT) (Luan, Korman et al. 1993).

Endonucleases, often encoded by the elements themselves, aid in retrotransposition by cleaving the target DNA to form a 3'-OH primer. Because this process involves the introduction of a new DNA fragment without the loss of the original insertion, LINE elements tend to accumulate in genomes and are found to comprise large

portions of the genomes they inhabit. For instance LINE-1 elements comprise about 20% of the human genome (Lander, Linton et al. 2001).

Figure 2.1 Schematic representation of retrotransposition mechanism of CR1 elements

LINE elements are thought to follow the master gene model of amplification in the genome (Vandergon and Reitman 1994). Briefly, this model suggests that retrotransposons in a given family will have only one or very few active ‘master’ elements at any given time. As such, any retrotransposition events will give rise to elements that are identical to the master element from which they arose. Therefore, if we find elements that are essentially identical to one another (i.e. have low divergence values compared to the consensus), they are likely the result of recent retrotransposition from a common source.

Several studies have been published assessing LINE diversity, which has resulted in their separation based on the number and characteristics of their Open Reading frames (ORF’s). Further classification is made based on the reverse transcriptase (RT) portion resulting in several clusters (Malik, Burke et al. 1999). The major groups of elements identified thus far are CRE, R2, R4, LINE-1, RTE, Tad, R1, LOA, I, Jockey, and

Chicken Repeat 1 (CR1) (Malik, Burke et al. 1999). This study will focus one particular group of LINEs, the CR1-like elements.

CR1-like elements are a widely distributed family of LINEs that have been identified in a variety of organisms including vertebrates –e.g. chicken (Haas, Grabowski et al. 1997) and turtle (Kajikawa, Ohshima et al. 1997) and invertebrates. Invertebrates with CR1-like TEs include the roundworm *Caenorhabditis elegans* (Jurka, Kapitonov et al. 2005), the sea urchin *Stroglyocentrotus purpuratus* (Jurka, Kapitonov et al. 2005), and the human blood fluke *Schistosoma mansoni* (Drew and Brindley 1997). Arthropods known to harbor CR1-like elements include Order Scorpiones (scorpions) (Glushkov, Novikova et al. 2006), and Maculinea (butterflies) (Novikova, Sliwinska et al. 2007), as well as the dipteran family Drosophila (Biedler and Tu 2003). Until now, the LINE landscape of carrion fly genomes (Diptera: Calliphoridae and Sarcophagidae) has gone uninvestigated.

Because of this lack of information and because we are interested in the eventual utilization of LINE elements for phylogenetic analysis and species identification, the goals of this study were; 1) to determine whether CR1-like elements are a component of representative carrion fly genomes, 2) to categorize those elements into the known CR1-like families, and 3) to determine CR1 relative divergence values and thereby estimate the potential for recent activity. The eventual development of a reliable transposable element based species identification system is one additional goal.

Materials and Methods

DNA was extracted from six carrion fly taxa representing two families of forensically important flies - *Calliphora vicina*, *Calliphora vomitoria*, *Phormia regina*, *Cochliomyia macellaria*, and *Lucilia sericata* of family Calliphoridae, and *Sarcophaga bullata* of family Sarcophagidae. Adult specimens were collected from the wild using raw liver as bait and a standard sweep net. Species identifications were confirmed using a dichotomous key (Whitworth 2006) and specimens were preserved in 95% ethanol overnight for DNA extraction the following day. The fly was dissected to obtain the thoracic muscle tissue and DNA extraction of that tissue was accomplished using the Qiagen Puregene Tissue Core Kit A (Gentra, Minneapolis MN).

CR1 primer pairs (CR1-S and CR1-A) had been previously developed by Novikova et al. (2007) for the identification of CR1 elements in butterflies (Lepidoptera: *Maculinea*). We used these to amplify a portion of an ORF from each species. PCR amplification was conducted in 25 µl reactions using 50 ng of target DNA, 7 pM of each oligonucleotide primer, 200 mM dNTPs, in 50 mM KCl, 10 mM Tris-HCl (pH 8.4), 2.0 mM MgCl₂, and Taq DNA polymerase (1.25 units). This mix was then subjected to 32 cycles of 95° denaturation for 30 seconds, 56° annealing for 30 seconds, and a 2 min extension at 72°. A final 72° extension was done for seven minutes. After agarose gel electrophoresis and UV visualization using ethidium bromide, the resulting amplicons (Figure 2.2) were cut from a 2% agarose gel with 0.25 µg ethidium bromide and cleaned using the Wizard SV gel and PCR clean up system (Promega, Madison WI).

Figure 2.2 Gel electrophoresis results illustrating amplification of CR1- like fragments in two taxa *L. sericata* (Lane 2) and *C. vomitoria* (Lane 3). Lane 1 contains a 1kb DNA ladder for reference.

The fragments were cloned into the TOPO TA (Invitrogen, Carlsbad CA) vector and transformed into Top10 cells using the manufacturer's protocol. Colonies were grown on LB/Kanamycin (2 μ l/ml) plates overnight. Individual colonies were grown in LB/Kanamycin (2 μ l/ml) broth overnight and plasmids were isolated using Fast Plasmid Mini kit (Eppendorf, Hamburg GER). Purified plasmids were sequenced using Big Dye termination sequencing on an ABI 3130xl Genetic Analyzer with M13 primers. Sequences used for this work have been deposited in GenBank under accession numbers FJ940924 through FJ941019.

Vector sequence was removed from the resulting data using SeqMan (DNASTAR, Madison, WI). Sequences were generally binned according to taxon of origin, however sequences obtained from the closely related taxa *C. vomitoria* and *Calliphora vicina* were very similar to one another and were therefore considered as a single group, hereafter referred to as *C.vom/C.vic*. Sequences were then aligned using MUSCLE (Edgar 2004; Edgar 2004) and analyzed visually for obvious subgroups within each bin. Clusters of similar sequences containing at least three representatives were used to generate consensus sequences

(Supplemental Figures 1-5). Modeltest (Posada and Crandall 1998) as implemented in PAUP* v4b10 (Swofford 2002) was used to select the best (of 56) model of DNA sequence evolution for the given sequence clusters (Table 2.1). Base frequencies, substitution models and among site variation rates from Modeltest were then used to calculate maximum likelihood genetic distances between each representative sequence and its corresponding consensus.

Consensus sequences were confirmed as CR1-derived using BlastX (Altschul, 1990) searches of GenBank. BlastX hits were also used to establish the reading frame for sequence translation. Alignment of the translated sequences and several ORF 2 portions of known non-LTR elements (Genbank accession numbers: XP_001193594.1, XP_001949771.1, BAC57926.1, ABH11542.1, BAC57904.1, BAC57908.1, BAC57912.1, CAB99192.1, AAX07241.1, AAZ15237.1, PIR: T25782, AAA53489.1, AAX07243.1, AAQ57129.1, ABR08300.1, ABI15188.1, ABI15187.1, AAC06264.1, XP_001200675.1, AAA49027.1, AAP88020.1, BAA88337.1, AAX07244.1, AAA29354.1, CAJ13354.1, AAB26437.2. Repbase submissions: RTE-1_MD, LINE-1_AA, CR1-1_DW1, CR1-2_HM, RTE-1_AG) was performed using MUSCLE (Edgar 2004; Edgar 2004). Phylogenetic analysis of the aligned translated CR1-derived RT portions was accomplished in MEGA(Kumar, Tamura et al. 2004) by performing a neighbor joining analysis using the equal input option and 500 bootstrap replicates.

Table 2.1 Results of Modeltest analysis.

Grouping consensus	Model chosen	Proportion of invariable sites	Gamma distribution shape parameter
<i>S. bullata</i> CR1A	TMV	0.8662	N/A – Equal distribution
<i>S. bullata</i> CR1B	HKY	0	N/A - Equal distribution
<i>C. macellaria</i> CR1A	TMV	0.6074	N/A – Equal distribution
<i>L. sericata</i> CR1A1	HYK	0.9747	N/A - Equal distribution
<i>L. sericata</i> CR1A2	K80	0	N/A - Equal distribution
<i>L. sericata</i> CR1B	F81	0	N/A- Equal distribution
<i>C.vom/C.vic</i> CR1A	HKY	0	N/A - Equal distribution
<i>C.vom/C.vic</i> CR1B1	HKY	0	N/A - Equal distribution
<i>C.vom/C.vic</i> CR1B2	HKY	0	N/A - Equal distribution
<i>P. regina</i> CR1A	HKY	0.9302	0.6242
<i>P. regina</i> CR1B	HKY	0.9587	N/A - Equal distribution
<i>P. regina</i> CR1C	F81	0	N/A - Equal distribution

Results

PCR analysis produced a single discrete band for each taxon examined. Each amplicon was found to be ~550 bases (Figure 2.2), which was the expected length. Cloning of each of these bands was successful and sequences from the clones were obtained. Some resulting sequences showed no similarity to at least two other sequences and were therefore excluded from further analysis. The number of analyzed sequences obtained from each taxa and the number of consensus sequences generated from them are shown in Table 2.2. For most taxa (*C. macellaria* being the lone exception) at least two distinct clusters of sequences were observed.

Table 2.2 Number of sequences obtained along with number of consensus sequences obtained from them for each examined taxa.

Taxa	Number of sequences obtained	Number of consensus sequences generated
<i>Lucilia sericata</i>	10	3
<i>Sarcophaga bullata</i>	27	2
<i>Calliphora vomitoria/vicina</i>	38	3
<i>Phormia regina</i>	13	3
<i>Cochliomyia macellaria</i>	8	1

A BlastX search using the consensus sequence from each grouping resulted in high similarity to known CR1 elements thus confirming the recovered sequences as portions of the RT encoding ORF of a CR1-like element (Table 2.3). The reading frame established from this search revealed no premature stop codons upon translation of the consensus sequences.

Table 2.3 Similarity results as given by BlastX of CR1-like nucleic acid consensus sequence to known CR1 amino acid sequences.

Consensus	Most similar accession	Organism	E value	Bit Score
<i>S. bullata</i> CR1A	CAB99192.1	<i>D. melanogaster</i>	2e-44	181
<i>S. bullata</i> CR1B	XP_001950444.1	<i>A. pisum</i>	2e-35	152
<i>C. macellaria</i> CR1A	AAK39265.1	<i>C. elegans</i>	2e-24	115
<i>L. sericata</i> CR1A1	CAB21860.1	<i>T. brucei</i>	2e-08	62
<i>L. sericata</i> CR1A2	AAK39265.1	<i>C. elegans</i>	2e-30	135
<i>L. sericata</i> CR1B	CAB99192.1	<i>D. melanogaster</i>	9e-51	202
<i>C.vom/C.vic</i> CR1A	CAB99192.1	<i>D. melanogaster</i>	2e-39	165
<i>C.vom/C.vic</i> CR1B1	ABI15187.1	<i>M. nausithous</i>	3e-49	197
<i>C.vom/C.vic</i> CR1B2	ABI15187.1	<i>M. nausithous</i>	9e-50	199
<i>P. regina</i> CR1A	CAB99192.1	<i>D. melanogaster</i>	4e-43	177
<i>P. regina</i> CR1B	BAC57910.1	<i>A. gambiae</i>	3e-45	184
<i>P. regina</i> CR1C	AAZ15237.1	<i>A. aegypti</i>	1e-33	146

Results of the phylogenetic analysis of the translated amino acid sequences are presented in Figure 2.3. An inclusive carrion fly cluster was not observed when compared to CR1 elements from a wide variety of outgroup taxa. A subset of carrion fly consensus sequences was found to form a monophyletic cluster with R1-like elements

such as the Pilger element from *D. melanogaster*. *S. bullata* CR1A falls out separately from the carrion fly R1-like elements and forms a cluster with various elements from *A. gambiae*. However, there is little support for excluding the CR1A consensus derived from *S. bullata* from carrion fly elements in the R1-like clade, (i.e. those recovered from *L. sericata*, *C. vomitoria*, *C. vicina*, and two elements from *P. regina*). Overall support for their classification as members of the R1 family of CR1-like elements is therefore high.

C. macelleria CR1A along with *L. sericata* CR1A1 and *L. sericata* CR1A2 formed a cluster which then formed a larger cluster with Jockey-like elements from a variety of insects but there is little bootstrap support for this association. On the other hand, support for their own cluster is high, suggesting a common ancestral element. *P. regina* CR1C and a CR1-like element from *A. aegypti* are strongly clustered.

C.vom/C.vic CR1B1 and *C.vom/C.vic* CR1B2 appear to be members of the Zenon family of elements based on the strong support found for the cluster including elements from butterflies (*Shijimiaeoides divina* and *Maculinea spp.*) and moths (*Bombyx mori*). It is interesting that an element from a very distantly related organism, the cnidarian *Hydra magnipapillata*, is also a member of this cluster.

Finally, the consensus *S. bullata* CR1B finds itself as part of a cluster that includes elements from the taxon from which the classical CR1 element originally described, the chicken (*Gallus gallus*). The clade includes elements occupying the genomes of vertebrates (*Gallus*, *Chelonia* and *Platemys*), blood flukes (*Schistosoma*), and sea urchins (*Strongylocentrotus*) among others. However, the element from *S. bullata* is clearly most strongly associated with a CR1 from a fellow dipteran *Drosophila willistoni*.

Figure 2.3 Phylogenetic tree inferred from translated carrion fly consensus sequences and several outgroups comprising known CR1-like elements. Carrion fly taxa are highlighted in red. The +2 indicates the reading frame for recovered sequences when compared to the original consensus sequence.

Analysis of divergence values within taxa revealed that there is little diversity within each presumed subfamily in several lineages (Table 2.4). When comparing each respective sequence to the consensus sequence, all *P. regina* clusters (CR1A, CR1B and CR1C) and the *L. sericata* CR1A1 cluster revealed over 99% sequence identities. The clusters *C.vom/C.vic* CR1A, *L. sericata* CR1B and *S. bullata* CR1B also showed high sequence identities (above 98%). Standard deviation values also show there is little difference between sequences residing in the same cluster.

Table 2.4: Divergence and standard deviation values calculated for each cluster of elements.

Consensus	Average divergence value	Standard Deviation
<i>P. regina</i> CR1A	0.005282	0.002767
<i>P. regina</i> CR1B	0.006222	0.007761
<i>P. regina</i> CR1C	0.006908	0.011965
<i>C.vom/C.vic</i> CR1A	0.012033	0.021723
<i>C.vom/C.vic</i> CR1B1	0.030555	0.011378
<i>C.vom/C.vic</i> CR1B2	0.029534	0.021355
<i>S. bullata</i> CR1A	0.030447	0.016793
<i>S. bullata</i> CR1B	0.015637	0.022969
<i>L. sericata</i> CR1A1	0.003882	0.002814
<i>L. sericata</i> CR1A2	0.029915	0.002005
<i>L. sericata</i> CR1B	0.012513	0.009294
<i>C. macelleria</i> CR1A	0.024084	0.022988

Discussion

While in mammals, one typically finds only a single lineage of active non-LTR retrotransposons, having multiple lineages of active non-LTR elements is not uncommon in non-mammalian animal taxa (Furano, Duvernell et al. 2004). For example, 21 families of non-LTR retrotransposons were found to have been recently active in the genome of the African malaria mosquito, *Anopheles gambiae* (Biedler and Tu 2003). While not as extreme an example, most of the carrion fly families examined here also appear to harbor multiple recently active non-LTR retrotransposons. Each examined species shows

evidence of at least one lineage of CR1-like elements present in their genome and in many taxa, more than one lineage of elements is apparent.

Comparison of each representative sequence to its respective consensus sequence revealed high sequence identities suggesting some of these elements have been recently active. This is indicative of the master gene model where the elements are likely the result of recent retrotransposition from a common source. This is especially true for the clusters that showed above a 98% sequence identity. It is unfortunate that neutral mutation rate data for the nuclear genome is unavailable for carrion flies. Such information would allow us to attach possible time frames to the divergence values we observed. Additional evidence of recent activity is the lack of any unexpected stop codons or other mutations that might suggest that they are nonfunctional elements.

One example is the *S. bullata* CR1B cluster. It exhibited one of the lowest divergence values between its representative amplicons and the consensus. Another example is found within *P. regina* where all three clusters (CR1A, CR1B and CR1C) showed over a 99% sequence identity. Though these exhibit such a high similarity within the cluster, the phylogenetic analysis reveals they show little similarity between clusters. This supports the hypothesis that there are separate lineages that have propagated throughout the genome. *C.vom/C.vic* CR1A with eight representative sequences forming the cluster retained over 98% sequence identity suggesting it too is recently active. All other families recovered showed at least 96% sequence similarity suggesting they have been active relatively recently, but may not be as young as the other families.

The observation that numerous recently active families of CR1-like elements are present in representative carrion flies suggests that we will eventually be able to identify

taxon-specific insertion events that will be useful for species identification at a later date. This will enable the eventual development of a TE-based method for species identification that will be of particular use in determining taxon identity for specimens collected at crime scenes. Additional applications are also possible for phylogenetic analyses of these complex taxonomic assemblages.

Further research will be done to characterize the elements identified here. This research will begin with recovering the complete ORF2 sequence from the *S. bullata* CR1B cluster. We chose the CR1B lineage from *S. bullata* because it consisted of the largest amount of sequences used to create the consensus, and showed one of the lowest divergence values. This suggested that intact copies of the master element are likely still present in the genome. Moreover, when compared to the known non-LTR elements it was the one of only three consensus clusters to form in the clade of CR1 elements with a high bootstrap value.

Chapter 3: Characterization of CR1 element identified within Sarcophagidae

Abstract

The goal of this study was to characterize the *S. bullata* CR1B element identified in the previous chapter though further sequencing in both the 5' and 3' direction. This was accomplished using a genome walk begun from the original consensus sequence. The final constructed sequence is presumed to be the complete Open Reading Frame 2 (ORF2) portion of the element containing both the reverse transcriptase (RT) and endonuclease (EN) domains. These domains were used to identify conserved amino acid regions in the recovered consensus via comparison to known non-LTR retrotransposons. A phylogenetic analysis of the full RT domain revealed the recovered ORF in *S. bullata* also compares favorably with previously documented CR1-like elements.

Introduction

Non-LTR retrotransposons have variable structures, but usually contain one or two open reading frames (ORFs). The function of ORF1 in non-LTR retrotransposons that contain it remains questionable, in part due to their absence in some non-LTR elements. Conserved domains have been identified in what ORF1 representatives we have. LINE 1 (L1) elements reveal there is a high probability of a coiled-coil domain along with nucleic acid binding domain being encoded within ORF1 suggesting a single-stranded binding function (Martin, Li et al. 2000). A zinc finger is proposed to be encoded in ORF 1 of both I and Jockey elements (Martin 2006). Also, an esterase domain (ES) or plant homeodomain (PHD) has been identified in ORF1 of CR1 elements in a variety of taxa (Kapitonov and Jurka 2003).

Though the function of ORF 1 remains inconclusive, ORF2 is well known to encode enzymes essential for retrotransposition. ORF2 has been shown to encode

enzymes with combined endonuclease/ reverse transcriptase (EN/RT) activity. While clearly distinct, CR1 elements are clustered with the L1 family of elements based on the reverse transcriptase encoded within ORF2. What separates them from the L1 elements is the differing protein sequences also encoded within the ORF2.

Phylogenetic analysis of the reverse transcriptase portion of non-LTR elements has enabled differentiation among classes of elements. This is often done with focus on the finger/palm region which corresponds to the amino terminal half of the RT domain of HIV (Unge, Knight et al. 1994). Eleven clades of non-LTR elements have been found based on analysis of the entire RT domain: Jockey, Chicken Repeat 1 (CR1), LINE 1 (L1), CRE, I, R1, R2, R4, RTE, Tad and LOA (Malik, Burke et al. 1999). As seen in Figure 3.1, the combined EN/RT coding region comprises a majority of several average complete elements (Tad, R1, LOA, I, Jockey and CR1).

Though the full element is much larger, a vast number of copies of CR1 elements within the chicken genome, where the element was first discovered, and in other taxa, are shorter than 400bp (ICGSC 2004). This is most likely due to truncation of the 5' element end during mobility (Haas, Grabowski et al. 2001).

Though the 5' end of the element is often truncated the 3' end shows characteristic features. The *Drosophila* CR1-like elements contain a specific sequential repeat on the 3' element end that is often followed or preceded by a polyadenylation signal (Kapitonov and Jurka 2003). This eight base pair direct repeat region is yet another character distinguishing CR1-family elements from the rest of the L1 elements which simply have a poly-A tail.

Figure 3.1: A neighbor joining tree of 11 major clades of non-LTR elements inferred from the reverse transcriptase domains encoded by them (Malik, Burke et al. 1999). Enzymatic domains encoded in each element (RT -reverse transcriptase, APE -apurinic/apyrimidinic endonuclease, REL-endo - restriction like endonuclease and RNH - RNase H domain) are shown in the shaded boxes. Vertical bars indicate cysteine-histidine motifs.

The purpose of this research is to characterize the EN/RT domain of a CR1-like element from *Sarcophaga bullata*. This will aid in determining positive identification for the element and allow the development of better amplification primers for additional analysis in other closely related taxa. Amplification in other taxa will further cement the groundwork of TEs as a maker system for species identification in forensically important carrion flies.

Materials and Methods

DNA was extracted from the thoracic tissue of *Sarcophaga bullata* using the Qiagen Puregene Tissue Core Kit A (Gentra, Minneapolis MN) and diluted to 0.1ug/ul. The manufacturer's protocol provided in the GenomeWalker Universal Kit (Clontech, Mountain View CA), was followed to digest each of four aliquots of genomic DNA with one of four restriction enzymes (Dra I, EcoR V, Pvu II and Stu I). Resulting fragments larger than 1,000 bp were cleaved from a 1% sodium borate agarose gel, cleaned with the Wizard SV gel and PCR clean up system (Promega, Madison WI) and linkers from the GenomeWalker Universal kit were ligated using the manufacturer's protocol.

Two consecutive primers were designed, *round 1 Right Out* (RO) and *round 1 RO nested* to amplify the 3' direction and two primers, *round 1 Left Out* (LO) and *round 1 LO nested* were developed for the 5' direction using the partial CR1 original consensus sequence of *S. bullata* CR1B described in Chapter 2 (Figure 3.2). They were used along with the GenomeWalker Universal Kit linker primers to obtain several amplicons >1kb which were visualized in a 1% sodium borate gel, cleaved from that gel, and purified using the Wizard SV gel and PCR clean up system (Promega, Madison WI). The resulting fragments were ligated into the TOPO TA (Invitrogen, Carlsbad CA) vector using the manufacturer's protocol, transformed into Top10 cells and grown on LB/Kanamycin (2μl/ml) plates overnight. Individual colonies were grown in LB/Kanamycin (2μl/ml) broth overnight and plasmids were isolated using Fast Plasmid Mini kit (Eppendorf, Hamburg GER). Purified plasmids were sequenced using Big Dye Termination sequencing on an ABI 3100 Genetic Analyzer.

Figure 3.2 Original primer pairs (blue arrows) developed for both the 5' and 3' direction of the element. Numbers indicate position of the base pairs relative to the full element. Black lines below the primers indicate the resultant fragments and their relative positions inferred after sequence analysis. These sequences were used to develop new primers for additional genome walk rounds to expand our analysis of the CR1-like element.

Vector sequence was removed from the resulting sequence data using SeqMan (DNASTAR, Madison, WI). Sequences were confirmed as CR1-derived using Blastn and BlastX (Altschul, 1990) searches of GenBank. The recovered first round sequence consensus showed high similarity to the CR1 element from *Anopheles gambiae* (accession number AAA53489.1). We used this sequence as a reference for the remainder of the genome walk.

The genome walk was then continued for several rounds with two new primers in each direction. Primers sequences for each round are described in Table 3.1. Occasional gaps and ambiguities in the sequence data were seen, usually because sequence data (averaging ~600 bp) for larger fragments (some larger than 1300 bp) was insufficient to obtain the entire fragment. In order to remedy this, additional primers were developed to amplify these regions and are denoted by half rounds (e.g. round 3.5) in Table 3.1.

At the 5' end, what appeared to be the end of the ORF was reached as evidenced by a lack of sequence similarity in any cloned fragments beyond this point. A similar observation was used to identify the 3' end.

Sequences from each round of sequencing were aligned and a complete contig sequence consensus was constructed (Supplemental Figure 6). The resulting consensus sequence was entered into the NCBI ORF finder (<http://www.ncbi.nlm.nih.gov/gorf/gorf.html>) and one large ORF was identified. Querying Blast (BlastX) with the sequence revealed high similarity to several RT/EN encoding ORFs. Several of these were extracted and MUSCLE (Edgar 2004; Edgar 2004) was used to align the recovered contig consensus *S. bullata* sequence with these known retroelement RT (Accession numbers: AAC72810.1, AAC51279.1, AAC72298.1, AAA21781.1, AAC13649.1, AAB92389.1, AAA28675.1, AAA29354.1, AAA28291.1, AAA53489.1, AAC06263.1, AAA49027.1, and CAA29181.1) and EN domains. Shading of similarity was done using BioEdit graphic view option. All sequences generated for this work have been deposited in GenBank under accession numbers FJ941020 through FJ941066.

Phylogenetic analysis of the RT domain from the translated *S. bullata* contig consensus and known CR1-like non-LTR elements (Accession numbers: BAA88337.1, AAC60281.1, U66331.1, AAR31731.1, AAA53489.1, AAZ15240.1, AAD19348.1, CAA29181.1, CAB41693.1, AAB65093.1, AAB92389.1, AAA21781.1, AAC72298.1, AAA29363.1, AAC13649.1, AAA28675.1, AAB04627.1, AAA29354.1, AAA28291.1, ABH11541.1, ABI15177.1, AAC72810.1, and AAC51279.1) was accomplished by performing a neighbor joining analysis using the equal input option and 500 bootstrap replicates.

Table 3.1: Sequence of primers used in conjunction with the GenomeWalker Universal Kit protocol to collect walk out data for each round.

Primer Name	Sequence (5'-3')	5' Position in final alignment
Round 1 RO	CTTACTCGTTCATAAGCTTTATCAAC	2260
Round1 Nested RO	GCAGTGCGTTAAATTCAGGAACACA	2340
Round 2 RO	CCCAATTCTTGAATATGGATCTGTAA	2857
Round 2 Nested RO	GTGGTTTACAATGGGATCCTAATGT	2959
Round 1 Nested LO	GGAGGGAAAATGGCCCAATTTAAGTGATTTG	1955
Round 1 LO	GAGATATCAGCTTTAGATCCCGATT	1982
Round 1.5 Forward	CCTGAAGACAAATATCATCCGACAC	1124
Round 1.5 Reverse	GGAATACAATCAACGAAACAATCGT	1341
Round 2 LO	CTAATACGCATATCAACTCAATATG	734
Round 2 Nested LO	GAAGGAAACTTCTTCAGACGAGAA	698
Round 3 LO	CTACTACTGAGCCAAGTTTCAGTG	553
Round 3 Nested LO	GAAGATAATTTGAGTTAATCCCTCT	507
Round 3.5 Right In	CCTGTTCCATATACCTTAATC	78

Results:

The final contig consensus sequence built from all genome walk data was just over 3,400 bases. When translated in the +2 frame just over 800 amino acid residues were obtained to produce a ~90 kD protein. This translation was compared to known non-LTR retrotransposons ORFs and found to be of average length.

We found several highly conserved regions common to the reconstructed *S. bullata* CR1 ORF contig consensus sequence and previously confirmed CR1 ORF sequences they are shown in Figure 3.3. Previous analyses had established eight conserved regions, located in the Fingers/Palm region, and three in the thumb region across all non-LTRs (Xiong and Eickbush 1990; Malik, Burke et al. 1999).

Similarity to known non-LTR retrotransposons was also assessed in the EN domain. The *S. bullata* consensus sequence is shown alongside known endonuclease domains (Figure 3.5). Areas shaded in black are identical amino acids while areas shaded in grey show greater than 80% similarity within the alignment. There are several highly conserved regions seen in this alignment indicating the element portion from *S. bullata* likely codes for endonuclease activity.

Representative sequences from eight of the non-LTR element groups were used to infer a phylogeny of known RT domains including the *S. bullata* presumed RT domain. For the sake of brevity seven non-LTR elements most closely related to CR1 were chosen for this analysis. As Figure 3.4 shows, the *S. bullata* CR1 presumed RT domain falls into the 'classical' CR1 clade with 77% bootstrap support. This result reinforces results from the previous chapter using a smaller fragment from the same RT domain. We also see that the *S. bullata* CR1-like sequence clusters with known CR1-like elements from two

other dipterans, the mosquitoes *Anopheles gambiae* and *Aedes aegypti* with relatively high support values.

Specific amino acid residue polymorphisms between the CR1 clade and other element clades were identified. For example Tyrosine and Aspartate residues were found to be consistent among the CR1-like elements only at residue numbers 314 and 333 respectively.

Figure 3.3 Alignment of *S. bullata* CR1B ORF2 with sequences of known non-LTR RT Fingers/palm region and one in the thumb region (area 7). Areas shaded in black are identical while areas shaded in grey show 80% similarity. Numbers above sequence denote the seven highly conserved areas previously described.

Figure 3.4 Results of a neighbor joining phylogenetic analysis of the RT domain of CR1-like non-LTR elements with the RT portion of the recovered element from *S. bullata*. Values on nodes are the proportion of bootstrap replicates supporting that node.

Figure 3.5 Sequence alignment showing similarity of a portion from *S. bullata* to known endonuclease domains. Accession numbers and species of origin are shown alongside each sequence.

Discussion

The *S. bullata* contig consensus sequence shares certain highly conserved regions with all non-LTR elements. The RT domain reconstructed in this work contains all seven highly conserved regions in the finger/palm region of typical non-LTR RT domains. These domains allow for classification of this element. For instance the *S. bullata* contig consensus sequence contains area 0, termed the Z domain, which is found to be only consistently found in retrotransposons (McClure 1991). The best conservation across all element types is found in areas two and four.

Separation of the *S. bullata* CR1 sequence from the R2, R4, and CRE-like element families is clear due to the presence of an AP endonuclease (APE) in the sequence where these families do not contain this domain (Malik, Burke et al. 1999). All of the other element families contain both the RT and APE domains and with the exception of a few I elements are all lacking the RNase H domain (Eickbush and Malik 2002). Further element family separation is indicated by at least 20% sequence divergence in the RT domain (Biedler and Tu 2003).

The RT regions recovered from this work show high similarity to known CR1 from a wide variety of taxa including reptiles, birds, insects, echinoderms, humans, rodents, protists, worms, anemones and fungi indicating it is likely a ‘classical’ CR1 element.

CR1 elements were first described in the chicken, *Gallus gallus*, and were originally thought to be a type of SINE because of their tendency to be truncated at the 5’ end (van het Schip, Samallo et al. 1987). We don’t know yet if CR1 elements in carrion flies suffer this same fate. However, given that they share the same basic structure and well-conserved amino acid motifs, presumably necessary for retrotransposition, as the classical CR1 elements, it is likely to be the case. Additional genome level data will be required before this can be determined.

It is clear that the RT and EN domains of the *S. bullata* CR1-like element are present and correspond well with similar elements found in other taxa. The phylogenetic analysis revealed the RT domain formed a cluster with other dipterian CR1s, suggesting that this element has been transferred to the genome vertically rather than horizontally as is often seen for non-LTR retrotransposons. This is not surprising due the low instances

of observed horizontal transfer of non-LTR elements (Eickbush and Malik 2002).

Moreover, many non-LTRs previously believed to replicate through horizontal transfer are now described through phylogenetic incongruence to indeed be replicated through vertical transfer (Eickbush and Malik 2002).

Overall the *S. bullata* CR1-like element is very similar to the ‘classical’ CR1 elements and shows signs of functionality as a marker for species identification due to its transmission. It has likely retained its ability to propagate through the genome and therefore intact copies of the master element are still present in the genome.

Chapter 4: Conclusions

This study shows the first documentation of LINEs within carrion flies. CR1-like elements were identified in several taxa and one very interesting family *S. bullata* CR1B, was investigated further. Briefly, the three main observations were made in the course of this study; 1) that carrion flies often harbor several CR1-like lineages, 2) that these lineages often exhibit signs of recent activity and, 3) that highly conserved regions typical of classical CR1-like elements are found in *S. bullata* CR1B. Below, these major findings will be elaborated. Additionally, extensions and implications of the work will be addressed.

Each species examined with the exception of *C. macelleria* contains several distinct clusters of CR1-like elements. These clusters were often found to show high sequence identities and therefore low divergence values suggesting that they were recently active. Several clusters (*P. regina* CR1A, *P. regina* CR1B, *P. regina* CR1C, *C.vom/C.vic* CR1A and *S. bullata* CR1B) showed 99% sequence identity or higher.

Comparison of the recovered sequence portion of carrion fly element families to known CR1-like element sequences revealed an exclusive carrion fly cluster was not present. This is most likely due to the variety of CR1-like lineages present in the examined species. A subset of carrion fly element clusters from *S. bullata*, *L. sericata*, *C. vomitoria*, *C. vicina* and *P. regina* are likely from the R1 family of elements due to their formation of a cluster with these elements. Another subset of elements from *L. sericata* and the only element from *C. macelleria* formed a cluster with Jockey-like elements from a variety of insects with little bootstrap support indicating they are likely from the Jockey element family. The Zenon family is likely the classification of the remaining two *C.vom/C.vic* clusters due to their cluster formation.

S. bullata CR1B, was found to cluster with, and therefore likely be from the CR1 family of elements. The closest association was with a fellow dipteran then further clustered with other CR1 elements from a wide variety of taxa including vertebrates, blood flukes, and sea urchins. This cluster also showed one of the lowest divergence values (0.015637) likely indicating recent activity. Due to these observations this cluster was chosen for further analysis.

Further sequencing of this cluster revealed several highly conserved regions in comparison to known CR1-like ORF2s. This ORF is known to contain the RT and EN domains which were both identified with high conservation. The RT domain has previously been used to characterize non-LTR element families (Malik, Burke et al. 1999) Phylogenetic analysis of the presumed RT domain revealed for this element showed this element falls into the ‘classical’ CR1 clade with fellow dipterans the mosquitoes *Anopheles gambiae* and *Aedes aegypti*.

The signs of recent activity suggest that we will eventually be able to identify taxon-specific insertion events that will be useful for species identification at a later date. This will enable the eventual development of a TE-based method for species identification that will be of particular use in determining taxon identity for specimens collected at crime scenes.

The need for a reliable identification method for species has become apparent for additional purposes. One such example is the need to correctly identify specific carrion flies for use in wound cleaning by the medical community. Though the COI gene has been investigated for this purpose (Williams, Cronje et al. 2008), this analysis method poses another identification possibility.

Applications are also possible for phylogenetic analyses of these complex taxonomic assemblages. For example the phylogeny of the carrion fly genus *Protophormia* is not completely resolved due to the large number of species (Sabrosky, Bennett et al. 1989).

Creating transgenic animals with the use of TEs has also become an active area of interest. For example, Class 2 elements known as piggyBacs have been used to investigate genetic modification in the tobacco budworm (Ren, Han et al. 2006) sheep carrion fly, *Lucilia cuprina* (Heinrich, Li et al. 2002) and the New World screwworm, *Cochliomyia hominivorax* (Allen, Handler et al. 2004). Use of the Herves element from *A. gambiae* to disable the mosquitoes' ability to transmit malaria has also been investigated (Arensburger, Kim et al. 2005). These studies present utilization of transposons, but it is possible to use retrotransposons as vectors as well. Insertion of gene sequences into transposons is done by replacing the transposase gene, whereas inserting gene sequences into retrotransposons involves insertion into the 3'UTR (Largaespada 2003).

Retrotransposons boast a wide variety of uses, and the elements recovered in this work are no exception. Though a significant amount research will need to be done to implement the recovered elements for any of the aforementioned uses, this study lays the groundwork.

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Supplemental Data

<i>CVic12r</i>	GATCCCCA - - A	ATGAAATCAT	A - - GCTATAG	TCTGTGAGCA	CTGGCCGGAT	ATATTTATGG
<i>CVic21</i>	GATCCCCA - - A	ATGAAATCAT	A - - GCTATAG	TCTGTGAGCA	CTGGCCGGAT	ATATTTATGG
<i>CVic26</i>	GATCCCCA - - A	ATGAAATCAT	A - - GCTATAG	TCTGTGAGCA	CTGGCCGGAT	ATATTTATGG
<i>CVic29</i>	GATCCCCA - - A	ATGAAATCAT	A - - GCTATAG	TCTGTGAGCA	CTGGCCGGAT	ATATTTATGG
<i>CVic7</i>	GATCCCCA - - A	ATGAAATCAT	A - - GCTATAG	TCTGTGAGCA	CTGGCCGGAT	ATATTTATGG
<i>CVic20</i>	GATCCCCA - - A	ATGAAATCAT	A - - GCTATAG	TCTGTGAGCA	CTGGCCGGAT	ATATTTATGG
<i>Cvom15_2</i>	GATCCCCA - - A	ATGAAATCAT	C - - ACTATAG	TCTGTGAGAA	CTGGCCGGAT	ATATTTACGG
<i>Cvom1_2</i>	GATCCCCA - - A	ATGAAATCAT	C - - ACTATAG	TCTGTGAGCA	CTGGCCGGAT	GTATTTACGG
<i>CvomCvic.CRIA.Con</i>	GATCCCCA - - A	ATGAAATCAT	A - - GCTATAG	TCTGTGAGCA	CTGGCCGGAT	ATATTTATGG
<i>Cvom7_2</i>	CATACCAGCG	CTGGTCTTGA	A - - ACAGTGC	TCTTCGA - CG	TTAGCTCG - T	GCATTAGCTA
<i>Cvom7</i>	TATACCAGCA	CTGGTCTTGA	A - - ACAGTAT	TCT - - - - -	- - - - -	- - - - -
<i>Cvom6_2</i>	TATACCAGCA	CTATTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCTCG - T	CCATTAGCTA
<i>Cvom2</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CT - - - - CG - T	CCATTAGCTA
<i>CVic27</i>	TATACCAGC -	- - - - TCTTGA	A - - GCAATGT	TCTTCGA - TG	CTAGCTCG - T	CCATTAGTTA
<i>CVic34</i>	TATACCAGCA	CTGATCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCTCG - C	CCATT - TCTA
<i>Cvom8</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTAT	TCTTCGA - CG	CTAGCTCG - T	CCATTAGCTA
<i>Cvom3_2</i>	TATACCAGCA	CTGGTCTTGA	A - - ACAGTGT	TCTTCG - - - G	CTAGCTCG - T	CCATTAGCTA
<i>Cvom2_2</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCTCG - T	CCATTAGCTA
<i>CVic24</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCTCG - T	CCATTAGCTA
<i>CVic10</i>	TATACCAGCA	CTTGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCTCG - T	CCATTAGCTA
<i>CVic16</i>	TATACCAGCA	CTTGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCTCG - T	CCATTAGCTA
<i>CVic8</i>	TATACCAGCA	CTTGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCTCG - T	CCATTAGCTA
<i>CVic1</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCTCG - T	CCATTAGCTA
<i>CVic14</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCTCG - T	CCATTAGCTA
<i>CVic15</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCTCG - T	CCATTAGCTA
<i>CVic31</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - TG	CTAGCTCG - T	CCATTAGCTA
<i>CvomCvic.CRIB1.Con</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCTCG - T	CCATTAGCTA
<i>Cvom10_2</i>	TATACCAGCA	GTGGTCTTGA	A - - GCAATGT	TCTTCGA - TG	CTAGCCCG - T	CCGTTAGCAA
<i>CVic22</i>	TATACCAGCA	CTGGACTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCCCG - T	CCATTAGCAA
<i>Cvom5_2</i>	TATACCAGCA	CTGGTCTTGA	ATTGTATTGT	TCTTCGA - CG	TTAGCCCG - T	CCGTTAGCAA
<i>Cvom8_2</i>	TATACCAGCA	CTGGTCTTGA	A - - ACAGTAT	TCTTCGA - CA	GTAGCCCG - C	CCGTTAGCAA
<i>Cvom5</i>	TATACCAACA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCCCA - T	CCGTTAGCAA
<i>Cvom4</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCCCG - T	CCGTTAGCAA
<i>Cvom3</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCCCG - T	CCATTAGCAA
<i>Cvom11_2</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCCCG - T	CCGTTAGCAA
<i>CVic11</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCCCG - T	CCGTTAGCAA
<i>CVic33</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCCCG - T	CCGTTAGCAA
<i>Cvom14_2</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCCCG - T	CCGTTAGCAA
<i>Cvom16</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCCCG - T	CCGTTAGCAA
<i>CVic32</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCTA - -	- - - - -	- - - - -
<i>CVic30</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TTTTTCGT - -	- - - - - TTT	CCGTTAGAAA
<i>CvomCvic.CRIB2.Con</i>	TATACCAGCA	CTGGTCTTGA	A - - GCAGTGT	TCTTCGA - CG	CTAGCCCG - T	CCGTTAGCAA
<i>CVic12r</i>	ATACATTTAA	CATTTGTCTC	AAAGAAAGAG	TTTTTCCAAA	ACTTTGGAAA	AAACAATATC
<i>CVic21</i>	ATACATTTAA	CATTTGTCTC	AAAGAAAGAG	TTTTTCCAAA	ACTTTGGAAA	AAACAATATC
<i>CVic26</i>	ATACATTTAA	CATTTGTCTC	AAAGAAAGAG	TTTTTCCAAA	ACTTTGGAAA	AAACAATATC
<i>CVic29</i>	ATACATTTAA	CATTTGTCTC	AAAGAAAGAG	TTTTTCCAAA	ACTTTGGAAA	AAACAATATC
<i>CVic7</i>	ATACATTTAA	CATTTGTCTC	AA - GAAGGAG	TTTTTCCAAA	ACTTTGGAAA	AAACAATATC
<i>CVic20</i>	ATACATTTAA	CATTTGTCTC	AAAGAAAGAG	TTTTTCCAAA	ACTTTGGAAA	AAACAATATC
<i>Cvom15_2</i>	ATACMTTTAA	CATTTGCCTC	AAGGAAGGAG	TTTTTCCAAA	ACTCTGGAAA	AGACAATATC
<i>Cvom1_2</i>	GTACATTTAA	CATTTGCCTC	AAGGAAGGAG	TTTTTCCAAA	ACTTTGGAAA	AGACAATATC
<i>CvomCvic.CRIA.Con</i>	ATACATTTAA	CATTTGTCTC	AAAGAAAGGAG	TTTTTCCAAA	ACTTTGGAAA	AAACAATATC
<i>Cvom7_2</i>	ACCTTATCAG	CACCTTATAC	CGTGCCGGCG	TATTACCACT	ATGTTGGAAG	GTTGCTAATG
<i>Cvom7</i>	- - - - -	- - - - TTATAC	CGTGCCGGCA	AATTTCCCTGT	ATGTTGGAAG	GTTGCTAATG
<i>Cvom6_2</i>	ACCTTTTCAG	CACCTCTATAC	CATCCCGGCA	AATTTCCCTCT	ATGTTGGAAG	GTTGCTAATG
<i>Cvom2</i>	ACCTTTTCAG	CAGTTTATAC	CGTGCCGGCA	AATTTCCAGT	ATGTTGGAAG	GTTGCTAATG
<i>CVic27</i>	ACCTTTTCAG	CACATTATAC	AGTGCCGGCA	AATTTCCAGT	ATGTTGGAAG	GTTGCTAATG
<i>CVic34</i>	ACCTTTTCAG	CACCTTATAC	CGTGCCGGCA	AATTTCCAGT	ATGTTGGAAG	GTTGCTAATG
<i>Cvom8</i>	AGTTTTTCAG	CACCTTATAC	CGTGCTGAAA	AATTTCCCTGT	ATGTTGGAAG	GTTGCTAATG
<i>Cvom3_2</i>	ACCTTTTCAG	CACCTTATAT	CGTGCCGGCA	AATTTCCAGT	ATGTTGGAAG	GTTGCTAATG
<i>Cvom2_2</i>	ACCTTTTCAG	CACCTTATAC	CGTGCCGGCA	AATTTCCCTGT	ATGTTGGAAG	GTTGCTAATG
<i>CVic24</i>	ACGTTTTTCAG	CACCTTATAC	CGTGCCGGCA	AATTTCCATGT	ATGTTGGAAG	GTTGCTAATG
<i>CVic10</i>	ACCTTTTCAG	CACCTTATAC	CGTGCCGGCA	AATTTCCAGT	ATGTTGGAAG	GTTGCTAATG
<i>CVic16</i>	ACCTTTTCAG	CACCTTATAC	CGTGCCGGCA	AATTTCCAGT	ATGTTGGAAG	GTTGCTAATG
<i>CVic8</i>	ACCTTTTCAG	CACCTTATAC	CGTGCCGGCA	AATTTCCAGT	ATGTTGGAAG	GTTGCTAATG
<i>CVic1</i>	ACCTTTTCAG	CACCTTATAA	CGTGCCGGCA	AATTTCCAGT	ATGTTGGAAG	GTTGCTAATG
<i>CVic14</i>	ACCTGTTTCAG	CACCTTATAC	CGTGCCGGCA	AATTTCCAGT	ATGTTGGAAG	GTTGCTAATG
<i>CVic15</i>	ACCTTTTCAG	CACCTTATAC	CGTGCCGGCA	AATTTCCAGT	ATGTTGGAAG	GTTGCTAATG
<i>CVic31</i>	ACCTTTTCAG	CACCTTATAC	CGTGCCGGCA	AATTTCCAGT	ATGTTGGAAG	GTTGCTAATG
<i>CvomCvic.CRIB1.Con</i>	ACCTTTTCAG	CACCTTATAC	CGTGCCGGCA	AATTTCCAGT	ATGTTGGAAG	GTTGCTAATG
<i>Cvom10_2</i>	ACCTTTTCAG	TATATTATAC	CTTGCCGGAG	AATTTCCCTAT	ATGTTGGAAG	GTTGCTAATG
<i>CVic22</i>	ATCTTTTCAG	GATATTATAC	CGTGCCGGAA	AATTTCCCTAT	ATGTTGGAAG	GTTT - - - -
<i>Cvom5_2</i>	ACCTTTTCAG	C - - - - -	- - - - CGGAG	AATTTCCCTAT	ATGTTAGAAAG	GTTGCTAATG
<i>Cvom8_2</i>	ACCTTTTCAG	CATATTATAT	CGTGTCGGAG	AATTTCCCTAT	ATGTTGGAAA	GTTGCTAATG
<i>Cvom5</i>	ACCTTTTCAG	CATATTATAC	CGTGCCGGAG	AATTTCCCTTC	ATGTTGGAAG	GTTGCTAATG
<i>Cvom4</i>	ACCTTTTCAG	CTTATTATAC	CGTGCCGGAG	AATTTCCATAT	ATGTTGGAAG	GTTGGTAAATG
<i>Cvom3</i>	ACCTTTTCAG	CATATTATAC	AGTGCCGGTG	AATTTCCCTAT	ATGTTGGAAG	GTTGCTAATG
<i>Cvom11_2</i>	ACCTTTTCAG	CATATTATAC	CGTGCCGGTG	AATTTCCCTAT	ATGTTGGAAG	GTTGCTAATG
<i>CVic11</i>	ACCTTTTCAG	CATATTA - AC	CGTGCCGGTG	AATTTCCAAAT	ATGTTGGAAG	GTTGCTAATG
<i>CVic33</i>	ACCTTTTCAG	CATATTA - AC	CGTGCCGGTG	AATTTCCAAAT	ATGTTGGAAG	GTTGCTAATG
<i>Cvom14_2</i>	ACCTTTTCAG	CATATTATAC	CGTGCCGGAG	AATTTCCCTAT	ATGTTGGAAG	GTTGCTAATG
<i>Cvom16</i>	ACCTTTTCAG	CATATTATAC	CGTGCCGGTG	AATTTCCCTAT	ATGTTGGAAG	GTTGCTAATG
<i>CVic32</i>	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<i>CVic30</i>	ACCTTTTCAG	CATATTATAC	CGTGCCGGAA	AATTTCC - AT	GTGTTAGAAAG	GTTTCTAATG
<i>CvomCvic.CRIB2.Con</i>	ACCTTTTCAG	CATATTATAC	CGTGCCGGAG	AATTTCCCTAT	ATGTTGGAAG	GTTGCTAATG

<i>CVic12r</i>	CTTGTGA - - -	- - - TGGAAAT	AAACGAAAAA	GGAGGTTTCT	CACATAT - - G	CAGTTTGGAT
<i>CVic21</i>	CTTGTGA - - -	- - - TGGAAAT	AAACGAAAAA	GGAGGTTTCT	CACATAT - - G	CAGTTTGGAT
<i>CVic26</i>	CTTGTGA - - -	- - - TGGAAAT	AAACGAAAAA	GGAGGTTTCT	CACATAT - - G	CAGTTTGGAT
<i>CVic29</i>	CTTGTGA - - -	- - - TGGAAAT	AAACGAAAAA	GGAGGTTTCT	CACATAT - - G	CAGTTTGGAT
<i>CVic7</i>	CTTGTGA - - -	- - - TGGAAAT	AAACGAAAAA	GGAGGTTTCT	CACATAT - - G	CAGTTTGGAT
<i>CVic20</i>	CTTGTGA - - -	- - - TGGAAAT	AAACGAAAAA	GGAGGTTTCT	CACATAT - - G	CAGTTTGGAT
<i>Cvom15_2</i>	CTTGTGA - - -	- - - TGGAAAT	AAACGAAAAA	GGAGGTTTCT	CACATAT - - G	CAGTTTGGAT
<i>Cvom1_2</i>	CTTGTGA - - -	- - - TGGAAAT	AAACGAAAAA	GGAGGTTTCT	CACATAT - - G	CAGTTTGGAT
<i>CvomCvic.CRIA.Con</i>	CTTGTGA - - -	- - - TGGAAAT	AAACGAAAAA	GGAGGTTTCT	CACATAT - - G	CAGTTTGGAT
<i>Cvom7_2</i>	TTTGTGAAAT	AT - - - - -	- - - - -	- - - - -	- - GGTAACCGG	CAGTATGGCT
<i>Cvom7</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTATG	CAGCGACCGG	CAGTATGGCT
<i>Cvom6_2</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTACT	CAGCGAACCGG	CAGTATGGCT
<i>Cvom2</i>	CTTGTGAAAC	ATTTGGAGTT	CAAC - - - - -	- - AATTTAAT	CAGCGACCGG	CTGTATGGCT
<i>CVic27</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTACT	CAGCGACCGG	CAGTATGGCT
<i>CVic34</i>	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - G	CAGTATGGCT
<i>Cvom8</i>	CT - - - GAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTACT	- - - - -	CAGAATGGCT
<i>Cvom3_2</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATATACT	CAGTGACCGA	CAGTATGGCT
<i>Cvom2_2</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTACT	TAGCGACCGG	CAGTATGGAT
<i>CVic24</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTTCT	CAGCGACCGG	CAGTATGGCT
<i>CVic10</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTACT	CAGCGACCGG	CAGTATGGAT
<i>CVic16</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTACT	CAGCGACCGG	CAGTATGGAT
<i>CVic8</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTACT	CAGCGACCGG	CAGTATGGAT
<i>CVic1</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTACT	CAGCGACCGG	CAGAATGGCT
<i>CVic14</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTACT	CAGCGACCGG	CAGTATGGCT
<i>CVic15</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTACT	CAGCGACCGG	CAGTATGGCT
<i>CVic31</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTACT	CAGCGACCGG	CAGTATG - -
<i>CvomCvic.CRIB1.Con</i>	CTTGTGAAAT	ATTTAGAGTC	CAAC - - - - -	- - AATTTACT	CAGCGACCGG	CAGTATGGCT
<i>Cvom10_2</i>	CTTGTGAAAT	ATCTAGAGTC	GAAC - - - - -	- - AATTTACT	TAGCAACCGG	CAGTGGGGCA
<i>CVic22</i>	CTTGTGAAAT	ATCTAGAGTC	GAAC - - - - -	- - AATTTACT	TAGCGACCGG	CAGTACGGCT
<i>Cvom5_2</i>	CTTGTAAAAC	ATCTAGAGTC	GAAC - - - - -	- - AATTTACT	TAGCGACCGG	TAGTACGGCT
<i>Cvom8_2</i>	CTTGTAAAAT	ATCTAGAGTC	GAAC - - - - -	- - AATTTTCT	TAGCGACCGG	CAGTACGGCT
<i>Cvom5</i>	CTTGTGAAAT	ATCTAGAATC	GAAC - - - - -	- - AATTTACT	TAGCGACC - -	- - - - -
<i>Cvom4</i>	CTTGTGAAAT	ATCTAGAGTC	GAAC - - - - -	- - AATTTACT	TAGCGACCGG	CAGTATGGCT
<i>Cvom3</i>	CTTGTGAAAT	ATCTAGAGTC	GAAC - - - - -	- - AATTTACT	TAGCGGCGCG	CAGTACGGCT
<i>Cvom11_2</i>	CTTGTGAAAT	ATCTAGAGTC	GAAC - - - - -	- - AATTTACT	TAGCGACCGG	CAGTACGGCT
<i>CVic11</i>	CTTGTGAAAT	ATCTAGAGTC	GAAC - - - - -	- - AATTTACT	TAGCGACTGG	CAGTACGGCT
<i>CVic33</i>	CTTGTGAAAT	ATCTAGAGTC	GAAC - - - - -	- - AATTTACT	TAGCGACTGG	CAGTACGGCT
<i>Cvom14_2</i>	CTTGTGAAAT	ATCTAGAGTC	GAAC - - - - -	- - AATTTACT	TAACGACCGG	CAGTACGGCT
<i>Cvom16</i>	CTTGTGAAAT	ATCTAGAGTC	GAAC - - - - -	- - AATTTACT	TAGCGACCGG	CATTACGGCT
<i>CVic32</i>	CTTGTGAAAT	ATCTAGAGTC	GAAC - - - - -	- - AATTTACT	TAGCGACCGG	CAGTAC - - -
<i>CVic30</i>	CTTGTGAAAT	ATCTAGAGTT	GAAC - - - - -	- - AATTTACT	TAGCGAC - -	- - - - - GGCT
<i>CvomCvic.CRIB2.Con</i>	CTTGTGAAAT	ATCTAGAGTC	GAAC - - - - -	- - AATTTACT	TAGCGACCGG	CAGTACGGCT
<i>CVic12r</i>	TCGTGAAAGG	TAAATCCACT	GTAGG - - - - -	- AGCCATCCG	TGAGGTGGTA	AATACTGCAA
<i>CVic21</i>	TCGTGAAAGG	TAAATCCACT	GTAGG - - - - -	- AGCCATCCG	TGAGGTGGTA	AATACTGCAA
<i>CVic26</i>	TCGTGAAAGG	TAAATCCACT	GTAGG - - - - -	- AGCCATCCG	TGAGGTGGTA	AATACTGCAA
<i>CVic29</i>	TCGTGAAAGG	TAAATCCACT	GTAGG - - - - -	- AGCCATCCG	TGAGGTGGTA	AATACTGCAA
<i>CVic7</i>	TCGTGAAAGG	TAAATCCACT	GTAGG - - - - -	- AGCCATCCG	TGAGGTGGTA	AATACTGCAA
<i>CVic20</i>	TCGTGAAAGG	TAAATCCACT	GTAGG - - - - -	- AGCCATCCG	TGAGGTGGTA	AATACTGCAA
<i>Cvom15_2</i>	TCGTGAAAGG	TAAATCCACT	GTAGG - - - - -	- AGCCATCCG	TGAGGTGGTA	AATACTGCAA
<i>Cvom1_2</i>	TCGTGAAAGG	TAAATCCACT	GTAGG - - - - -	- AGCCATCCG	TGAGGTGGTA	AATACTGCAA
<i>CvomCvic.CRIA.Con</i>	TCGTGAAAGG	TAAATCCACT	GTAGG - - - - -	- AGCCATCCG	TGAGGTGGTA	AATACTGCAA
<i>Cvom7_2</i>	TTTCGTAGAGG	ACGCTCTACG	GGAGACTTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>Cvom7</i>	TTTCGTAGAGG	ATGCTCTACG	GGAGACTTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>Cvom6_2</i>	TTTCGTAGAGG	ACGCTCTACG	GAAGACTTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>Cvom2</i>	TTTCGTAGAGG	ACGCTCTACG	GGAGACTTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>CVic27</i>	TTTCGTAGAGG	ACGCTCTACG	GGAGACTTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>CVic34</i>	TTTCGTAGAGG	ACGCTCTACG	GGATACCTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>Cvom8</i>	TTAGTAGAGG	ACGCT - - - -	- - - - -	- - - - - TCC -	- - - - -	- - TATCGGTA
<i>Cvom3_2</i>	TTTCGTAGAGG	ACGCTCTACG	GGAGACTTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>Cvom2_2</i>	TTTCGTAGAGG	TCGCTCTACG	GGAGACTTGC	TAGCCTTCT -	- - - - -	- - TATCGGAA
<i>CVic24</i>	TTTCGTAGAGG	ACGCTCTACG	CGTGACTTGC	TAGCCTTTC -	- - - - -	- - TATCAAAA
<i>CVic10</i>	TTTCGTAGAGG	ACGCTCTACG	GGAGACTTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>CVic16</i>	TTTCGTAGAGG	ACGCTCTACG	GGAGACTTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>CVic8</i>	TTTCGTAGAGG	ACGCTCTACG	GGAGACTTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>CVic1</i>	TTTCGTAGAGG	ACGCTCTACG	GGAGACTTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>CVic14</i>	TTTCGTAGAGG	ACGCTCTACG	GGGACTTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>CVic15</i>	TTTCGTAGAGG	ACGCTCTACG	GGAGACTTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>CVic31</i>	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - TATCGGAA
<i>CvomCvic.CRIB1.Con</i>	TTTCGTAGAGG	ACGCTCTACG	GGAGACTTGC	TAGCCTTCC -	- - - - -	- - TATCGGAA
<i>Cvom10_2</i>	TTTCATAAAAG	ACGTTCTATG	GGGAACTTGC	TTCGCTTCC -	- - - - -	- - TATCGGAA
<i>CVic22</i>	TTTCGTAGAGG	CCGCTCTACG	GGGGACTTAC	TTCGCTTCC -	- - - - -	- - TATCGGAA
<i>Cvom5_2</i>	TTTCGTAGAGG	CCGCTCTAGG	GGGGACTTGC	TAGCCTTAC -	- - - - -	- - TATCGGAA
<i>Cvom8_2</i>	TTTCGTAGAGG	ACGCTCTACG	GGGGACTTGC	TTCGCTTCC -	- - - - -	- - TATCGGAA
<i>Cvom5</i>	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - TATCGGAA
<i>Cvom4</i>	TTTCGTAGAGG	ACGCTCTACG	GGGGACTTGC	TTCGCTTCC -	- - - - -	- - TATCGGAA
<i>Cvom3</i>	TTTCGTAGAGG	ACGCTCTACG	GGGGACTTGC	TTCGCTTCC -	- - - - -	- - TATCGGAA
<i>Cvom11_2</i>	TTTCGTAGAGG	ACGCTCTACG	GGGGACTTGC	TTCGCTTCC -	- - - - -	- - TATCGGAA
<i>CVic11</i>	TTTCGTAGAGG	ACGCTCTACG	GGGGACTTGC	TTCGCTTCC -	- - - - -	- - TATCGGAA
<i>CVic33</i>	TTTCGTAGAGG	ACGCTCTACG	GGGGACTTGC	TTCGCTTCC -	- - - - -	- - TATCGGAA
<i>Cvom14_2</i>	TTTCGTAGAGG	ACGCTCTACG	GGGGACTTGC	TTCGCTTCC -	- - - - -	- - TATCGGAA
<i>Cvom16</i>	TTTCGTAGAGG	ACGCTCTACG	GGGGACTTGC	TTCGCTTCC -	- - - - -	- - TATCGGAA
<i>CVic32</i>	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - TATCGGAA
<i>CVic30</i>	TTTCGTAGAGG	ACGCTCTACG	GGGGACTTGC	TTCGCTTCC -	- - - - -	- - TATCGGAA
<i>CvomCvic.CRIB2.Con</i>	TTTCGTAGAGG	ACGCTCTACG	GGGGACTTGC	TTCGCTTCC -	- - - - -	- - TATCGGAA

<i>CVic12r</i>	AGGAAGCTTT	TGAGCACTTG	CGATTTTGCT	CCA - - - - -	TCGTCAACCCT	GGACATCAAG
<i>CVic21</i>	AGGAAGCTTT	TGAGCACTTG	CGATTTTGCT	CCA - - - - -	TCGTCAACCCT	GGACATCAAG
<i>CVic26</i>	AGGAAGCTTT	TGAGCACTTG	CGATTTTGCT	CCA - - - - -	TCGTCAACCCT	GGACATCAAG
<i>CVic29</i>	AGGAAGCTTT	TGAGCACTTG	CGATTTTGCT	CCA - - - - -	TCGTCAACCCT	GGACATCAAG
<i>CVic7</i>	AGGAAGCTTT	TGAGCACTTG	CGATTTTGCT	CCA - - - - -	TCGTCAACCCT	GGACATCAAG
<i>CVic20</i>	AGGAAGCTTT	TGAGCACTTG	CGATTTTGCT	CCA - - - - -	TCGTCAACCCT	GGACATCAAG
<i>Cvom15_2</i>	AGGAAGCTTT	TGAACACATG	CGATTTTGTT	CCA - - - - -	TCGTCAACCCT	GGACATCAAG
<i>Cvom1_2</i>	AGGAAGCTTT	TGAACACATG	CGATTTTGTT	CCA - - - - -	TCGTCAACCCT	GGACATCAAG
<i>CvomCvic.CRIA.Con</i>	AGGAAGCTTT	TGAGCACTTG	CGATTTTGCT	CCA - - - - -	TCGTCAACCCT	GGACATCAAG
<i>Cvom7_2</i>	AAATGGTGTC	GTTCCATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>Cvom7</i>	AAATTTATGTC	GTTCCATACA	CCGTTTTGGC	AAAAGCAAAAG	TGGTGGCTCT	AGATATTTCT
<i>Cvom6_2</i>	- - - - -	GTTCCATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>Cvom2</i>	AAATGGTGTC	GTTCCATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CVic27</i>	AAATGGT - - -	GTTCTATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTATCTCT	AGATATTTCT
<i>CVic34</i>	AAATGGTGTC	GTTCCATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>Cvom8</i>	AAATGGTGTC	GTACCATATA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>Cvom3_2</i>	AAATGGTGCC	ATTCCATACA	CCGTTTTGGC	GAAAGTAAAG	TACTGGCTCT	AGATATTTCT
<i>Cvom2_2</i>	AAATGGTGTC	GTTCCATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CVic24</i>	AAAAAGTGTC	GTTCTATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCACT	AGATATTTCT
<i>CVic10</i>	AAATGGTGCC	GTTCCATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CVic16</i>	AAATGGTGCC	GTTCCATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CVic8</i>	AAATGGTGTC	GTTCCATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CVic1</i>	AAATGGTGTC	GTTCCATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CVic14</i>	AAATGGTGTC	GTTCCATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CVic15</i>	AAATGGTGTC	GTTCCATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CVic31</i>	- - - - -	GTTCCATACG	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CvomCvic.CRIB1.Con</i>	AAATGGTGTC	GTTCCATACA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>Cvom10_2</i>	AAGTGGTGCC	GTTCTATTCA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCC	ACATCTTTCT
<i>CVic22</i>	ATATGGTGTC	GTTCCATTCA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>Cvom5_2</i>	AAATGGTGCC	GTTCCATTCA	CCGTTTTGGC	GAAAGTAAAG	TGA TGGCTCT	AGATATTTCT
<i>Cvom8_2</i>	AAATGGTGCC	GTTTCATTCA	CTGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>Cvom5</i>	AA - TGGTCCC	GTTCCATTCA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>Cvom4</i>	AAATGGTGCC	GTTCCATTCA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>Cvom3</i>	AAATGGTGCC	GTTCCATTCA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>Cvom11_2</i>	AAATGGTGCC	GTTCCATTCA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CVic11</i>	AAGTGGTGCC	GTTCCATTCA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CVic33</i>	AAGTGGTGCC	GTTCCATTCA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>Cvom14_2</i>	AAATGGTGCC	GTTCCATTCA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>Cvom16</i>	AAATGGTGCC	GTTCCATTCA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CVic32</i>	AAATGGTGTC	GTTCCATTCA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CVic30</i>	AAATGGTGTC	GTTCCATTCA	CCGTTTTGGC	GAAAGTAAAG	TGGGCGCTCC	AGATATTTCT
<i>CvomCvic.CRIB2.Con</i>	AAATGGTGCC	GTTCCATTCA	CCGTTTTGGC	GAAAGTAAAG	TGGTGGCTCT	AGATATTTCT
<i>CVic12r</i>	AACGCATTCA	ACTCTGCAAA	CTGGAATGTA	ATTTCGACAAA	CAATGCGAGA	GCGAAATTTTC
<i>CVic21</i>	AACGCATTCA	ACTCTGCAAA	CTGGAATGTA	ATTTCGACAAA	CAATGCGAGA	GCGAAATTTTC
<i>CVic26</i>	AACGCATTCA	ACTCTGCAAA	CTGGAATGTA	ATTTCGACAAA	CAATGCGAGA	GCGAAATTTTC
<i>CVic29</i>	AACGCATTCA	ACTCTGCAAA	CTGGAATGTA	ATTTCGACAAA	CAATGCGAGA	GCGAAATTTTC
<i>CVic7</i>	AACGCATTCA	ACTCTGCAAA	CTGGAATGTA	ATTTCGACAAA	CAATGCGAGA	GCGAAATTTTC
<i>CVic20</i>	AACGCATTCA	ACTCTGCAAA	CTGGAATGTA	ATTTCGACAAA	CAATGCGAGA	GCGAAATTTTC
<i>Cvom15_2</i>	AATGCAATTCA	ACTCTGCTAA	CTGGAATGTA	ATTTCGACAAA	CAATGCGAGA	GCGAAATTTTC
<i>Cvom1_2</i>	AATGCAATTCA	ACTCTGCTAA	CTGGAATGTA	ATTTCGACAAA	CAATGCGAGA	GCGAAATTTTC
<i>CvomCvic.CRIA.Con</i>	AACGCATTCA	ACTCTGCAAA	CTGGAATGTA	ATTTCGACAAA	CAATGCGAGA	GCGAAATTTTC
<i>Cvom7_2</i>	AAAGCGTTTTG	A - - - - -	- CAGAAATATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>Cvom7</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	ACATGGTGCT	CTTTT - - - - A	GCAAAACTTTA
<i>Cvom6_2</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>Cvom2</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GTA TGGTGCA	CTTTT - - - - -	- - - - -
<i>CVic27</i>	AAAGCGTTTTG	A - - - - -	- CAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>CVic34</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>Cvom8</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>Cvom3_2</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>Cvom2_2</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>CVic24</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>CVic10</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>CVic16</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>CVic8</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>CVic1</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>CVic14</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA T - TGCG	CTTTT - - - - A	GCAAAACTTTA
<i>CVic15</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>CVic31</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>CvomCvic.CRIB1.Con</i>	AAAGCGTTTTG	A - - - - -	- TAGAGTATG	GCA TGGTGCG	CTTTT - - - - A	GCAAAACTTTA
<i>Cvom10_2</i>	AAAGCGTTTCG	A - - - - -	- TAAGGTGTG	GCAAGA - - -	- - - - -	- - - - -
<i>CVic22</i>	AAAGCGTTTCG	A - - - - -	- TAGGGTGTG	GCA TGGTGCG	CTCTT - - - - A	TGAAACTTTA
<i>Cvom5_2</i>	AAAGCGTTTCG	A - - - - -	- TAGGGTGTG	GCA TGGTGCG	CTCGT - - - - A	TGAAACTTTA
<i>Cvom8_2</i>	AAAGCGTTTCG	A - - - - -	- TAGGGTGTG	GCA TGGTGCG	CTCTT - - - - A	TGAAACTTTA
<i>Cvom5</i>	AAAGCGTTTCG	A - - - - -	- TAGGGTGTG	GCA TGGTGCG	CTCTT - - - - A	TGAAACTTTA
<i>Cvom4</i>	AAAGCGTTTCG	A - - - - -	- TAGGGTGTG	GCA TGGTGCG	CTCTT - - - - A	TGAAACTTTA
<i>Cvom3</i>	AAAGCGTTTCG	A - - - - -	- TAGGGTGTG	GCA TGGTGCG	CTCTT - - - - A	TGAAACTTTA
<i>Cvom11_2</i>	AAAGCGTTTCG	A - - - - -	- TAGAGTGTG	GCA TGGTGCG	CTCTT - - - - A	TGAAACTTTA
<i>CVic11</i>	AAAGCGTTTCG	A - - - - -	- TAGGGTGTG	GCA TGGTGCG	CTCTT - - - - A	TGAAACTTTA
<i>CVic33</i>	AAAGCGTTTCG	A - - - - -	- TAGGGTGTG	GCA TGGTGCG	CTCTT - - - - A	TGAAACTTTA
<i>Cvom14_2</i>	AAAGCGTTTCG	A - - - - -	- TAGGGTGTG	GCA TGGTGCG	CTCTT - - - - A	TGAAACTTTA
<i>Cvom16</i>	AAAGCGTTTCG	A - - - - -	- TAGGGTGTG	GTA TGGTGCG	CTCTT - - - - A	TGAAACTTTA
<i>CVic32</i>	AAAGCGTTTCG	A - - - - -	- TAGGGTGTG	GCA TGGTGCG	CTCTT - - - - A	TGAAACTTTA
<i>CVic30</i>	AAAGCGTTTCG	A - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<i>CvomCvic.CRIB2.Con</i>	AAAGCGTTTCG	A - - - - -	- TAGGGTGTG	GCA TGGTGCG	CTCTT - - - - A	TGAAACTTTA

<i>CVic12r</i>	TCAGAAATATT	TGGTAAAAAAT	GG-----TT	GAT-----	-AATTATCTG	GAAGATAGAA
<i>CVic21</i>	TCAGAAATATT	TGGTAAAAAAT	GG-----TT	GAT-----	-AATTATCTG	GAAGATAGAA
<i>CVic26</i>	TCAGAAATATT	TGGTAAAAAAT	GG-----TT	GAT-----	-AATTATCTG	GAAGATAGAA
<i>CVic29</i>	TCAGAAATATT	TGGTAAAAAAT	GG-----TT	GAT-----	-AATTATCTG	GAAGATAGAA
<i>CVic7</i>	TCAGAAATATT	TGGTAAAAAAT	GG-----TT	GAT-----	-AATTATCTG	GAAGATAGAA
<i>CVic20</i>	TCAGAAATATT	TGGTAAAAAAT	GG-----TT	GAT-----	-AATTATCTG	GAAGATAGAA
<i>Cvom15_2</i>	TCAGGATATT	TGGTGAGAAAT	GG-----TT	GAT-----	-AATTACCTG	GAAGATAGAA
<i>Cvom1_2</i>	TCAGGATATT	TGGTGAGAAAT	GG-----TG	GAT-----	-AATTACCTG	GAAGATAGAA
<i>CvomCvic.CRI1A.Con</i>	TCAGAAATATT	TGGTAAAAAAT	GG-----TT	GAT-----	-AATTATCTG	GAAGATAGAA
<i>Cvom7_2</i>	TTGATTTTGG	TGTCGGTAATC	AACCTTCTATC	GATTTATATC	GAGCTTTCTC	AGAAATCGCA
<i>Cvom7</i>	TTGCTTTTGG	TGTCGATAAT	AACCTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>Cvom6_2</i>	TTGCTTTTGG	TGTCGATAAT	AACCTTCTCTA	GACTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>Cvom2</i>	-----GG	TGTCGGTAAT	AACCTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>CVic27</i>	TTGCTTTTGG	TGTCATAAAT	AACCTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>CVic34</i>	TTGCTTTTGG	TGTCGGTAAT	AGCTTCTCTC	GATTTATATC	GATCTTT- -	- - - - ACCGCA
<i>Cvom8</i>	TTGCTTTTGG	TGTCGGTAAT	AA-----	- - - - -C	GAGCTTTCTC	AGAGATCGCA
<i>Cvom3_2</i>	TTGCTTTTGG	TGTCGATAAT	AACCTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>Cvom2_2</i>	TTGCTGTTGG	TGTCGGTAAT	AATTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>CVic24</i>	TTGCTTTTGG	TGTCGGTAAT	AATTTCTCTC	GATTTATATC	GAACCTTCTC	AGAGATCGCA
<i>CVic10</i>	TTGCTTTTGG	TGTCGGTAAT	AGCTTCTCTC	GATTTATATC	GAGTTTCTC	AGAAATCGCA
<i>CVic16</i>	TTGCTTTTGG	TGTCGGTAAT	AGCTTCTCTC	GATTTATATC	GAGTTTCTC	AGAAATCGCA
<i>CVic8</i>	TTGCTTTTGG	TGTCGGTAAT	AGCTTCTCTC	GATTTATATC	GAGTTTCTC	AGAAATCGCA
<i>CVic1</i>	TTGCTTTTGG	TGTCGGTAAT	AACCTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>CVic14</i>	TTGCTTTTGG	TGTTGGTAAT	AACCTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>CVic15</i>	TTGCTTTTGG	TGTTGGTAAT	AACCTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>CVic31</i>	TTGCTTTTGG	TGTTGGTAAT	AAATTTCTGTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>CvomCvic.CRI1B1.Con</i>	TTGCTTTTGG	TGTCGGTAAT	AACCTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>Cvom10_2</i>	CTGTTTTTGG	TGTCGCTAAT	TACTTCTCTC	GATTTATATC	GAGCTTTCTT	AGAGATCGCA
<i>CVic22</i>	TTGCTTTTGG	TGTCGGTAAC	GACTTCTCTC	GATTTATATC	GAGCTTTTCT	AGAGATCGCA
<i>Cvom5_2</i>	TTGCTTTTGG	TGTCGGTAAT	ATCTTCTCTC	GATTTATATC	GAGGTTTCTC	AGAGATCGCA
<i>Cvom8_2</i>	TTGCTTTTGA	TGTCGGTAAT	GCCTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>Cvom5</i>	CTGCTTTTGG	TGTCGGTAAT	GACTTCTCTC	GATTTATATC	GAGCCTTCTC	AGAGATCGCA
<i>Cvom4</i>	TTGCTTTTGG	TGTCGGTAAT	GACTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>Cvom3</i>	TTGCTTTTGG	TGTCGGTAAT	GACTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>Cvom11_2</i>	TTGCTTTTGG	TGTCGGTAAT	GACTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>CVic11</i>	TTGCTTTTGG	TGTCGGTAAT	GACTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>CVic33</i>	TTGCTTTTGG	TGTCGGTAAT	GACTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>Cvom14_2</i>	TTGCTTTTGG	-----	-----	-----	-----	-----
<i>Cvom16</i>	TTGCTTTTGG	TGTCGGTAAT	GACTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>CVic32</i>	TTTCTTTTGG	TATCGGTAAC	GACTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>CVic30</i>	-----	-----TAAC	GACTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>CvomCvic.CRI1B2.Con</i>	TTGCTTTTGG	TGTCGGTAAT	GACTTCTCTC	GATTTATATC	GAGCTTTCTC	AGAGATCGCA
<i>CVic12r</i>	TCCTTGAATA	TGA- - TACTG	AAGATGGAAT	- - - - -AAAA	AGCTACGAAG	TGACAGCT
<i>CVic21</i>	TCCTTGAATA	TGA- - TACTG	AAGATGGAAT	- - - - -AAAA	AGCTACGAAG	TGACAGCT
<i>CVic26</i>	TCCTTGAATA	TGA- - TACTG	AAGATGGAAT	- - - - -AAAA	AGCTACGAAG	TGACAGCT
<i>CVic29</i>	TCCTTGAATA	TGA- - TACTG	AAGATGGAAT	- - - - -AAAA	AGCTACGAAG	TGACAGCT
<i>CVic7</i>	TCCTTGAATA	TGA- - TACTG	AAGATGGAAT	- - - - -AAAA	AGCTACGAAG	TGACAGCT
<i>CVic20</i>	TCCTTGAATA	TGA- - TACTG	AAGATGGAAT	- - - - -AAAA	AGCTACGAAG	TGACAGCT
<i>Cvom15_2</i>	CCCTTGAATA	TGA- - TACTG	AAGATGGAAT	- - - - -AAAA	AGCTACGAAG	TGACAGCT
<i>Cvom1_2</i>	TCCTTGAATA	TGA- - TACTG	AAGATGGAAT	- - - - -AAAA	AGCTACGAAG	TGACAGCT
<i>CvomCvic.CRI1A.Con</i>	TCCTTGAATA	TGA- - TACTG	AAGATGGAAT	- - - - -AAAA	AGCTACGAAG	TGACAGCT
<i>Cvom7_2</i>	CT- - - - -ATA	CGAGTTGTTA	TAGATGGGAT	CTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>Cvom7</i>	CA- - - - -ATA	CGAGTTGTTA	TAGACGGAAT	TTCATTAAC	GAGTTCAAGA	TCAATTCA
<i>Cvom6_2</i>	CT- - - - -ATA	CGAATTGTTA	TAGATGGAAT	CTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>Cvom2</i>	CA- - - - -GTA	CGAGTTGTTA	TAGATGGAAT	CTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>CVic27</i>	CT- - - - -ATA	CGAGTTGTTA	TGGATGGAAT	TTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>CVic34</i>	CT- - - - -ATA	CGAGTTGTTA	TAGATGGAAT	TTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>Cvom8</i>	CT- - - - -ATA	CGAGTTGTTA	TAGATGGAAT	CTCATCAAAC	GAGTTCAATA	TCAACTCA
<i>Cvom3_2</i>	CT- - - - -ATA	CGAGTTGTTA	TAGATGGAAT	CTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>Cvom2_2</i>	CT- - - - -ATA	CGAGTTGTTA	TAGATGGAAT	CTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>CVic24</i>	CT- - - - -ATA	CGAGTTGTTA	TAGATGGAAT	CTCATCAAAC	AAGTTCAAGA	TCAATTCA
<i>CVic10</i>	CT- - - - -ATA	CGAGTTGTTA	TAGATGGAAT	CTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>CVic16</i>	CT- - - - -ATA	CGAGTTGTTA	TAGATGGAAT	CTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>CVic8</i>	CT- - - - -ATA	CGAGTTGTTA	TAGATGGAAT	CTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>CVic1</i>	CT- - - - -ATG	CGAGTTGTTA	TAGATGGAAT	TTCATCAAGC	GAGTTCAAGA	TCAATTCA
<i>CVic14</i>	CT- - - - -ATA	TGAGTTGTTA	TAGATGGAAT	TTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>CVic15</i>	CT- - - - -ATA	CGAGTTGTTA	TAGATGGAAT	TTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>CVic31</i>	CT- - - - -ATA	CGAGTTGTTA	TAGATGGAAT	TTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>CvomCvic.CRI1B1.Con</i>	CT- - - - -ATA	CGAGTTGTTA	TAGATGGAAT	CTCATCAAAC	GAGTTCAAGA	TCAATTCA
<i>Cvom10_2</i>	CT- - - - -ATA	CGAGTTATTG	TAGATGAGAT	CTCATCAAAT	GAGTTCAAAA	TTAATTCA
<i>CVic22</i>	CT- - - - -ATA	CGAATTGTTG	TAGATAGGAT	CTCATCAAAT	GAGTTCAAGA	TTAATTCA
<i>Cvom5_2</i>	CT- - - - -TTA	CGATTTGTTG	TAGATGGGAT	CT- - - - -	GAGCTCAAGA	TTAATTCA
<i>Cvom8_2</i>	CT- - - - -ATA	CGAGTTGTTG	TAGATGGGAT	CTCATCAAAT	GAGTTCAAGA	TTAATGCA
<i>Cvom5</i>	CT- - - - -ATA	CGAGTTGTTG	TAGATGGGAT	CTCATCAAAT	GAGTTCAAGA	TTAATTCA
<i>Cvom4</i>	CT- - - - -ATA	CGAGTTGTTG	TAGATGGGAT	CTCATCAAAT	GAGTTCAAGA	TTAATTCA
<i>Cvom3</i>	CT- - - - -ATA	CGAGTTGTTG	TAGATGGGAT	CTCATCAAAT	GAGTTCAAGA	TTAATTCA
<i>Cvom11_2</i>	CT- - - - -ATA	CGAGTTGTTG	TAGATGGGAT	CTCATCAAAT	GAGTTCAAGA	TTAATTCA
<i>CVic11</i>	CT- - - - -ATA	CGAGTTGTTG	TAGATGGGAT	CTCATCAAAT	GAGTTCAAGA	TTAATTCA
<i>CVic33</i>	CT- - - - -ATA	CGAGTTGTTG	TAGATGGGAT	CTCATCAAAT	GAGTTCAAGA	TTAATTCA
<i>Cvom14_2</i>	-----	-----TGTTG	TAGATGGGAT	CTCATCAAAT	AAGTTCAAGA	TTAATTCA
<i>Cvom16</i>	CT- - - - -ATA	CGAGTTGTTG	TAGATGGGAT	CTCATCAAAT	GAGTTCAAGA	TTAATTCA
<i>CVic32</i>	CT- - - - -ATA	AGATTTGTTG	TAGATGGGAT	CTCATCAAAT	GAGTTCAAGA	TTAATTCA
<i>CVic30</i>	CT- - - - -ATA	CGAGTTGTTG	TAGATGGGAT	CTCATCAAAT	GAGTTCAAGA	TTAATTCA
<i>CvomCvic.CRI1B2.Con</i>	CT- - - - -ATA	CGAGTTGTTG	TAGATGGGAT	CTCATCAAAT	GAGTTCAAGA	TTAATTCA

Supplemental Figure 1 Sequences obtained from *C.vom/C.vic* clones alongside consensus clusters

Lser6_2	CATATCCATG	CTGATGCTGA	AACACCTTGG	CGTACGGGAA	GTCGAGTACT	TGACAATGGT
Lser7	CATATCCATG	CTGATGCTGA	AACACCTTGG	CGTACGGGAA	GTCGAGTACT	TGACAATGGT
Lser5	CATATCCATG	CTGATGCTGA	AACACCTTGG	CGTACGGGAA	GTCGAGTACT	TGACAATGGT
Lser.CRI1A1.Con	CATATCCATG	CTGATGCTGA	AACACCTTGG	CGTACGGGAA	GTCGAGTACT	TGACAATGGT
Lser7_2	CATATCCATG	CAGATGCTGA	GACTCCTTGG	CGAACGTGGA	GTCGAGTACT	TGACAATGGT
Lser10_2	CATATCCATG	CTGATGCTGA	AACACCTTGG	CGAACGGGGA	GTCGAGTACT	TGACAATGGT
Lser3_2	CATATCCATG	CTGATGCTGA	AACACCTTGG	CGAACGGGGA	GTCGAGTACT	TGACAATGGT
Lser.CRI1A2.Con	CATATCCATG	CTGATGCTGA	AACACCTTGG	CGAACGGGGA	GTCGAGTACT	TGACAATGGT
Lser8_2	CATACCAAAAC	GCAGCTTTTA	AGCTCGCAAT	CAGGAAAAGTG	CCTAAATTAT	TTGCCGACCT
Lser6	-----	-----	-----	-----	-----	-----
Lser1	CATACCAAAAC	GCAGCTTTTA	AGCTCGCAAT	CAGGAAAAGTG	CCTAAATTAT	TTGCCGACCT
Lser9_2	CATACCAAAAC	GCAGCTTTTA	AGCTCGCAAT	CAGGAAAAGTG	CCTAAATTAT	TTGCCGACCT
Lser.CRI1B2.Con	CATACCAAAAC	GCAGCTTTTA	AGCTCGCAAT	CAGGAAAAGTG	CCTAAATTAT	TTGCCGACCT
Lser6_2	TTTAAACATG	TCAATAAGCA	GTCTGATAAT	ACCC---AAT	GCCTGGAAAA	GGGGTAGAGT
Lser7	TTTAAACATG	TCAATAAGCA	GTCTGATAAT	ACCC---AAT	GCCTGGAAAA	GGGGTAGAGT
Lser5	TTTAAACATG	TCAATAAGCA	GTCTGATAAT	ACCC---AAT	GCCTGGAAAA	GGGGTAGAGT
Lser.CRI1A1.Con	TTTAAACATG	TCAATAAGCA	GTCTGATAAT	ACCC---AAT	GCCTGGAAAA	GGGGTAGAGT
Lser7_2	TTTAAACCTG	TCAATGAGCA	GCCTGATAAT	ACCC---AAT	GCCTGGAAAA	AGGGTAGAGT
Lser10_2	CTTAAACCTG	CCAATGAGCA	GCCTGATAAT	ACCC---AAT	GCCTGGAAAA	GGGGTAGAGT
Lser3_2	CTTAAACCTG	TCAATGAGCA	GCCTGATAAT	ACCC---AAT	GCCTGGAAAA	AGGGTAGAGT
Lser.CRI1A2.Con	TTTAAACATG	TCAATGAGCA	GCCTGATAAT	ACCC---AAT	GCCTGGAAAA	AGGGTAGAGT
Lser8_2	GTTTAACCAA	GTCTTGAGGG	AATGTATTTT	CCCA---GAC	CCCTGGAAGA	AACAGACACT
Lser6	-----	-----GGGAA	AAGGTATTTT	CCCCATGACC	CCTTGGAAGA	AACAGACACT
Lser1	GTTTAACCAA	TGCTCGAGGG	AAGGTATTTT	CCCA---GAC	CCCTGGAAGA	AACAGACACT
Lser9_2	GTTTAACCAA	TGCTTGAGGG	AAGGTATTTT	CCCA---GAC	CCCTGGAAGA	AACAGACACT
Lser.CRI1B2.Con	GTTTAACCAA	TGCTTGAGGG	AAGGTATTTT	CCCA---GAC	CCCTGGAAGA	AACAGACACT
Lser6_2	CATCCCCATA	CTGAAACCAG	GGC-----	---GGATCG	ACAGAGGGTC	TATTCTACAG
Lser7	CATCCCCATA	CTGAAACCAG	GGC-----	---GGATCG	ACAGAGGGTC	TATTSTACAG
Lser5	CATCCCCATA	CTGAAACCAG	GGC-----	---GGATCG	ACAGAGGGTC	TATTCTACAG
Lser.CRI1A1.Con	CATCCCCATA	CTGAAACCAG	GGC-----	---GGATCG	ACAGAGGGTC	TATTCTACAG
Lser7_2	CATCCCCATA	CTGAAACCAG	GGAAG-----	---AACGCG	ACAGAGGGTC	AATCTACAG
Lser10_2	CATCCCCGATA	CTGAAACCAG	GGAAG-----	---AACGCG	ACAGAGGGTC	AATCCTACAG
Lser3_2	CATCCCCGATA	CTGAAACCAG	GGAAG-----	---AACGCG	ACAGAGGGTC	AAACCTACAG
Lser.CRI1A2.Con	CATCCCCATA	CTGAAACCAG	GGAAG-----	---AACGCG	ACAGAGGGTC	AATCCTACAG
Lser8_2	GGTACTAATC	CAAAAAACCAA	ATAAACCTAT	TGATGAGCCG	TCGT-----	---CGTACAG
Lser6	GGTACTAATC	CAAAAAACCAA	ATAAACCTAT	TGGTGACCCG	TCGT-----	---CGTACAG
Lser1	GGTACTAATC	CAAAAAACCAA	ATAAACCTAT	TTTTGACCCG	TCGT-----	---CGTACAG
Lser9_2	GGTACTAATC	CAAAAAACCAA	ATAAACCTAT	GGT-GACCCG	TCGT-----	---CGTACAG
Lser.CRI1B2.Con	GGTACTAATC	CAAAAAACCAA	ATAAACCTAT	TGTTGACCCG	TCGT-----	---CGTACAG
Lser6_2	GCCGATTTCC	CTCCTGCCAC	CAGTCGCGAA	GACTCTTGAG	GCTCTCCTCC	TCCCCAGTT
Lser7	GCCGATTTCC	CTCCTGCCAC	CAGTCGCGAA	GACTCTTGAG	GCTCTCCTCC	TCCCCAGTT
Lser5	GCCGATTTCC	CTCCTGCCAC	CAGTCGCGAA	GACTCTTGAG	GCTCTCCTCC	TCCCCAGTT
Lser.CRI1A1.Con	GCCGATTTCC	CTCCTGCCAC	CAGTCGCGAA	GACTCTTGAG	GCTCTCCTCC	TCCCCAGTT
Lser7_2	GCCGATTTCC	CTCCTGTAC	CAGTCGCGAA	GACTCTTGAG	GCGCTCCTCC	TCCCCAGTT
Lser10_2	GCCGATTTCC	CTCCTGTAC	CAGTCGCGAA	GAGTCTTGAG	GCGCTCCTCC	TCCCCAGTT
Lser3_2	GCCGATTTCC	CTCCTGTAC	CAGTCGCGAA	GACTCTTGAG	GCGCTCCTCC	TCCCCAGTT
Lser.CRI1A2.Con	GCCGATTTCC	CTCCTGTAC	CAGTCGCGAA	GACTCTTGAG	GCGCTCCTCC	TCCCCAGTT
Lser8_2	ACCAATATGT	CTACTGGACA	CAATAGGGAA	ACTACTGGAG	AAAAATAAT	ACAGTCGCTT
Lser6	ACCAATATGT	CTACTGGACA	CAATAGGGAA	ACTACTGGAG	AAAAATAAT	ACAGTCGCTT
Lser1	ACCAATATGT	CTACTGGACA	CAATAGGGAA	ACTACTGGAG	AAAAATAAT	ACAGTCGCTT
Lser9_2	ACCAATATGT	CTACTGGACA	CAATAGGGAA	ACTACTGGAG	AAAAATAAT	ACAGTCGCTT
Lser.CRI1B2.Con	ACCAATATGT	CTACTGGACA	CAATAGGGAA	ACTACTGGAG	AAAAATAAT	ACAGTCGCTT
Lser6_2	--GTCCAGTC	ATC-----CA	ACAGCAGCT-	-----CGC	CATCAT----	-----
Lser7	--GTCCAGTC	ATC-----CA	ACAGCAGCT-	-----CGC	CATCAT----	-----
Lser5	--GTCCAGTC	ATC-----CA	ACAGCAGCT-	-----CGC	CATCAT----	-----
Lser.CRI1A1.Con	--GTCCAGTC	ATC-----CA	ACAGCAGCT-	-----CGC	CATCAT----	-----
Lser7_2	--GTCTTGCC	ATC-----TA	ACAACAGCTC	G-----CCAC	CAGCATGGAT	TCCGTAAGAT
Lser10_2	--GTCTTGCC	ATC-----TT	ATAGCAGCTC	G-----CCAC	CAGCATGGAT	TCCGTAAGAT
Lser3_2	--GTCTTGCC	ATC-----TT	ACAGCAGCTC	G-----CCAC	CAGCATGGAT	TCCGTAAGAT
Lser.CRI1A2.Con	--GTCTTGCC	ATC-----TA	ACAGCAGCTC	G-----cCAC	CAGCATGGAT	TCCGTAAGAT
Lser8_2	GTTACCAATC	GTTGAAGCGA	AAAACGGTCT	GTCAAAGCTAC	CAATATGGCT	TTCGTAAGGC
Lser6	GTTACCAATC	GTTGAAGCGA	AAAACGGTCT	GTCAAAGCTAC	CAATATGGCT	TTCGTAAGGC
Lser1	GTTACCAATC	GTTGAAGCGA	AAAACGGTCT	GTCAAAGCTAC	CAATATGGCT	TTCGTAAGGC
Lser9_2	GTTACCAATC	GTTGAAGCGA	AAAACGGTCT	GTCAAAGCTAC	CAATATGGCT	TTCGTAAGGC
Lser.CRI1B2.Con	GTTACCAATC	GTTGAAGCGA	AAAACGGTCT	GTCAAAGCTAC	CAATATGGCT	TTCGTAAGGC
Lser6_2	-----	-----	-----TAAC	CGCCATAAACC	ACTCAGATCT	CATAGGGCTT
Lser7	-----	-----	-----TAAC	CGCCATAAACC	ACTCAGATCT	CATAGGGCTT
Lser5	-----	-----	-----TAAC	CGCCATAAACC	ACTCAGATCT	CATAGGGCTT
Lser.CRI1A1.Con	-----	-----	-----TAAC	CGCCATAAACC	ACTCAGATCT	CATAGGGCTT
Lser7_2	GC-----	-----A	CAGCATTTAAC	CGCCATAAACC	GCTCAGATCT	CACAAGGCTT
Lser10_2	GACAGCAC-	-----CACCT	CAGCATTTAAC	CGCCATAAACC	ACTCAGATCT	CACAAGGCTT
Lser3_2	GACAGCAC-	-----CACCT	CAGCATTTAAC	CGCCATAAACC	ACTCAGATCT	CACAAGGCTT
Lser.CRI1A2.Con	GACAGCAC-	-----CACCT	CAGCATTTAAC	CGCCATAAACC	ACTCAGATCT	CACAAGGCTT
Lser8_2	AAGATCAACC	ATAGACGCAA	TCCATATGGT	CACGGAACA	GCACAAAAGG	CAA-----TA
Lser6	AAGATCAACC	ATAGACGCAA	TTCATATGGT	CACGGAACA	GCACAAAAGG	CAA-----TA
Lser1	AAGATCAACC	ATAGACGCAA	TTCATATGGT	CACGGAACA	GCACAAAAGG	CAA-----TA
Lser9_2	AAGATCAACC	ATAGACGCAA	TTCATATGGT	CACGGAACA	GCACAAAAGG	CAA-----TA
Lser.CRI1B2.Con	AAGATCAACC	ATAGACGCAA	TTCATATGGT	CACGGAACA	GCACAAAAGG	CAA-----TA

<i>Cmac15</i>	AATCTCCATG	CTAATGCTGA	AGAAATCTTGG	CGAGCGGGGA	GTAGAATATT	TGACAATGGT
<i>Cmac1</i>	AATCTCCATG	CTAATGCTGA	AAAATCTTGG	CGAGCGGGGA	GTAGAATATT	TGACAATGGT
<i>Cmac5</i>	AATCTCCATG	CTAATGCTGA	AAAACTTGG	CGAGCGGGGA	GTAGAATATT	TGACAATGGT
<i>Cmac2</i>	AATCTCCATG	CTAATGCACA	AAAATCTTGG	CGAGCGGGGA	GTAGAATACT	TGACAATGGT
<i>Cmac4</i>	AATCTCCATG	CTAATGCTAA	AAAACCTTGG	CGAGCGGGGA	GTAGAATACT	TGACAATGGT
<i>Cmac7</i>	AATCTCCATG	CTAATGCTAA	AAATACCTTGG	CGAGCGGGGA	GTAGAATACT	TGACAATGGT
<i>Cmac8</i>	AATCTCCATG	CTAATGCTAA	AAAACCTTGG	CGAGCGGGGA	GTAGAATACT	TGACAATGGT
<i>Cmac9</i>	GATCTCCATG	CTAATGCTAA	AAAACCTTGG	CGAGCGGGGA	GTAGAATACT	TGACAATGGT
<i>Cmac.CRIA.Con</i>	AATCTCCATG	CTAATGCTAA	AAAACCTTGG	CGAGCGGGGA	GTAGAATACT	TGACAATGGT
<i>Cmac15</i>	ATTTAATCTG	TCAATTAAGA	GCTTAGTAAT	ACCCAATGCC	TGGAAATCGG	GTAGAGTCAT
<i>Cmac1</i>	ATTTAACCTG	TCAATTAAGA	GCTTAGTAAT	ACCCAACGCC	TGGAAATCGG	GTAGAGTCAT
<i>Cmac5</i>	TTTTAACCTG	TCAATTAGGA	GCTTGATAAT	ACCCAACGCC	TGGAAATCGG	GTAGAGTCAT
<i>Cmac2</i>	TTTTAACCTG	TCAATTAGGA	GCTTGATAAT	ACCCAACGCC	TGGAAATCGG	GTAGAGTCAT
<i>Cmac4</i>	TTTTAACCTG	TCAATTAGGA	GCTTGATAAT	ACCCAACGCC	TGGAAATCGG	GTAGAGTCAT
<i>Cmac7</i>	TTTTAACCTG	TCAATTAGGA	GCTTGATAAT	ACCCAACGCC	TGGAAATCGG	GTAGAGTCAT
<i>Cmac8</i>	TTTTAACCTG	TCAATTAGGA	GCTTGATAAT	ACCCAACGCC	TGGAAATCGG	GTAGAGTCAT
<i>Cmac9</i>	TTTTAACCTG	TCAATTAGGA	GCTTGATAAT	ACCCAACGCC	TGGAAATCGG	GTAGAGTCAT
<i>Cmac.CRIA.Con</i>	TTTTAACCTG	TCAATTAGGA	GCTTGATAAT	ACCCAACGCC	TGGAAATCGG	GTAGAGTCAT
<i>Cmac15</i>	CCCAATTTTG	AAACCAGGGA	AAGACGCGAA	CAAGGGTTTA	TATTACAGGT	CGATATCCCT
<i>Cmac1</i>	CCCAATTTTG	AAACCAGGGA	AAGACGCGAG	CGAGGGTTTA	TCGTACAGGC	CGATATCCCT
<i>Cmac5</i>	CCCAATTTTG	AAACCAGGGA	AAGACGCGAG	CGAGGGTTTA	TCGTACAGGC	CGATATCCCT
<i>Cmac2</i>	CCCAATTTTG	AAACCAGGGA	AAGACGCGAG	CGAGGGTTTA	TCGTACAGGC	CGATATCCCT
<i>Cmac4</i>	CCCAATTTTG	AAACCAGGGA	AAGACGCGAG	CGAGGGTTTA	TCGTACAGGC	CGATATCCCT
<i>Cmac7</i>	CCCAATTTTG	AAACCAGGGA	AAGACGCGAG	CGAGGGTTTA	TCGTACAGGC	CGATATCCCT
<i>Cmac8</i>	CCCAATTTTG	AAACCAGGGA	AAGACGCGAG	CGAGGGTTTA	TCGTACAGGC	CGATATCCCT
<i>Cmac9</i>	CCCAATTTTG	AAACCAGGGA	AAGACGCGAG	CGAGGGTTTA	TCGTACAGGC	CGATATCCCT
<i>Cmac.CRIA.Con</i>	CCCAATTTTG	AAACCAGGGA	AAGACGCGAG	CGAGGGTTTA	TCGTACAGGC	CGATATCCCT
<i>Cmac15</i>	CTTATCACCA	GTCGCGAAGA	CTCTTGAGGC	TCTTCTACTC	CACCAGCTAA	ATCACCACCT
<i>Cmac1</i>	CTTATCACCA	GTCGCGAAGA	CTCTTGAGGC	TCTTTTACTC	CCCCAGCTAA	ATCACCACCT
<i>Cmac5</i>	CTTATCACCA	GTCGCGAAGA	CTCTTGAGGC	TCTTCTACTC	CCCCAGCTGA	ATCACCACCT
<i>Cmac2</i>	CTTATCACCA	GTCGCGAAGA	CTCTTGAGGC	TCTTCTACTC	CCCCAGCTGA	ATCACCACCT
<i>Cmac4</i>	CTTATCACCA	GTCGCGAAGA	CTCTTGAGGC	TCTTCTACTC	CCCCAGCTGA	ATCACCACCT
<i>Cmac7</i>	CTTATCACCA	GTCGCGAAGA	CTCTTGAGGC	TCTTCTACTC	CCCCAGCTGA	ATCACCACCT
<i>Cmac8</i>	CTTATCACCA	GTCGCGAAGA	CTCTTGAGGC	TCTTCTACTC	CCCCAGCTGA	ATCACCACCT
<i>Cmac9</i>	CTTATCACCA	GTCGCGAAGA	CTCTTGAGGC	TCTTCTACTC	CCCCAGCTGA	ATCACCACCT
<i>Cmac.CRIA.Con</i>	CTTATCACCA	GTCGCGAAGA	CTCTTGAGGC	TCTTCTACTC	CCCCAGCTGA	ATCACCACCT
<i>Cmac15</i>	TATAGCAGCT	CGCCACCAAC	TTGGATTCCG	TAAT - TGCAT	AGTACCACCA	CAGCATTAAAC
<i>Cmac1</i>	TATAGCAGCT	CGTCACCAGC	ATGGATTCCG	TAGTATGTCAT	AG - - CACCA	CAGCATTAAAC
<i>Cmac5</i>	TATAGCAGCT	CGTCACCAGC	ATGGATTCCG	TAATATGTCAT	AGTACCACCA	CAGCATTAAAC
<i>Cmac2</i>	TATAGCAGCT	CGTCACCAGC	ATGGATTCCG	TAATATGTCAT	AGTACCACCA	CAGCATTAAAC
<i>Cmac4</i>	TATAGCAGCT	CGCCACCAAC	ATGGATTCCG	TAATATGTCAT	AGTACCACCA	CAGCATTAAAC
<i>Cmac7</i>	TATAGCAGCT	-----	-----	-----	-----	-----
<i>Cmac8</i>	TATAGCAGCT	CGTCACCAGC	ATGGATTCCG	TAATATGTCAT	AGTACCACCA	CAGCATTAAAC
<i>Cmac9</i>	TATAGCAGCT	CGTCACCAGC	ATGGATTCCG	TAATATGTCAT	AGTACCACCA	CAGCATTAAAC
<i>Cmac.CRIA.Con</i>	TATAGCAGCT	CGTCACCAGC	ATGGATTCCG	TAATATGTCAT	AGTACCACCA	CAGCATTAAAC
<i>Cmac15</i>	GACCGTATCC	AATCAAAATAG	CCCATGGTTT	GAACCAGCAG	AGACCATGTG	AGCGAACCAAT
<i>Cmac1</i>	GACCGTATCC	ACTCAAAATAG	CCCATGGTTT	GAACCAGCAG	AGACCGTGTG	AGCGAACCAAT
<i>Cmac5</i>	GACCGTATCC	ACTCAAAATAG	CCCATGGTTT	GAACCAGCAG	AGACCGTGTG	AGCGAACCAAT
<i>Cmac2</i>	GACCGTATCC	ACTCAAAATAG	CCCACGGTTT	GAACCAGCAG	AGACCGTGTG	AGCGAACCAAT
<i>Cmac4</i>	GACCGTATCC	ACTCAAAATAG	CCCATGGTTT	GAACCAGCAG	AGACCGTGTG	AGCGAACCAAT
<i>Cmac7</i>	-----	-----	-----	-----	-----	-----
<i>Cmac8</i>	GACCGTATCC	ACTCAAAATAG	CCCATGGTTT	GAACCAGCAG	AGACCGTGTG	AGCGAACCAAT
<i>Cmac9</i>	GACCGTATCC	ACTCAAAATAG	CCCATGGTTT	GAACCAGCAG	AGACCGTGTG	AGCGAACCAAT
<i>Cmac.CRIA.Con</i>	GACCGTATCC	ACTCAAAATAG	CCCATGGTTT	GAACCAGCAG	AGACCGTGTG	AGCGAACCAAT
<i>Cmac15</i>	CCTTGTTGGCA	CTTGACCTGT	CAAAAAGCATT	TGACACAGTC	AGCCATACTG	TACTCTTTCCA
<i>Cmac1</i>	CCTTGTTGGCA	CTTAACCTGA	CAAAAAGCATT	TGACACGGTC	AGCCATACTG	TACTCTTTCCA
<i>Cmac5</i>	CCTTGTTGGCA	CTTGACCTGT	CAAAAAGCATT	TGACACAGTC	AGCCATACTG	TACTCTTTCCA
<i>Cmac2</i>	CCTTGTTGGCA	CTTGACCTGT	CAAAAAGCATT	TGACACAGTC	AGCCATACTG	TACTCTTTCCA
<i>Cmac4</i>	CCTTGTTGGCA	CTTGACCTGT	CAAAAAGCATT	TGACACGGTC	AGCCACACAG	TACTCTTTCCA
<i>Cmac7</i>	-----	-----	-----	-----	-----	-----
<i>Cmac8</i>	CCTTGTTGGCA	CTTGACCTGT	CAAAAAGCATT	TGACACGGTC	AGCCACACAG	TACTCTTTCCA
<i>Cmac9</i>	CCTTGTTG - -	- - - ACCTGT	CAAAAAGCATT	TGACACGGTC	AGCCACACAG	TACTCTTTCCA
<i>Cmac.CRIA.Con</i>	CCTTGTTGGCA	CTTGACCTGT	CAAAAAGCATT	TGACACGGTC	AGCCAYACAG	TACTCTTTCCA
<i>Cmac15</i>	GGACATCCTG	CAGTCCTCCT	TGCCAAACTA	CACGAAGAGA	TGGATTGTGA	ATTATTTGAG
<i>Cmac1</i>	GGACATGCTG	CAGTCCTCCT	TGCCAAACTA	CACGAAGAAA	TGGATAGTGA	ATTATTTGAG
<i>Cmac5</i>	GGACATCCTG	CAGTCCTCCT	TGCCGAACAA	CACGAAGAGA	TGGATTGTGA	ATTATTTGAG
<i>Cmac2</i>	GGACATCCCG	CAGTCCTCCT	TGCCGAACAA	CACGAAGAGA	TGGATTGTGA	ACTATTTTAG
<i>Cmac4</i>	GGACATCCTG	CAGTCCTCCT	TGCCGAACAA	CACGAAGAGA	TGGATTGTGA	ACTATTTGAG
<i>Cmac7</i>	-----	-----	-----	-----	-----	-----
<i>Cmac8</i>	GGACATCCTG	CAGTCCTCCT	TGCCGAACAA	CACGAAGAGA	TGGATTGTGA	ATTATTTGAG
<i>Cmac9</i>	GGACATCCTG	CAGTCCTCCT	TGCCGAACAA	CACGAAGAGA	TGGATTGTGA	ATTATTTGAG
<i>Cmac.CRIA.Con</i>	GGACATCCTG	CAGTCCTCCT	TGCCGAACAA	CACGAAGAGA	TGGATTGTGA	ATTATTTGAG

<i>Cmac15</i>	TGGAAGACAG	TCATTCGTTG	AGTTTCGAGA	CCGAAAGTCC	AAATCCCGTA	GAGTTAAAGA
<i>Cmac1</i>	AGGAAGACAG	TCATTCGTTG	AGTTTCGAGA	CCGAAAGTCC	AAAACCCGTA	GAGTTAAACA
<i>Cmac5</i>	TGGAAGACAG	TCATTCGTTG	AGTTTCGAGA	CCGAAAGTCC	AAAACCCGTA	GTGTTAAACA
<i>Cmac2</i>	TGGAAGACAG	TCATTCGTTG	AGTTTCGAGT	CCGAAAGTTC	AAAACCCGTA	GAGTTAAACA
<i>Cmac4</i>	CGGAAGACAG	TCATTCGTTG	AGTTTCGAGA	CCGAAAGTCC	AAAACCCGTA	GAGTTAAACA
<i>Cmac7</i>	-----	-----	-----	-----	-----	-----
<i>Cmac8</i>	CGGAAGACAG	TCATTCGTTG	AGTTTCGAGA	CCGAAAGTCC	AAAACCCGTA	GAGTTAAACA
<i>Cmac9</i>	CGGAAGACAG	TCATTCGTTG	AGTTTCGAGA	CCGATAGTCC	AAAACCCGTA	GAGTTAAACA
<i>Cmac.CRIA.Con</i>	HGGAAGACAG	TCATTCGTTG	AGTTTCGAGA	CCGAAAGTCC	AAAACCCGTA	GAGTTAAACA

Supplemental Figure 3 Sequences obtained from *C. macelleria* clones alongside consensus clusters

<i>PReg28</i>	TATCTTCTTC	TCC - TGGGCC	TGACGGGATC	CCAAATGAGA	TAATAACTTT	GGTTTGTGAA
<i>PReg3</i>	TATCTTCTTC	TCC - GGGTCC	GGACGGGATC	CCAAATGAGA	TAATAACTTT	GGTTTGTGAA
<i>PReg21</i>	TATCTTCTTC	TCC - TGGTCC	AGATGGGATC	CCAAATGAGA	TAATAACTTT	GGTTTGTGAA
<i>PReg18</i>	TATCTTCTTC	TCC - AGGGCC	AGACGGGATC	CCAAATGAGA	TAATAACTTT	GGTTTGTGAA
<i>PReg7</i>	TATCTTCTTC	TCCCMGGACC	AGATGGGATC	CCAAATGAGA	TAATAACTTT	GGTTTGTGAA
<i>Preg.Cr1A.Con</i>	TATCTTCTTC	TCC - NGGNCC	DGAYGGGATC	CCAAATGAGA	TAATAACTTT	GGTTTGTGAA
<i>PReg22r</i>	TATCTTCTTC	TCC - CGGACC	AGATGGGATA	CCCAATGAGG	TTATAAAATT	GGTAGGTGAG
<i>PReg27</i>	TATCTTCTTC	TCC - AGGTCC	AGACGGTATA	CCCAATGAGG	TTATAAAATT	GGTAGGTGAG
<i>PReg31</i>	TATCTTCTTC	TCC - AGGTCC	AGACGGTATA	CCCAATGAGG	TTATAAAATT	GGTAGGTGAG
<i>PReg8r</i>	-----	-----	-----	-----	-----	-----GAG
<i>PReg12r</i>	TATCTTCTTC	TCC - TGGACC	AGATGGGATA	CCCAATGAGG	TTATAAAATT	GGTAGGTGAG
<i>Preg.Cr1B.Con</i>	TATCTTCTTC	TCC - NGGWCC	AGAYGGGATA	CCCAATGAGG	TTATAAAATT	GGTAGGTGAG
<i>PReg29</i>	TATCTTCTTC	TCC - TGGACC	GGACGGACTC	TCACCTTAGGT	TACTAAAACT	AATTTT - - - -
<i>PReg17</i>	TATCTTCTTC	TCC - TGGACC	GGACGGACTC	TCACCTTAGGT	TACTAAAACT	AATTTT - - - -
<i>PReg20</i>	TATCTTCTTC	TCC - GGGACC	GGACGGACTC	TCACCTTAGGT	TCCTAAAACT	AATTTT - - - -
<i>Preg.Cr1C.Con</i>	TATCTTCTTC	TCC - KGGACC	GGACGGACTC	TCACCTTAGGT	TACTAAAACT	AATTTT - - - -
<i>PReg28</i>	AATTGGCCAG	ATTTGTTTAA	AGAGACATTC	AACATGTGTC	TGAGAAATGGG	TACC - - - - -
<i>PReg3</i>	AATTGGCCAG	ATTTGTTTAA	AGAGACATTC	AACATGTGTC	TGAGAAATGGG	TACC - - - - -
<i>PReg21</i>	AATTGGCCAG	ATTTGTTTAA	AGAGACATTC	AACATGTGTC	TGAGAAATGGG	TACC - - - - -
<i>PReg18</i>	AATTGGCCAG	ATTTGTTTAA	AGAGACATTC	AACATGTGTC	TGAGAAATGGG	TACC - - - - -
<i>PReg7</i>	AATTGGCCAG	ATTTGTTTAA	AGAGACATTC	AACATGTGTC	TGAGAAATGGG	TACC - - - - -
<i>Preg.Cr1A.Con</i>	AATTGGCCAG	ATTTGTTTAA	AGAGACATTC	AACATGTGTC	TGAGAAATGGG	TACC - - - - -
<i>PReg22r</i>	ATATGGCCCG	AATCATTAGT	CAGAATCTTT	AATTCATGCC	TAAAGGCCGG	TATC - - - - -
<i>PReg27</i>	ATATGGCCCG	AATCATTAGT	CAGAATCTTT	AATTCATGCC	TAAAGGCCGG	TATC - - - - -
<i>PReg31</i>	ATATGGCCCG	AATCATTAGT	CAGAATCTTT	AATTCATGCC	TAAAGGCCGG	TATC - - - - -
<i>PReg8r</i>	ATATGGCCCG	AATCATTAGT	CAGAATCTTT	AATTCATGCC	TAAAGGCCGG	TATC - - - - -
<i>PReg12r</i>	ATATGGCCCG	AATCATTAGT	CAGAATCTTT	AATTCATGCC	TAAAGGCCGG	TTTC - - - - -
<i>Preg.Cr1B.Con</i>	ATATGGCCCG	AATCATTAGT	CAGAATCTTT	AATTCATGCC	TAAAGGCCGG	TATC - - - - -
<i>PReg29</i>	- - - - - TA	CCTCATGTCT	TGCGACATTT	TACACATATT	TTTAAATAGTG	TTTTGACTTG
<i>PReg17</i>	- - - - - TA	CCTCATGTCT	TGCGACATTT	TACACATATT	TTTAAATAGTG	TTTTGACTTG
<i>PReg20</i>	- - - - - TA	CCTCATGTCT	TGCGACATTT	TACACATATT	TTCAATAGTG	TTTTGACTTG
<i>Preg.Cr1C.Con</i>	- - - - - TA	CCTCATGTCT	TGCGACATTT	TACACATATT	TTTAAATAGTG	TTTTGACTTG
<i>PReg28</i>	- - - - - TTT	CCTAGGATAT	GGAAGAGGCA	ATTTCTTGTT	TTGC - - - - TA	CGCAAAGGCG
<i>PReg3</i>	- - - - - TTT	CCTAGGATAT	GGAAGAGGCA	ACTTCTTGTT	TTGC - - - - TA	CGCAAAGGCG
<i>PReg21</i>	- - - - - TTT	CCTAGGATAT	GGAAGAGGCA	ATTTCTTGTT	TTGC - - - - TA	CGCAAAGGCG
<i>PReg18</i>	- - - - - TTT	CCTAGGATAT	GGAAGAGGCA	ATTTCTTGTT	TTGC - - - - TA	CGCAAAGGCG
<i>PReg7</i>	- - - - - TTT	CCTAGGATAT	GGAAGAGGCA	ATTTCTTGTT	TTGC - - - - TA	CGCAAAGGCG
<i>Preg.Cr1A.Con</i>	- - - - - TTT	CCTAGGATAT	GGAAGAGGCA	ATTTCTTGTT	TTGC - - - - TA	CGCAAAGGCG
<i>PReg22r</i>	- - - - - TTT	CCCGCTAGAT	GGAAGATACA	GAAATTAGTT	TTAC - - - - TA	CGAAAGGGAA
<i>PReg27</i>	- - - - - TTT	CCCGCTAGAT	GGAAGATACA	GAAATTAGTT	TTAC - - - - TA	CGAAAGGGAA
<i>PReg31</i>	- - - - - TTT	CCCGCTAGAT	GGAAGATACA	GAAATTAGTT	TTAC - - - - TA	CGAAAGGGAA
<i>PReg8r</i>	- - - - - TTT	CCCGCTAGAT	GGAAGATACA	GAAATTAGTT	TTAC - - - - TA	TGAAAGGGAA
<i>PReg12r</i>	- - - - - TTT	CCCGCTAGAT	GGAAGATACA	GAAATTAGTT	TTAC - - - - TA	CGAAAGGGAA
<i>Preg.Cr1B.Con</i>	- - - - - TTT	CCCGCTAGAT	GGAAGATACA	GAAATTAGTT	TTAC - - - - TA	CGAAAGGGAA
<i>PReg29</i>	CTCTAAATAT	CCACAAGCCT	GGAATAATATC	AAGA - - - GTT	TTGCCCATTC	CCAAAATGAA
<i>PReg17</i>	CTCTAAATAT	CCACAAGCCT	GGAATAATATC	AAGA - - - GTT	TTGCCCATTC	CCAAAATGAA
<i>PReg20</i>	CTCTAAATAT	CCACAAGCCT	GGAATAATATC	AAGA - - - GTT	CTGCCCATTC	CCAAAATGAA
<i>Preg.Cr1C.Con</i>	CTCTAAATAT	CCACAAGCCT	GGAATAATATC	AAGA - - - GTT	TTGCCCATTC	CCAAAATGAA
<i>PReg28</i>	AGAAACCCCT	CGACAATCCT	TCTTCATATA	GGCCGATATG	CCTACTGAAC	ACTTGTGGAA
<i>PReg3</i>	AGAAACCCCT	CGACAATCCT	TCTTCATATA	GGCCGATATG	CCTACTGAAC	ACTTGTGGAA
<i>PReg21</i>	AGAAACCCCT	CGATAATCCT	TCTTCATATA	GGCCGATATG	CCTACTGAAC	ACTTGTGGAA
<i>PReg18</i>	AGAAACCCCT	CGATAATCCT	TCTTCATATA	GGCCGATATG	CCTACTGAAC	ACTTGTGGAA
<i>PReg7</i>	AGAAACCCCT	CGATAATCCT	TCTTCATATA	GACCGATATG	CCTACTGAAC	ACTTGTGGAA
<i>Preg.Cr1A.Con</i>	AGAAACCCCT	CGATAATCCT	TCTTCATATA	GGCCGATATG	CCTACTGAAC	ACTTGTGGAA
<i>PReg22r</i>	ATAAACCAATT	GAATGAACCT	AGTACTTATA	GGCCGCTTTG	CATGTTGGAT	TCATTAGGAA
<i>PReg27</i>	ATAAACCAATT	GAATGAACCT	AGTACTTATA	GGCCGCTTTG	CATGTTGGAT	TCATTAGGAA
<i>PReg31</i>	ATAAACCAATT	GAATGAACCT	AGTACTTATA	GGCCGCTTTG	CATGTTGGAT	TCATTAGGAA
<i>PReg8r</i>	ATAAACCAATT	GAATGAACCT	AGTACTTATA	GGCCGCTTTG	CATGTTGGAT	TCATTAGGAA
<i>PReg12r</i>	ATAAACCAATT	GAATGAACCT	AGTACTTATA	GGCCGCTTTG	CATGTTGGAT	TCATTAGGAA
<i>Preg.Cr1B.Con</i>	ATAAACCAATT	GAATGAACCT	AGTACTTATA	GGCCGCTTTG	CATGTTGGAT	TCATTAGGAA
<i>PReg29</i>	AAACGCGACA	CTC - - - TGT	AGTGAATATC	GTCCGATCTG	TATTGTATCT	GATATGTTCTA
<i>PReg17</i>	AAACGCGACA	CTC - - - TGT	AGTGAATATC	GTCCGATCTG	TATTGTATCT	GATATGTTCTA
<i>PReg20</i>	AAACGCGACA	CTC - - - TGT	AGTGAATATC	GTCCGATCTG	TATTGTATCT	GATATGTTCTA
<i>Preg.Cr1C.Con</i>	AAACGCGACA	CTC - - - TGT	AGTGAATATC	GTCCGATCTG	TATTGTATCT	GATATGTTCTA

PReg28	AGTTTCTGGA	GAAATTGATA	ACAAAGAGAC	TAGAGGCGGA	AATTGAAGGA	AAGGGTGGAT
PReg3	AGTTTCTGGA	GAAACTGATA	ACAAAGAGAC	TAGAGGCGGA	AATTGAAGGA	AAGGGTGGAT
PReg21	AGTTTCTGGA	GAAACTGATA	ACAAAGAGAC	TAGAGGCGGA	AATTGAAGGA	AAGGGTGGAT
PReg18	AGTTTCTGGA	GAAACTGATA	ACAAAGAGAC	TAGAGGCGGA	AATTGAAGGA	AAGGGTGGAT
PReg7	AGTTTCTGGA	GAAACTGATA	ACAAAGAGAC	TAGAGGCGGA	AATTGAAGGA	AAGGGTGGAT
Preg.Cr1A.Con	AGTTTCTGGA	GAAACTGATA	ACAAAGAGAC	TAGAGGCGGA	AATTGAAGGA	AAGGGTGGAT
PReg22r	AACTCTTAGA	GTGTGTAATA	CTGAAACGGC	TAGAGGAAAA	CATAGATATC	CTTGGAGGAT
PReg27	AACTCTTAGA	GTGTGTAATA	CTGAAACGGC	TAGAGGAAAA	CATAGATATC	CTTGGAGGAT
PReg31	AACTCTTAGA	GTGTGTAATA	CTGAAACGGC	TAGAGGAAAA	CATAGATATC	CTTGGAGGAT
PReg8r	AACTCTTAGA	GTGTGTAATA	CTGAAACGGC	TAGAGGAAAA	CATAGATATC	CTTGGAGGAT
PReg12r	AACTCTTAGA	GTGTGTAATA	CTGAAACGGC	TAGAGGAAAA	CATAGATATC	CTTGGAGGAT
Preg.Cr1B.Con	AACTCTTAGA	GTGTGTAATA	CTGAAACGGC	TAGAGGAAAA	CATAGATATC	CTTGGAGGAT
PReg29	AGGTTTTTGA	AACATTAGTT	CATGATCAAA	TGTTAGGCTA	TATCAATGAA	AGAAATTTGT
PReg17	AGGTTTTTGA	AACATTAGTT	CATGATCAAA	TGTTAGGCTA	TATCAATGAA	AGAAATTTGT
PReg20	AGGTTTTTGA	AACATTAGTT	AAATGATCAAA	TGTTAGGCTA	TATCAATGAA	AGAAATTTGT
Preg.Cr1C.Con	AGGTTTTTGA	AACATTAGTT	AAATGATCAAA	TGTTAGGCTA	TATCAATGAA	AGAAATTTGT
PReg28	TCTCGCGAAT	GCAGTTTGGG	TTT - GTAAGG	GGAAGATCGA	CGATTGATGC	TATCCGGGAG
PReg3	TCTCGCGAAT	GCAGTTTGGG	TTT - GTAAGG	GGAAGATCGA	CGATTGATGC	TATCCGGGAG
PReg21	TCTCGCGAAT	GCAGTTTGGG	TTT - GTAAGG	GGAAGATCGA	CGATTGATGC	TATCCGGGAG
PReg18	TCTCGCGAAT	GCAGTTTGGG	TTT - GTAAGG	GGAAGATCGA	CGATTGATGC	TATCCGGGAG
PReg7	TCTCGCGAAT	GCAGTTTGGG	TTT - GTAAGG	GGAAGATCGA	CGATTGATGC	TATCCGGGAG
Preg.Cr1A.Con	TCTCGCGAAT	GCAGTTTGGG	TTT - GTAAGG	GGAAGATCGA	CGATTGATGC	TATCCGGGAG
PReg22r	TATCTCATA	GCAGCATGGT	TTTCGTAAAG	GGACGAGT - A	CAGTTGACGC	CATTAGCGAG
PReg27	TATCTCATA	GCAGCATGGT	TTTCGTAAAG	GGACGAGT - A	CAGTTGACGC	CATTAGCGAG
PReg31	TATCTCATA	GCAGCATGGT	TTTCGTAAAG	GGACGAGT - A	CAGTTGACGC	CATTAGCGAG
PReg8r	TATCTCATA	GCAGCATGGT	TTTCGTAAAG	GGACGAGT - A	CAGTTGACGC	CATTAGCGAG
PReg12r	TATCTCATA	GCAGCATGGT	TTTCGTAAAG	GGACGAGT - A	CAGTTGACGC	CATTAGCGAG
Preg.Cr1B.Con	TATCTCATA	GCAGCATGGT	TTTCGTAAAG	GGACGAGT - A	CAGTTGACGC	CATTAGCGAG
PReg29	TATCCGAAAT	CCAATCTGGT	TTTCAGACACC	GCCATAAC - A	CTACTGCCCC	TATGATTGAT
PReg17	TATCCGAAAT	CCAATCTGGT	TTTCAGACACC	GCCATAAC - A	CTACTGCCCC	TATGATTGAT
PReg20	TATCCGAAAT	CCAATCTGGT	TTTCAGACACC	GCCATAAC - A	CTACTGCCCC	TATGATTGAT
Preg.Cr1C.Con	TATCCGAAAT	CCAATCTGGT	TTTCAGACACC	GCCATAAC - A	CTACTGCCCC	TATGATTGAT
PReg28	GTAGTGAGTA	CTGCAGCTAG	CGCTATGAGA	T - GCATGAG	ATT - TTGTTC	CATTGTCAAC
PReg3	GTAGTGAGTA	CTGCAGCTAG	CGCTATGAGA	T - GCATGAG	ATT - TTGTTC	CATTGTCAAC
PReg21	GTAGTGAGTA	CTGCAGCTAG	CGCTATGAGA	T - GCCTGAG	ATT - TTGTTC	CATTGTCAAC
PReg18	GTAGTGAGTA	CTGCAGCTAG	CGCTATGAGA	T - GCATGAG	ATT - TTGTTC	CATTGTCAAC
PReg7	GTAGTGAGTA	CTGCAGCTAG	CGCTATGAGA	T - GCATGAG	ATT - TTGTTC	CATTGTCAAC
Preg.Cr1A.Con	GTAGTGAGTA	CTGCAGCTAG	CGCTATGAGA	T - GCATGAG	ATT - TTGTTC	CATTGTCAAC
PReg22r	GTTTGTAATA	AAGCAGTACA	AGC - AAAAAAC	A - GCGGGAG	AATAC TGCGC	GATAATAACA
PReg27	GTTTGTAATA	AAGCAGTACA	AGC - AAAAAAC	A - GCGGGAG	AATAC TGCGC	GATAATAACA
PReg31	GTTTGTAATA	AAGCAGTACA	AGC - AAAAAAC	A - GCGGGAG	AATAC TGCGC	GATAATAACA
PReg8r	GTTTGTAATA	AAGCAGTACA	AGC - AAAAAAC	A - GCGGGAG	AATAC TGCGC	GATAATAACA
PReg12r	GTTTGTAATA	AAGCAGTACA	AGC - AAAAAAC	A - GCGGGAG	AATAC TGCGC	GATAATAACA
Preg.Cr1B.Con	GTTTGTAATA	AAGCAGTACA	AGC - AAAAAAC	A - GCGGGAG	AATAC TGCGC	GATAATAACA
PReg29	ATATTACACG	AAGTGGGAGA	TGG - ATTAGA	TCAGCATAAAG	TT - CTGTGC	TATGAAAAGT
PReg17	ATATTACACG	AAGTGGGAGA	TGG - ATTAGA	TCAGCATAAAG	TT - CTGTGC	TATGAAAAGT
PReg20	ATATTACACG	AAGTGGGAGA	TGG - ATTAGA	TCAGCATAAAG	TT - CTGTGC	TATGAAAAGT
Preg.Cr1C.Con	ATATTACACG	AAGTGGGAGA	TGG - ATTAGA	TCAGCATAAAG	TT - CTGTGC	TATGAAAAGT
PReg28	TTGGACATTA	GGAACGCCTT	TAACCTCTGCG	GACTGGAATG	TCATTTGTCA	GACAATG - -
PReg3	TTGGACATTA	GGAACGCCTT	TAACCTCTGCG	GACTGGAATG	TCATTTGTCA	GACAATG - -
PReg21	TTGGACATTA	GGAACGCCTT	TAACCTCTGCG	GACTGGAATG	TCATTTGTCA	GACAATG - -
PReg18	TTGGACATTA	GGAACGCCTT	TAACCTCTGCG	GACTGGAATG	TCATTTGTCA	GACAATG - -
PReg7	TTGGACATTA	GGAACGCCTT	TAACCTCTGCG	GACTGGAATG	TCATTTGTCA	GACAATG - -
Preg.Cr1A.Con	TTGGACATTA	GGAACGCCTT	TAACCTCTGCG	GACTGGAATG	TCATTTGTCA	GACAATG - -
PReg22r	CTAGATGTCA	AAAACGCTTT	CAATACCGTG	AAATGGAAGG	TGGTACTAGA	TGCGTTTC - -
PReg27	CTAGATGTCA	AAAACGCTTT	CAATACCGTG	AAATGGAAGG	TGGTACTAGA	TGCGTTTC - -
PReg31	CTAGATGTCA	AAAACGCTTT	CAATACCGTG	AAATGGAAGG	TGGTACTAGA	TGCGTTTC - -
PReg8r	CTAGATGTCA	AAAACGCTTT	CAATACCGTG	AAATGGAAGG	TGGTACTAGA	TGCGTTTC - -
PReg12r	CTAGATGTCA	AAAACGCTTT	CAATACCGTG	AAATGGAAGG	TGGTACTAGA	TGCGTTTC - -
Preg.Cr1B.Con	CTAGATGTCA	AAAACGCTTT	CAATACCGTG	AAATGGAAGG	TGGTACTAGA	TGCGTTTC - -
PReg29	CTAGATTTCA	GTAGGGTATT	TGAAACCAATT	TCTCATGAAAG	TGCTACTAAA	TAAACTTTTT
PReg17	CTAGATTTCA	GTAGGGTATT	TGAAACCAATT	TCTCATGAAAG	TGCTACTAAA	TAAACTTTTT
PReg20	CTAGATTTCA	GTAGGGTATT	TGAAACCAATT	TCTCATGAAAG	TGCTACTAAA	TAAACTTTTT
Preg.Cr1C.Con	CTAGATTTCA	GTAGGGTATT	TGAAACCAATT	TCTCATGAAAG	TGCTACTAAA	TAAACTTTTT
PReg28	AGAGAGAGAG	GATTTTCAGG	ATATTTGATC	AACATTGTGG	ATGACTATCT	GCGGGACAGG
PReg3	AGAGAGAGAG	GATTTTCAGG	ATATTTGATC	AACATTGTGG	ATGACTATCT	GCGGGACAGG
PReg21	AGAGAGAGAG	GATTTTCAGG	ATATTTGATC	AACATTGTGG	ATGACTATCT	GCGGGACAGG
PReg18	AGAGAGAGAG	GATTTTCAGG	ATATTTGATC	AACATTGTGG	ATGACTATCT	GCGGGACAGG
PReg7	- - - AGAGAG	GATTTTCAGG	ATATTTGATC	AACATTGTGG	ATGACTATCT	GCGGGACAGG
Preg.Cr1A.Con	AGAGAGAGAG	GATTTTCAGG	ATATTTGATC	AACATTGTGG	ATGACTATCT	GCGGGACAGG
PReg22r	AAGAAGAAAA	GAGTGGACAA	CTATCTCTAC	AACATAATAG	CAGATTACCT	GGATAATAGA
PReg27	AAGAAGAAAA	GAGTGGACAA	CTATCTCTAC	AACATAATAG	CAGATTACCT	GGATAATAGA
PReg31	AAGAAGAAAA	GAGTGGACAA	CTATCTCTAC	AACATAATAG	CAGATTACCT	GGATAATAGA
PReg8r	AAGAAGAAAA	GAGTGGACAA	CTATCTCTAC	AACATAATAG	CAGATTACCT	GGATAATAGA
PReg12r	AAGAAGAAAA	GAGTGGACAA	CTATCTCTAC	AACATAATAG	CAGATTACCT	GGATAATAGA
Preg.Cr1B.Con	AAGAAGAAAA	GAGTGGACAA	CTATCTCTAC	AACATAATAG	CAGATTACCT	GGATAATAGA
PReg29	GCACAAATTTG	GATTCTCTTG	TAATGCTTTG	AAATTAATCC	AGTATTTTAA	TACTAACAGA
PReg17	GCACAAATTTG	GATTCTCTTG	TAATGCTTTG	AAATTAATCC	AGTATTTTAA	TACTAACAGA
PReg20	GCACAAATTTG	GATTCTCTTG	TAATGCTTTG	AAATTAATCC	AGTATTTTAA	TACTAACAGA
Preg.Cr1C.Con	GCACAAATTTG	GATTCTCTTG	TAATGCTTTG	AAATTAATCC	AGTATTTTAA	TACTAACAGA

<i>PReg28</i>	ATCCTAGAAAT	ATG - - - AAAC	CGAAAAATGGT	ATGGATCACT	ACGAAAGTGGC	AGC - - - TGGT
<i>PReg3</i>	ATCCTAGAAAT	ATG - - - AAAC	CGAAAAATGGT	ATGGATCACT	ACGAAAGTGAC	AGC - - - TGGC
<i>PReg21</i>	ATCCTAGAAAT	ATG - - - AAAC	CGAAAAATGGT	ATGGATCACT	ACGAAAGTGAC	AGC - - - TGGC
<i>PReg18</i>	ATCCTAGAAAT	ATG - - - AAAC	CGAAAAATGGT	ATGGATCACT	ACGAAAGTGAC	AGC - - - TGGC
<i>PReg7</i>	ATCCTAGAAAT	ATG - - - AAAC	CGAAAAATGGT	ATGGATCACT	ACGAAAGTGGC	AGC - - - TGGC
<i>Preg.Cr1A.Con</i>	ATCCTAGAAAT	ATG - - - AAAC	CGAAAAATGGT	ATGGATCACT	ACGAAAGTGAC	AGC - - - TGGN
<i>PReg22r</i>	ATTCTATTAT	ACG - - - AAAC	GGAAAAATGGC	ACAAAAAGAAT	ATCGAATAAC	GGC - - - TGGC
<i>PReg27</i>	ATTCTATTAT	ACG - - - AAAC	GGAAAAATGGC	ACAAAAAGAAT	ATCGAATAAC	AGC - - - TGGC
<i>PReg31</i>	ATTCTATTAT	ACG - - - AAAC	GGAAAAATGGC	ACAAAAAGAAT	ATCGAATAAC	AGC - - - TGGC
<i>PReg8r</i>	ATTCTATTAT	ACG - - - AAAC	GGAAAAATGGC	ACAAAAAGAAT	ATCGAATAAC	AGC - - - TGGC
<i>PReg12r</i>	ATTCTATTAT	ACG - - - AAAC	GGAAAAATGGC	ACAAAAAGAAT	ATCGAATAAC	AGC - - - TGGC
<i>Preg.Cr1B.Con</i>	ATTCTATTAT	ACG - - - AAAC	GGAAAAATGGC	ACAAAAAGAAT	ATCGAATAAC	AGC - - - TGGN
<i>PReg29</i>	ACTC - - - AAT	TTGTACAGAC	TATTAATGAA	AGTTCGTCCA	GCAAAATTTAC	ATTCCGTGGT
<i>PReg17</i>	ACTC - - - AAT	TTGTACAGAC	TATTAATGAA	AGTTCGTCCA	GCAAAATTTAC	ATTCCGTGGT
<i>PReg20</i>	ACTC - - - AAT	TTGTACAGAC	TATTAATGAA	AGTTCGTCCA	GCAAAATTTAC	ATACCGTGGC
<i>Preg.Cr1C.Con</i>	ACTC - - - AAT	TTGTACAGAC	TATTAATGAA	AGTTCGTCCA	GCAAAATTTAC	ATTCCGTGGN
<i>PReg28</i>	GTACCCCAAG	GC - AGTGTTT	TTG			
<i>PReg3</i>	GTACCCCAAG	GC - AGTGTTT	TTG			
<i>PReg21</i>	GTCCCAACAG	GCTAGTGTTT	TTG			
<i>PReg18</i>	GTTCCACAAG	GC - AGTGTTT	TTG			
<i>PReg7</i>	GTTCCACAAG	GC - AGTGTTT	TTG			
<i>Preg.Cr1A.Con</i>	GTNCCNCARG	GC - AGTGTTT	TTG			
<i>PReg22r</i>	GTTCCCAACAG	GC - AGTGTTT	TTG			
<i>PReg27</i>	GTCCCAACAG	GC - AGTGTTT	TTG			
<i>PReg31</i>	GTCCCAACAG	GC - AGTGTTT	TTG			
<i>PReg8r</i>	GTACCCCAAG	GC - AG - - - TT	GTA			
<i>PReg12r</i>	GTTCCCAACAG	GC - AGTGTTA	AGG			
<i>Preg.Cr1B.Con</i>	GTNCCNCARG	GC - AGTGTTT	TTG			
<i>PReg29</i>	GTCCCAACAG	GC - AGTGTTT	TTG			
<i>PReg17</i>	GTCCCAACAG	GC - AGTGTTT	TTG			
<i>PReg20</i>	GTACCCCAAG	GC - AGTGTTT	TTG			
<i>Preg.Cr1C.Con</i>	GTNCCNCARG	GC - AGTGTTT	TTG			

Supplemental Figure 4 Sequences obtained from *P. regina* clones alongside consensus clusters

<i>Sbul18</i>	GATCTCAAAC	CGGGCACTTA	AGGTGGCTAT	CAGGCATAGA	CCGGAA - AT -	- - GATCGCCA
<i>Sbul2</i>	GATCCCAAAC	CGGGCACTTA	AGGTGGCTAT	CAGGCATAGA	CCGGAT - AT -	- - GATCGCCA
<i>Sbul23</i>	GATCCCAAAC	CGGGCACTTA	AGGTGGCTGT	CAAGCATAGA	CCGGAT - AT -	- - GATCGCCA
<i>Sbul.CR1A.Con</i>	GATCCCAAAC	CGGGCACTTA	AGGTGGCTAT	CAGGCATAGA	CCGGAT - AT -	- - GATCGCCA
<i>Sbul27</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACC -	- - - - -	- - - - -	- - - - -
<i>Sbul12</i>	GGTTCTTAGC	- - AGTATTTT	CAAACACCAT	TC - TCAATTA	CTGAGTAAC	CCATTAACCT
<i>Sbul13</i>	GGTTCTTAGC	- - AGTATTTT	CAAACACCAT	TC - TCAATTA	CTGAGTAAC	CCATTAACCT
<i>Sbul24</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAACTA	CTGAGT - ACG	CCATTAACCT
<i>Sbul28</i>	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<i>Sbul29</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul11</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul5</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul22</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul26</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CC - TTAACCT
<i>Sbul25</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul32</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul15</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul3</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul7</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul17</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul10</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul30</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul14</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul21</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul4</i>	GGTTCTTAGT	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul9</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul31</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul6</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT
<i>Sbul.CR1B.Con</i>	GGTTCTTAGC	- - AGTATTTT	AAAAACACCAT	TC - TCAATTA	CTGAGT - ATT	CCATTAACCT

<i>Sbul18</i>	CCATCTGCCT	ACTTGACACG	ATGGGAAAAA	TACTTTAGAG	GATAGTATAC	AATCGACTGC
<i>Sbul2</i>	CCATCTGCCT	ACTTGACACG	ATGGGAAAAA	TACTGGAGAG	GATAATATAC	AATCGACTGC
<i>Sbul23</i>	CCATCTGCCT	ACTTGACACG	ATGGGAAAAA	TACTGGAGAG	GATAGTATAC	AATCGACTGC
<i>Sbul.CR1A.Con</i>	CCATCTGCCT	ACTTGACACG	ATGGGAAAAA	TACTGGAGAG	GATAATATAC	AATCGACTGC
<i>Sbul27</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul12</i>	GAATTGCTTA	AATCAACACT	ATACCCAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul13</i>	GAATTGCTTA	AATCAACACT	ATACCCAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul24</i>	GAATTGCTAA	ACTTAACACA	ATATCGAAAGC	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul28</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul29</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>SBul11</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>SBul5</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul22</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul26</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul25</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul32</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul15</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul3</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul7</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul17</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>SBul10</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul30</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>SBul14</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>SBul21</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul4</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul9</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul31</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>SBul6</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul.CR1B.Con</i>	GAATTGCTAA	ACTTAACACA	ATACCGAAAT	TATTTGAAAA	ACTCTTATGT	GATACACTGT
<i>Sbul18</i>	TGATACATGT	CGAGGCGAGA	GGAGCTCTCT	CGGACCTGCA	ATACAGATTT	AGGAAGGGAC
<i>Sbul2</i>	TGACACATGT	CGAGGCGAGA	GGAGCTCTCT	CGGACCTGCA	ATACGGATTT	AGGAAGGAAAC
<i>Sbul23</i>	TGACACATGT	CGAGGCGAGA	GGAGCTCTCT	CGGACCTGCA	ATACGGATTT	AGGAAGGGAC
<i>Sbul.CR1A.Con</i>	TGACACATGT	CGAGGCGAGA	GGAGCTCTCT	CGGACCTGCA	ATACGGATTT	AGGAAGGAAAC
<i>Sbul27</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul12</i>	- - - - CATTT	CAAGCATCGT	CTATCTTATC	TGCATAC - CA	GCAATGGATTC	TGTGCGTCTC
<i>Sbul13</i>	- - - - CATTT	CAAGCATCGT	CTATCTTATC	TGCATAC - CA	GCAATGGATTC	TGTGCGTCTC
<i>Sbul24</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCCATGGTTTC	TGTAAGTCTC
<i>Sbul28</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGCCTC
<i>Sbul29</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>SBul11</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>SBul5</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul22</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul26</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul25</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul32</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul15</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATAT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul3</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATAT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul7</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATAT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul17</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGCCTC
<i>SBul10</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul30</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>SBul14</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>SBul21</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul4</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul9</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul31</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>SBul6</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC
<i>Sbul.CR1B.Con</i>	- - - - CATTT	CAAGCATCGT	CCATCTTATC	TGCATCT - CA	GCAATGGTTTC	TGTAAGTCTC

<i>Sbul18</i>	C - GTTTAACC	CGGC GAATTG	GGGGCG - - -	GATTATGAGA	GCCCTTTTCA	ACATGG - - T
<i>Sbul2</i>	C - GTTTAACT	CGGC GGATTG	GGGGCG - - -	GATTATGAGA	GCCCTTTTCA	ACATGG - - CT
<i>Sbul23</i>	C - GTTTAACT	CGGC GAATTG	GGGGTG - - -	GATTATGAGA	GCCCTTTTCA	ACATGG - - CT
<i>Sbul.CR1A.Con</i>	C - GTTTAACT	CGGC GAATTG	GGGGCG - - -	GATTATGAGA	GCCCTTTTCA	ACATGG - - CT
<i>Sbul27</i>	C - ATTTGATA	AAATAAATCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul12</i>	C - ATTTGATA	GAGTAAATCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul13</i>	C - ATTTGATA	GAGTAAATCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul24</i>	C - ATATGATA	AAGTAAATCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul28</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul29</i>	CKATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>SBul11</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>SBul5</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTT	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul22</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTT	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul26</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul25</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul32</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul15</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul3</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul7</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul17</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>SBul10</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul30</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul14</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul21</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul4</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul9</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul31</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul6</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul.CR1B.Con</i>	C - ATTTGATA	AAGTAAACCA	TAACCTTACTC	GTTCCATAAG -	- - CTTTATCA	ACTTGGTTTT
<i>Sbul18</i>	ACGCCTCCAT	ACTTAATGGA	GATT - TGAAT	GATTACTTTTC	AGGACAGGAA	GGTAATATA -
<i>Sbul2</i>	ACGCCTCCAT	ACTTAATGGA	GATTCTGAAT	GATTACTTTTC	AGGACAGGAA	GGTAATATAC
<i>Sbul23</i>	ACGCCTCCAT	ACTTAATGGA	GATTCTGAAT	GATTACTTTTC	AGGACAGGAA	GGTAATATAC
<i>Sbul.CR1A.Con</i>	ACGCCTCCAT	ACTTAATGGA	GATTCTGAAT	GATTACTTTTC	AGGACAGGAA	GGTAATATAC
<i>Sbul27</i>	AGTTCATCAT	TACTAAACTG	GATT - - AAA	ACGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul12</i>	AGTTCATCAT	TACTAAACTG	GATT - - AAA	TCGTATTTAG	TAAAGAGGAA	GC - AGTGCCT
<i>Sbul13</i>	AGTTCATCAT	TACTAAACTG	GATT - - AAA	TCGTATTTAG	TAAAGAGGAA	GC - AGTGCCT
<i>Sbul24</i>	AGTTCATCAT	TACTAAACTG	GATT - - AAA	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul28</i>	AGTTGGTCAT	TACTAAATTG	GATT - - AAG	TCGTATTTAG	T - AACAGAAA	GC - AGTGCCT
<i>Sbul29</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>SBul11</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>SBul5</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul22</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul26</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul25</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul32</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul15</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul3</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul7</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul17</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>SBul10</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul30</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul14</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>SBul21</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul4</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul9</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul31</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>SBul6</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT
<i>Sbul.CR1B.Con</i>	AGTTCGTCAT	TACTAAACTG	GATT - - AAG	TCGTATTTAG	TAAACAGAAA	GC - AGTGCCT

<i>Sbul18</i>	CAAATGGATG	AATGGAGAAA	AAGA - - - - -	- - - - -	- - -
<i>Sbul2</i>	CAAACGGATG	- ATGGAGAAA	AGGAATACGT	- - - AGTGACG	GCG
<i>Sbul23</i>	CAAACGGATG	- ATGGAGAAA	AGGAATACGT	- - - AGTGACG	GCG
<i>Sbul.CR1A.Con</i>	CAAACGGATG	- ATGGAGAAA	AGGAATACGT	- - - AGTGACG	GCG
<i>Sbul27</i>	TAAATTTCAGG	AACATGCAAT	CGAAGTTTAT	TGATGTACTA	TCA
<i>Sbul12</i>	TAAATTTCAGG	AACACGCAAT	CGAACTTTAT	TGATGTACTG	TCA
<i>Sbul13</i>	TAAATTTCAGG	AACACGCAAT	CGAACTTTAT	TGATGTACTG	TCA
<i>Sbul24</i>	TAAATTTCAGG	AACACACAAT	CGAACTTAAAT	TGATGTACTG	TCA
<i>Sbul28</i>	TAAATTC - - -	- - - - -	- - - - -	- - - - -	- - -
<i>Sbul29</i>	TAAATTCAGG	AACACACAAT	CGAACTTAAAT	TGATGTACTG	TCA
<i>Sbul11</i>	TAAATTCAGG	AACACACAAT	CGAACTTAAAT	TGATGTACTG	TCA
<i>Sbul5</i>	TAAATTCAGG	AACACACAAT	CGAACTTAAAT	TGATGTACTG	TCA
<i>Sbul22</i>	TAAATTCAGG	AACACACAAT	CGAACTTAAAT	TGATGTACTG	TCA
<i>Sbul26</i>	TAAATTCAGG	AACACACAAT	CGGACTTAAAT	TGATGTACTG	TCA
<i>Sbul25</i>	TAAATTCAGG	AACACACAAT	CGGACTTAAAT	TGATGTACTG	TCA
<i>Sbul32</i>	TAAATTCAGG	AACACACAAT	CGGACTTAAAT	TGATGTACTG	TCA
<i>Sbul15</i>	TAAATTCAGG	AACACACAAT	CGGACTTAAAT	TGATGTACTG	TCA
<i>Sbul3</i>	TAAATTCAGG	AACACACAAT	CGGACTTAAAT	TGATGTACTG	TCA
<i>Sbul7</i>	TAAATTCAGG	AACACACAAT	CGGACTTAAAT	TGATGTACTG	TCA
<i>Sbul17</i>	TAAATTCAGG	AACACACAAT	CGAACTTAAAT	TGATGTACTG	TCT
<i>Sbul10</i>	TAAATTCAGG	AACACACAAT	CGAACTTAAAT	TGATGTACTG	TCA
<i>Sbul30</i>	TAAATTCAGG	AACACACAAT	CGAACTTAAAT	TGATGTACTG	TCA
<i>Sbul14</i>	TAAATTCAGG	AACACACAAT	CGAACTTAAAT	TGATGTACTG	TCA
<i>Sbul21</i>	TAAATTCAGG	AACACACAAT	CGAACTTAAAT	TGATGTACTG	TCA
<i>Sbul4</i>	TAAATTCAGG	AACACACAAT	CGAACTTAAAT	TGATGTACTG	TCA
<i>Sbul9</i>	TAAATTCAGG	AACACACAAT	CGGACTTAAAT	TGATGTACTG	TCA
<i>Sbul31</i>	TAAATTCAGG	AACACACAAT	CGGACTTAAAT	TGATGTACTG	TCA
<i>Sbul6</i>	TAAATTCAGG	AACACACAAT	CGGACTTAAAT	TGATGTACTG	TCA
<i>Sbul.CR1B.Con</i>	TAAATTCAGG	AACACACAAT	CGAACTTAAAT	TGATGTACTG	TCA

Supplemental Figure 5 Sequences obtained from *S. bullata* clones alongside consensus clusters

	10	20	30	40	50	60
RD3_LO_5	CTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCCTGTCAACTCTGCTCGTTTAATCA					
RD3_LO_4	CTATAGGGCACGCGTGGTCGACGGYCCGGGCTGGTCCTGTCAACTCTGCTCGTTTAATCA					
RD3_LO_2	-					
RD3_LO_1	-					
RD3.5_2	-					
RD3.5_1	-					
RD3.5_4	-					
RD2_LO_3	-					
RD2_LO_1	-					
RD2_LO_2	-					
RD1_LO_11	-					
RD1_LO_10	-					
RD1_LO_9	-					
RD1.5_LO_1	-					
RD1.5_LO_2	-					
RD1.5_LO_3	-					
RD1.5_LO_4	-					
RD1.5_LO_5	-					
RD1_LO_8	-					
RD1_LO_7	-					
RD1_LO_6	-					
RD1_LO_5	-					
RD1_LO_4	-					
RD1_LO_3	-					
RD1_LO_2	-					
RD1_LO_1	-					
S. bullata CRIB	-					
RD1_RO_1	-					
RD1_RO_2	-					
RD1_RO_3	-					
RD1_RO_4	-					
RD1_RO_5	-					
RD1_RO_6	-					
RD1_RO_7	-					
RD1_RO_8	-					
RD1_RO_9	-					
RD1_RO_10	-					
RD1_RO_11	-					
RD1_RO_12	-					
RD1_RO_13	-					
RD1_RO_14	-					
RD1_RO_15	-					
RD1_RO_16	-					
RD1_RO_17	-					
RD1_RO_18	-					
RD2_RO_1	-					
RD2_RO_2	-					
RD2_RO_3	-					
RD2_RO_4	-					
S. bullata consensus'	CTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCCTGTCAACTCTGCTCGTTTAATCA					

	70	80	90	100	110	120
RD3_LO_5	ATCTCGATGTTACATCTCCTGTTCCATATACCTTAAATCCAAATGCTTCTGTTGTGAATA					
RD3_LO_4	ATCTCGATGCTACTTCTCCTGTTCCATCAACCTTAAATCCAAATGCTTCTGTTGTGAATA					
RD3_LO_2	- - - - -					
RD3_LO_1	- - - - -					
RD3.5_2	- - - - - C C T G T T C C A T A T A C C T T A A T C C C A A A T A C T T C T G T T G T G A A T A					
RD3.5_1	- - - - - C C T G T T C C A T A T A C C T T A A T C C - A A A T G C T T C T G T T G T G A A T A					
RD3.5_4	- - - - - C C T G T T C C A T A T A C C T T A A T C C C A A A T A C T T C T G T T G T G A A T A					
RD2_LO_3	- - - - -					
RD2_LO_1	- - - - -					
RD2_LO_2	- - - - -					
RD1_LO_11	- - - - -					
RD1_LO_10	- - - - -					
RD1_LO_9	- - - - -					
RD1.5_LO_1	- - - - -					
RD1.5_LO_2	- - - - -					
RD1.5_LO_3	- - - - -					
RD1.5_LO_4	- - - - -					
RD1.5_LO_5	- - - - -					
RD1_LO_8	- - - - -					
RD1_LO_7	- - - - -					
RD1_LO_6	- - - - -					
RD1_LO_5	- - - - -					
RD1_LO_4	- - - - -					
RD1_LO_3	- - - - -					
RD1_LO_2	- - - - -					
RD1_LO_1	- - - - -					
S. bullata CRIB	- - - - -					
RD1_RO_1	- - - - -					
RD1_RO_2	- - - - -					
RD1_RO_3	- - - - -					
RD1_RO_4	- - - - -					
RD1_RO_5	- - - - -					
RD1_RO_6	- - - - -					
RD1_RO_7	- - - - -					
RD1_RO_8	- - - - -					
RD1_RO_9	- - - - -					
RD1_RO_10	- - - - -					
RD1_RO_11	- - - - -					
RD1_RO_12	- - - - -					
RD1_RO_13	- - - - -					
RD1_RO_14	- - - - -					
RD1_RO_15	- - - - -					
RD1_RO_16	- - - - -					
RD1_RO_17	- - - - -					
RD1_RO_18	- - - - -					
RD2_RO_1	- - - - -					
RD2_RO_2	- - - - -					
RD2_RO_3	- - - - -					
RD2_RO_4	- - - - -					
S. bullata consensus'	ATCTCGATGYTACWTCTCCTGTTCCATATACCTTAAATCCCAAATRCTTCTGTTGTGAATA					

	130	140	150	160	170	180
RD3_LO_5	ATCAAAATGCTTCTGCTGAAAATCATCCAAAGGAGTTGCGAACTATTTACCTAAAAAAA					
RD3_LO_4	ATCAAAATGCTTCTGCTGAAAATCATCCAAAGGAGTTGCGAACTATTTACCTAAAAAAA					
RD3_LO_2	-					
RD3_LO_1	-					
RD3.5_2	ATCAAAATGTTTCTGCTGAAAATCATCCAAATGAGTTGCGAACTATTTACCTAAAAAAA					
RD3.5_1	ATCAAAATGCTTCTGCTGAAAATCATCCAAAGGAGTTGCGAACTATTTACCTAAAAAAA					
RD3.5_4	ATCAAAATGTTTCTGCTGAAAATCATCCAAAGGAGTTGCGAACTATTTACCTAAAAAAA					
RD2_LO_3	-					
RD2_LO_1	-					
RD2_LO_2	-					
RD1_LO_11	-					
RD1_LO_10	-					
RD1_LO_9	-					
RD1.5_LO_1	-					
RD1.5_LO_2	-					
RD1.5_LO_3	-					
RD1.5_LO_4	-					
RD1.5_LO_5	-					
RD1_LO_8	-					
RD1_LO_7	-					
RD1_LO_6	-					
RD1_LO_5	-					
RD1_LO_4	-					
RD1_LO_3	-					
RD1_LO_2	-					
RD1_LO_1	-					
S. bullata CRIB	-					
RD1_RO_1	-					
RD1_RO_2	-					
RD1_RO_3	-					
RD1_RO_4	-					
RD1_RO_5	-					
RD1_RO_6	-					
RD1_RO_7	-					
RD1_RO_8	-					
RD1_RO_9	-					
RD1_RO_10	-					
RD1_RO_11	-					
RD1_RO_12	-					
RD1_RO_13	-					
RD1_RO_14	-					
RD1_RO_15	-					
RD1_RO_16	-					
RD1_RO_17	-					
RD1_RO_18	-					
RD2_RO_1	-					
RD2_RO_2	-					
RD2_RO_3	-					
RD2_RO_4	-					
S. bullata consensus'	ATCAAAATGYTTCTGCTGAAAATCATCCAAAGGAGTTGCGAACTATTTACCTAAAAAAA					

	190	200	210	220	230	240
RD3_LO_5	CAATATTTGCTACACGCTTTG	CAGTTGATACGAATGCTGAAG	ATATGAAATTGTATATTC			
RD3_LO_4	CAATATTTGCTACACGCTTTG	CAGTTGATACGAATGCTGAAG	ATATGAAATTGTATATTC			
RD3_LO_2	-	-	-	-	-	-
RD3_LO_1	-	-	-	-	-	-
RD3.5_2	CAATATTTGCTACACGCTTTG	CAGTTGATACGAATGCTGAAG	ATATGAAATTGTATATTC			
RD3.5_1	CAATATTTGCTACACGCTTTG	CAGTTGATACGAATGCTGAAG	ATATGAAATTGTATATTC			
RD3.5_4	CAATATTTGCTACACGCCTTG	CAGTTGATACGAATGCTGAAG	ATATGAAATTGTATATTC			
RD2_LO_3	-	-	-	-	-	-
RD2_LO_1	-	-	-	-	-	-
RD2_LO_2	-	-	-	-	-	-
RD1_LO_11	-	-	-	-	-	-
RD1_LO_10	-	-	-	-	-	-
RD1_LO_9	-	-	-	-	-	-
RD1.5_LO_1	-	-	-	-	-	-
RD1.5_LO_2	-	-	-	-	-	-
RD1.5_LO_3	-	-	-	-	-	-
RD1.5_LO_4	-	-	-	-	-	-
RD1.5_LO_5	-	-	-	-	-	-
RD1_LO_8	-	-	-	-	-	-
RD1_LO_7	-	-	-	-	-	-
RD1_LO_6	-	-	-	-	-	-
RD1_LO_5	-	-	-	-	-	-
RD1_LO_4	-	-	-	-	-	-
RD1_LO_3	-	-	-	-	-	-
RD1_LO_2	-	-	-	-	-	-
RD1_LO_1	-	-	-	-	-	-
S. bullata CRIB	-	-	-	-	-	-
RD1_RO_1	-	-	-	-	-	-
RD1_RO_2	-	-	-	-	-	-
RD1_RO_3	-	-	-	-	-	-
RD1_RO_4	-	-	-	-	-	-
RD1_RO_5	-	-	-	-	-	-
RD1_RO_6	-	-	-	-	-	-
RD1_RO_7	-	-	-	-	-	-
RD1_RO_8	-	-	-	-	-	-
RD1_RO_9	-	-	-	-	-	-
RD1_RO_10	-	-	-	-	-	-
RD1_RO_11	-	-	-	-	-	-
RD1_RO_12	-	-	-	-	-	-
RD1_RO_13	-	-	-	-	-	-
RD1_RO_14	-	-	-	-	-	-
RD1_RO_15	-	-	-	-	-	-
RD1_RO_16	-	-	-	-	-	-
RD1_RO_17	-	-	-	-	-	-
RD1_RO_18	-	-	-	-	-	-
RD2_RO_1	-	-	-	-	-	-
RD2_RO_2	-	-	-	-	-	-
RD2_RO_3	-	-	-	-	-	-
RD2_RO_4	-	-	-	-	-	-
S. bullata consensus'	CAATATTTGCTACACGCTTTG	CAGTTGATACGAATGCTGAAG	ATATGAAATTGTATATTC			

	250	260	270	280	290	300
RD3_LO_5	TATCAAAAAATCAAAAAATTGTAATCCAGATGAAATTCTTCTTTTCAAAATAAAATTCGGAGT					
RD3_LO_4	TATCAAAAAATCAAAAAATTGTAATCCAGATGAAATTCTTCTTTTCAAAATAAAATTCGAAAT					
RD3_LO_2	-	-	-	-	-	-
RD3_LO_1	-	-	-	-	-	-
RD3.5_2	TATCAAAAAATCAAAAAATTGTAATCCAGATGAAATTCTTCTTTTCAAAATAAAATTCGAGGT					
RD3.5_1	TATCAAAAAATCAAAAAATTGTAATCCAGATGAAATTCTTCTTTTCAAAATAAAATTCGAAGT					
RD3.5_4	TATCAAGAATCAAAAAATTGTAATCCAGATGGAATTCTTCTTTTCAAAATAAAATTCGAGGT					
RD2_LO_3	-	-	-	-	-	-
RD2_LO_1	-	-	-	-	-	-
RD2_LO_2	-	-	-	-	-	-
RD1_LO_11	-	-	-	-	-	-
RD1_LO_10	-	-	-	-	-	-
RD1_LO_9	-	-	-	-	-	-
RD1.5_LO_1	-	-	-	-	-	-
RD1.5_LO_2	-	-	-	-	-	-
RD1.5_LO_3	-	-	-	-	-	-
RD1.5_LO_4	-	-	-	-	-	-
RD1.5_LO_5	-	-	-	-	-	-
RD1_LO_8	-	-	-	-	-	-
RD1_LO_7	-	-	-	-	-	-
RD1_LO_6	-	-	-	-	-	-
RD1_LO_5	-	-	-	-	-	-
RD1_LO_4	-	-	-	-	-	-
RD1_LO_3	-	-	-	-	-	-
RD1_LO_2	-	-	-	-	-	-
RD1_LO_1	-	-	-	-	-	-
S. bullata CRIB	-	-	-	-	-	-
RD1_RO_1	-	-	-	-	-	-
RD1_RO_2	-	-	-	-	-	-
RD1_RO_3	-	-	-	-	-	-
RD1_RO_4	-	-	-	-	-	-
RD1_RO_5	-	-	-	-	-	-
RD1_RO_6	-	-	-	-	-	-
RD1_RO_7	-	-	-	-	-	-
RD1_RO_8	-	-	-	-	-	-
RD1_RO_9	-	-	-	-	-	-
RD1_RO_10	-	-	-	-	-	-
RD1_RO_11	-	-	-	-	-	-
RD1_RO_12	-	-	-	-	-	-
RD1_RO_13	-	-	-	-	-	-
RD1_RO_14	-	-	-	-	-	-
RD1_RO_15	-	-	-	-	-	-
RD1_RO_16	-	-	-	-	-	-
RD1_RO_17	-	-	-	-	-	-
RD1_RO_18	-	-	-	-	-	-
RD2_RO_1	-	-	-	-	-	-
RD2_RO_2	-	-	-	-	-	-
RD2_RO_3	-	-	-	-	-	-
RD2_RO_4	-	-	-	-	-	-
S. bullata consensus'	TATCAAAAAATCAAAAAATTGTAATCCAGATGAAATTCTTCTTTTCAAAATAAAATTCGARGT					

	310	320	330	340	350	360
RD3_LO_5	ACAGGGCATCATTCAAAATTATTGTTCTGAAAATCTGTTCCAGCAAATTGTTAATCAGG					
RD3_LO_4	ACAGGGCATCATTCAAAATTATTGTTCTGAAAATCTGTYCCAGCAAATTGTTAATCCGG					
RD3_LO_2	-	-	-	-	-	-
RD3_LO_1	-	-	-	-	-	-
RD3.5_2	ACAGGGCATCATTCAAAATTATTGTTCTGAAAATCTGTTCCAGCAAATTGTTAATCAGG					
RD3.5_1	ACAGGGCATCATTCAAAATTATTGTTCTGAAAATCTGTTCCAGCAAATTGTTAATCAGG					
RD3.5_4	ACAGGGCATCATTCAAAATTATTGTTCTGAAAATCTGTTCCAGCAAATTGTTAATCAGG					
RD2_LO_3	-	-	-	-	-	-
RD2_LO_1	-	-	-	-	-	-
RD2_LO_2	-	-	-	-	-	-
RD1_LO_11	-	-	-	-	-	-
RD1_LO_10	-	-	-	-	-	-
RD1_LO_9	-	-	-	-	-	-
RD1.5_LO_1	-	-	-	-	-	-
RD1.5_LO_2	-	-	-	-	-	-
RD1.5_LO_3	-	-	-	-	-	-
RD1.5_LO_4	-	-	-	-	-	-
RD1.5_LO_5	-	-	-	-	-	-
RD1_LO_8	-	-	-	-	-	-
RD1_LO_7	-	-	-	-	-	-
RD1_LO_6	-	-	-	-	-	-
RD1_LO_5	-	-	-	-	-	-
RD1_LO_4	-	-	-	-	-	-
RD1_LO_3	-	-	-	-	-	-
RD1_LO_2	-	-	-	-	-	-
RD1_LO_1	-	-	-	-	-	-
S. bullata CRIB	-	-	-	-	-	-
RD1_RO_1	-	-	-	-	-	-
RD1_RO_2	-	-	-	-	-	-
RD1_RO_3	-	-	-	-	-	-
RD1_RO_4	-	-	-	-	-	-
RD1_RO_5	-	-	-	-	-	-
RD1_RO_6	-	-	-	-	-	-
RD1_RO_7	-	-	-	-	-	-
RD1_RO_8	-	-	-	-	-	-
RD1_RO_9	-	-	-	-	-	-
RD1_RO_10	-	-	-	-	-	-
RD1_RO_11	-	-	-	-	-	-
RD1_RO_12	-	-	-	-	-	-
RD1_RO_13	-	-	-	-	-	-
RD1_RO_14	-	-	-	-	-	-
RD1_RO_15	-	-	-	-	-	-
RD1_RO_16	-	-	-	-	-	-
RD1_RO_17	-	-	-	-	-	-
RD1_RO_18	-	-	-	-	-	-
RD2_RO_1	-	-	-	-	-	-
RD2_RO_2	-	-	-	-	-	-
RD2_RO_3	-	-	-	-	-	-
RD2_RO_4	-	-	-	-	-	-
S. bullata consensus'	ACAGGGCATCATTCAAAATTATTGTTCTGAAAATCTGTTCCAGCAAATTGTTAATCAGG					

	370	380	390	400	410	420
RD3_LO_5	A	A	T	T	T	T
RD3_LO_4	A	A	T	T	T	T
RD3_LO_2	-	-	-	-	-	-
RD3_LO_1	-	-	-	-	-	-
RD3.5_2	-	-	-	-	-	-
RD3.5_1	-	-	-	-	-	-
RD3.5_4	-	-	-	-	-	-
RD2_LO_3	-	-	-	-	-	-
RD2_LO_1	-	-	-	-	-	-
RD2_LO_2	-	-	-	-	-	-
RD1_LO_11	-	-	-	-	-	-
RD1_LO_10	-	-	-	-	-	-
RD1_LO_9	-	-	-	-	-	-
RD1.5_LO_1	-	-	-	-	-	-
RD1.5_LO_2	-	-	-	-	-	-
RD1.5_LO_3	-	-	-	-	-	-
RD1.5_LO_4	-	-	-	-	-	-
RD1.5_LO_5	-	-	-	-	-	-
RD1_LO_8	-	-	-	-	-	-
RD1_LO_7	-	-	-	-	-	-
RD1_LO_6	-	-	-	-	-	-
RD1_LO_5	-	-	-	-	-	-
RD1_LO_4	-	-	-	-	-	-
RD1_LO_3	-	-	-	-	-	-
RD1_LO_2	-	-	-	-	-	-
RD1_LO_1	-	-	-	-	-	-
S. bullata CRIB	-	-	-	-	-	-
RD1_RO_1	-	-	-	-	-	-
RD1_RO_2	-	-	-	-	-	-
RD1_RO_3	-	-	-	-	-	-
RD1_RO_4	-	-	-	-	-	-
RD1_RO_5	-	-	-	-	-	-
RD1_RO_6	-	-	-	-	-	-
RD1_RO_7	-	-	-	-	-	-
RD1_RO_8	-	-	-	-	-	-
RD1_RO_9	-	-	-	-	-	-
RD1_RO_10	-	-	-	-	-	-
RD1_RO_11	-	-	-	-	-	-
RD1_RO_12	-	-	-	-	-	-
RD1_RO_13	-	-	-	-	-	-
RD1_RO_14	-	-	-	-	-	-
RD1_RO_15	-	-	-	-	-	-
RD1_RO_16	-	-	-	-	-	-
RD1_RO_17	-	-	-	-	-	-
RD1_RO_18	-	-	-	-	-	-
RD2_RO_1	-	-	-	-	-	-
RD2_RO_2	-	-	-	-	-	-
RD2_RO_3	-	-	-	-	-	-
RD2_RO_4	-	-	-	-	-	-
S. bullata consensus'	A	A	T	T	T	T

	430	440	450	460	470	480
RD3_LO_5	GTCTTCCTCACATTGCCGACACAAATCAAAAAAACTAATTTCCATTGTTTATCAAAATGT					
RD3_LO_4	GTCTTCCTCACATTGCCGACACAAATCAAAAAAACTAATTTCCATTGTTTATCAAAATGT					
RD3_LO_2	GTCTTCCTCACATTGCCGACACAAATCAAAAAAACTAATTTCCATTGTTTATCAAAATGT					
RD3_LO_1	- - CTTCTCACATTGCCGACACAAATCAAAAAAACTAATTTCCATTGTTTATCAAAATGT					
RD3.5_2	- - CTTCTCACATTGCCGACACAAATCAAAAAAACTAATTTCCATTGTTTATCAAAATGT					
RD3.5_1	- - - - -					
RD3.5_4	- - - - -					
RD2_LO_3	- - - - - TCAAAAAA - CTAATTTCCATTGTTTATCAAAATGT					
RD2_LO_1	GTCTTCCTCACATTGCCAACACAAATCAAAAAAACTAATTTCCATTGTTTATCAAAATGT					
RD2_LO_2	GTCTTCCTCACATTGCCGACACAAATCAAAAAAACTAATTTCCATTGCTTATCAAAATGT					
RD1_LO_11	- - - - -					
RD1_LO_10	- - - - -					
RD1_LO_9	- - - - -					
RD1.5_LO_1	- - - - -					
RD1.5_LO_2	- - - - -					
RD1.5_LO_3	- - - - -					
RD1.5_LO_4	- - - - -					
RD1.5_LO_5	- - - - -					
RD1_LO_8	- - - - -					
RD1_LO_7	- - - - -					
RD1_LO_6	- - - - -					
RD1_LO_5	- - - - -					
RD1_LO_4	- - - - -					
RD1_LO_3	- - - - -					
RD1_LO_2	- - - - -					
RD1_LO_1	- - - - -					
S. bullata CRIB	- - - - -					
RD1_RO_1	- - - - -					
RD1_RO_2	- - - - -					
RD1_RO_3	- - - - -					
RD1_RO_4	- - - - -					
RD1_RO_5	- - - - -					
RD1_RO_6	- - - - -					
RD1_RO_7	- - - - -					
RD1_RO_8	- - - - -					
RD1_RO_9	- - - - -					
RD1_RO_10	- - - - -					
RD1_RO_11	- - - - -					
RD1_RO_12	- - - - -					
RD1_RO_13	- - - - -					
RD1_RO_14	- - - - -					
RD1_RO_15	- - - - -					
RD1_RO_16	- - - - -					
RD1_RO_17	- - - - -					
RD1_RO_18	- - - - -					
RD2_RO_1	- - - - -					
RD2_RO_2	- - - - -					
RD2_RO_3	- - - - -					
RD2_RO_4	- - - - -					
S. bullata consensus'	GTCTTCCTCACATTGCCGACACAAATCAAAAAAACTAATTTCCATTGTTTATCAAAATGT					

	490	500	510	520	530	540
RD3_LO_5	TAGAGGGATTAACTCGAAATTATCTTCA					
RD3_LO_4	TAGAGGGATTAACTCGAAATTATCTTCA					
RD3_LO_2	TAGAGGGATTAACTCGAAATTATCTTCA					
RD3_LO_1	TAGAGGGATTAACTCGAAATTATCTTCA					
RD3.5_2	- - - - -					
RD3.5_1	- - - - -					
RD3.5_4	- - - - -					
RD2_LO_3	TAGAGGCATTAACCTCGAAATTATCTCCAATTTATTGTAATAGTTTTGGATTTAATTACCA					
RD2_LO_1	TAGAGGGATTAACTCGAAATTATCTTCAATTTATTGTAATAGTTTTGGATTTAATTACCA					
RD2_LO_2	TAGAGGTATTAACCTCGAAATTATCTTCAATTTATTGTAATAGTTTTGGATTTAATTACCA					
RD1_LO_11	- - - - -					
RD1_LO_10	- - - - -					
RD1_LO_9	- - - - -					
RD1.5_LO_1	- - - - -					
RD1.5_LO_2	- - - - -					
RD1.5_LO_3	- - - - -					
RD1.5_LO_4	- - - - -					
RD1.5_LO_5	- - - - -					
RD1_LO_8	- - - - -					
RD1_LO_7	- - - - -					
RD1_LO_6	- - - - -					
RD1_LO_5	- - - - -					
RD1_LO_4	- - - - -					
RD1_LO_3	- - - - -					
RD1_LO_2	- - - - -					
RD1_LO_1	- - - - -					
S. bullata CRIB	- - - - -					
RD1_RO_1	- - - - -					
RD1_RO_2	- - - - -					
RD1_RO_3	- - - - -					
RD1_RO_4	- - - - -					
RD1_RO_5	- - - - -					
RD1_RO_6	- - - - -					
RD1_RO_7	- - - - -					
RD1_RO_8	- - - - -					
RD1_RO_9	- - - - -					
RD1_RO_10	- - - - -					
RD1_RO_11	- - - - -					
RD1_RO_12	- - - - -					
RD1_RO_13	- - - - -					
RD1_RO_14	- - - - -					
RD1_RO_15	- - - - -					
RD1_RO_16	- - - - -					
RD1_RO_17	- - - - -					
RD1_RO_18	- - - - -					
RD2_RO_1	- - - - -					
RD2_RO_2	- - - - -					
RD2_RO_3	- - - - -					
RD2_RO_4	- - - - -					
S. bullata consensus'	TAGAGGGATTAACTCGAAATTATCTTCAATTTATTGTAATAGTTTTGGATTTAATTACCA					

	550	560	570	580	590	600
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	T	A	T	A	A	T
RD2_LO_1	T	A	T	A	A	T
RD2_LO_2	T	A	T	A	A	T
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	T	A	T	A	A	T

	610	620	630	640	650	660
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	C	C	C	C	A	A
RD2_LO_1	C	C	C	T	A	A
RD2_LO_2	C	C	C	T	A	A
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	C	C	C	T	A	A

	670	680	690	700	710	720
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	A	-	C	T	G	G
RD2_LO_1	A	A	C	T	G	G
RD2_LO_2	A	A	C	T	G	G
RD1_LO_11	-	-	-	-	-	-
RD1_LO_10	-	-	-	-	-	-
RD1_LO_9	-	-	-	-	-	-
RD1.5_LO_1	-	-	-	-	-	-
RD1.5_LO_2	-	-	-	-	-	-
RD1.5_LO_3	-	-	-	-	-	-
RD1.5_LO_4	-	-	-	-	-	-
RD1.5_LO_5	-	-	-	-	-	-
RD1_LO_8	-	-	-	-	-	-
RD1_LO_7	-	-	-	-	-	-
RD1_LO_6	-	-	-	-	-	-
RD1_LO_5	-	-	-	-	-	-
RD1_LO_4	-	-	-	-	-	-
RD1_LO_3	-	-	-	-	-	-
RD1_LO_2	-	-	-	-	-	-
RD1_LO_1	-	-	-	-	-	-
S. bullata CRIB	-	-	-	-	-	-
RD1_RO_1	-	-	-	-	-	-
RD1_RO_2	-	-	-	-	-	-
RD1_RO_3	-	-	-	-	-	-
RD1_RO_4	-	-	-	-	-	-
RD1_RO_5	-	-	-	-	-	-
RD1_RO_6	-	-	-	-	-	-
RD1_RO_7	-	-	-	-	-	-
RD1_RO_8	-	-	-	-	-	-
RD1_RO_9	-	-	-	-	-	-
RD1_RO_10	-	-	-	-	-	-
RD1_RO_11	-	-	-	-	-	-
RD1_RO_12	-	-	-	-	-	-
RD1_RO_13	-	-	-	-	-	-
RD1_RO_14	-	-	-	-	-	-
RD1_RO_15	-	-	-	-	-	-
RD1_RO_16	-	-	-	-	-	-
RD1_RO_17	-	-	-	-	-	-
RD1_RO_18	-	-	-	-	-	-
RD2_RO_1	-	-	-	-	-	-
RD2_RO_2	-	-	-	-	-	-
RD2_RO_3	-	-	-	-	-	-
RD2_RO_4	-	-	-	-	-	-
S. bullata consensus'	A	A	C	T	G	G

	730	740	750	760	770	780
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	T	C	-	-		
RD2_LO_1	T	C	A	-	-	
RD2_LO_2	T	C	-	-	-	
RD1_LO_11	T	C	A	T	G	A
RD1_LO_10	-	C	-	T	G	A
RD1_LO_9	T	C	A	T	G	A
RD1.5_LO_1	-	-	-	-	-	-
RD1.5_LO_2	-	-	-	-	-	-
RD1.5_LO_3	-	-	-	-	-	-
RD1.5_LO_4	-	-	-	-	-	-
RD1.5_LO_5	-	-	-	-	-	-
RD1_LO_8	-	-	-	-	-	-
RD1_LO_7	-	-	-	-	-	-
RD1_LO_6	-	-	-	-	-	-
RD1_LO_5	-	-	-	-	-	-
RD1_LO_4	-	-	-	-	-	-
RD1_LO_3	-	-	-	-	-	-
RD1_LO_2	-	-	-	-	-	-
RD1_LO_1	-	-	-	-	-	-
S. bullata CRIB	-	-	-	-	-	-
RD1_RO_1	-	-	-	-	-	-
RD1_RO_2	-	-	-	-	-	-
RD1_RO_3	-	-	-	-	-	-
RD1_RO_4	-	-	-	-	-	-
RD1_RO_5	-	-	-	-	-	-
RD1_RO_6	-	-	-	-	-	-
RD1_RO_7	-	-	-	-	-	-
RD1_RO_8	-	-	-	-	-	-
RD1_RO_9	-	-	-	-	-	-
RD1_RO_10	-	-	-	-	-	-
RD1_RO_11	-	-	-	-	-	-
RD1_RO_12	-	-	-	-	-	-
RD1_RO_13	-	-	-	-	-	-
RD1_RO_14	-	-	-	-	-	-
RD1_RO_15	-	-	-	-	-	-
RD1_RO_16	-	-	-	-	-	-
RD1_RO_17	-	-	-	-	-	-
RD1_RO_18	-	-	-	-	-	-
RD2_RO_1	-	-	-	-	-	-
RD2_RO_2	-	-	-	-	-	-
RD2_RO_3	-	-	-	-	-	-
RD2_RO_4	-	-	-	-	-	-
S. bullata consensus'	T	C	A	T	G	A

	790	800	810	820	830	840
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	A	T	T	C	A	T
RD1_LO_10	A	T	T	C	A	T
RD1_LO_9	A	T	T	C	A	T
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	A	T	T	C	A	T
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	A	T	T	C	A	T

	850	860	870	880	890	900
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	A	A	A	T	G	C
RD1_LO_10	A	A	A	T	G	C
RD1_LO_9	A	A	A	T	G	C
RD1.5_LO_1	A	A	A	T	G	C
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	A	A	A	T	G	C
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	A	A	A	T	G	C

	910	920	930	940	950	960
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	A	G	A	C	T	T
RD1_LO_10	A	G	A	C	T	T
RD1_LO_9	A	G	A	C	T	T
RD1.5_LO_1	A	G	A	C	T	T
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	A	G	A	C	T	T

	970	980	990	1000	1010	1020
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	A	G	T	T	A	G
RD1_LO_10	A	G	T	T	G	G
RD1_LO_9	A	G	T	T	A	G
RD1.5_LO_1	A	G	T	T	A	G
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	A	G	T	T	A	G

	1030	1040	1050	1060	1070	1080
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	T	C	A	A	A	T
RD1_LO_10	T	C	A	A	A	T
RD1_LO_9	T	C	A	A	A	T
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	T	C	A	A	A	T
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	T	C	A	A	A	T

	1090	1100	1110	1120	1130	1140
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	T	T	C	A	T	C
RD1_LO_10	C	T	C	A	T	C
RD1_LO_9	T	T	C	A	T	C
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	Y	T	C	A	T	C

	1150	1160	1170	1180	1190	1200
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	T	C	C	G	A	C
RD1_LO_10	T	C	C	G	A	C
RD1_LO_9	T	C	C	G	A	C
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	T	C	C	G	A	C

	1210	1220	1230	1240	1250	1260
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	A	A	A	A	C	A
RD1_LO_10	A	A	A	A	C	A
RD1_LO_9	A	A	A	A	C	A
RD1.5_LO_1	A	A	A	A	C	A
RD1.5_LO_2	A	A	A	A	C	A
RD1.5_LO_3	A	A	A	A	C	A
RD1.5_LO_4	A	A	A	A	C	A
RD1.5_LO_5	-	-	-	-	-	-
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	A	A	A	A	C	A

	1270	1280	1290	1300	1310	1320
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	T	G	A	A	A	T
RD1_LO_10	T	G	A	A	A	T
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	T	G	A	A	A	T
RD1.5_LO_2	T	G	A	A	A	T
RD1.5_LO_3	T	G	A	A	A	T
RD1.5_LO_4	T	G	A	A	A	T
RD1.5_LO_5	T	G	A	A	A	T
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	T	G	A	A	A	T

	1330	1340	1350	1360	1370	1380
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	G	A	A	A	T	T
RD1.5_LO_2	G	A	A	A	T	T
RD1.5_LO_3	G	A	A	A	T	T
RD1.5_LO_4	G	A	A	A	T	T
RD1.5_LO_5	G	A	A	A	T	T
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	G	A	A	A	T	T

	1390	1400	1410	1420	1430	1440
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	T	T	T	T	T	T
RD1.5_LO_2	T	T	T	T	T	T
RD1.5_LO_3	T	T	T	T	T	T
RD1.5_LO_4	T	T	T	T	T	T
RD1.5_LO_5	T	T	T	T	T	T
RD1_LO_8	T	T	T	T	T	T
RD1_LO_7	-	T	T	T	T	T
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	T	T	T	T	T	T

	1450	1460	1470	1480	1490	1500
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	T	A	A	G	T	T
RD1.5_LO_2	T	A	A	G	T	T
RD1.5_LO_3	T	A	A	G	T	T
RD1.5_LO_4	T	A	A	G	T	T
RD1.5_LO_5	T	A	A	G	T	T
RD1_LO_8	T	A	A	G	T	T
RD1_LO_7	T	A	A	G	T	T
RD1_LO_6	-	-	-	-	-	-
RD1_LO_5	-	-	-	-	-	-
RD1_LO_4	-	-	-	-	-	-
RD1_LO_3	-	-	-	-	-	-
RD1_LO_2	-	-	-	-	-	-
RD1_LO_1	-	-	-	-	-	-
S. bullata CRIB	-	-	-	-	-	-
RD1_RO_1	-	-	-	-	-	-
RD1_RO_2	-	-	-	-	-	-
RD1_RO_3	-	-	-	-	-	-
RD1_RO_4	-	-	-	-	-	-
RD1_RO_5	-	-	-	-	-	-
RD1_RO_6	-	-	-	-	-	-
RD1_RO_7	-	-	-	-	-	-
RD1_RO_8	-	-	-	-	-	-
RD1_RO_9	-	-	-	-	-	-
RD1_RO_10	-	-	-	-	-	-
RD1_RO_11	-	-	-	-	-	-
RD1_RO_12	-	-	-	-	-	-
RD1_RO_13	-	-	-	-	-	-
RD1_RO_14	-	-	-	-	-	-
RD1_RO_15	-	-	-	-	-	-
RD1_RO_16	-	-	-	-	-	-
RD1_RO_17	-	-	-	-	-	-
RD1_RO_18	-	-	-	-	-	-
RD2_RO_1	-	-	-	-	-	-
RD2_RO_2	-	-	-	-	-	-
RD2_RO_3	-	-	-	-	-	-
RD2_RO_4	-	-	-	-	-	-
S. bullata consensus'	T	A	A	G	T	T

	1510	1520	1530	1540	1550	1560
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	AGTAAGATCTGAATACACCATCGCCAACCAACGGGCTTATTACATCTACTTAAATAAAAGT					
RD1.5_LO_2	AGTAAGATCTGAATACACCATCGCCAACCAAGGGCTTATTACATCCACTTAAATAAAAGT					
RD1.5_LO_3	AGTAAGATCTGAATACACCATCGCCAACCAAGGGCTTATTACATCCACTTAAATAAAAGT					
RD1.5_LO_4	AGTAAGATCTGAATACACCATCGCCAACCAACGGGCTTATTACATCTACTTAAATAAAAGT					
RD1.5_LO_5	AGTAAGATC - - - - - CATCGCCAACCAAGGGCTTATTACATCTACTTAAATAAAAGT					
RD1_LO_8	AGTAAGATCTGAATACACCATCGCCAACCAAGGGCTTATTACATCTACTTAAATAAAAGT					
RD1_LO_7	AGTAAGATCTGAATACACCATCGCCAACCAAGGGCTTATTACATCTACTTAAATAAAAGT					
RD1_LO_6	AGTAAGATCTGAATACACCATCGCCAACCAAGGGCTTATTACATCTACTTAAATAAAAGT					
RD1_LO_5	AGTAAGATCTGAATACACCATCGCCAACCAAGGGCTTATTACATCTACTTAAATAAAAGT					
RD1_LO_4	AGTAAGATCTGAATACACCATCGCCAACCAAGGGCTTATTACATCTACTTAAATAAAAGT					
RD1_LO_3	- - - - - TAAAGT					
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	AGTAAGATCTGAATACACCATCGCCAACCAAGGGCTTATTACATCTACTTAAATAAAAGT					

	1570	1580	1590	1600	1610	1620
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	A	A	A	A	A	A
RD1.5_LO_2	A	A	A	A	A	A
RD1.5_LO_3	A	A	A	A	A	A
RD1.5_LO_4	A	A	A	A	A	A
RD1.5_LO_5	A	A	A	A	A	A
RD1_LO_8	A	A	A	A	A	A
RD1_LO_7	A	A	A	A	A	A
RD1_LO_6	A	A	A	A	A	A
RD1_LO_5	A	A	A	A	A	A
RD1_LO_4	A	A	A	A	A	A
RD1_LO_3	A	A	A	A	A	A
RD1_LO_2	A	A	A	A	A	A
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	A	A	A	A	A	A

	1630	1640	1650	1660	1670	1680
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	A	G	C	A	G	C
RD1.5_LO_2	A	G	C	A	G	C
RD1.5_LO_3	A	G	C	A	G	C
RD1.5_LO_4	A	G	C	A	G	C
RD1.5_LO_5	A	G	C	A	G	C
RD1_LO_8	A	G	C	A	G	C
RD1_LO_7	A	G	C	A	G	C
RD1_LO_6	A	G	C	A	G	C
RD1_LO_5	A	G	C	A	G	C
RD1_LO_4	A	G	C	A	G	C
RD1_LO_3	A	G	C	A	G	C
RD1_LO_2	-	-	-	-	-	-
RD1_LO_1	A	G	C	A	G	C
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	A	G	C	A	G	C

	1690	1700	1710	1720	1730	1740
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	T	A	T	A	A	G
RD1.5_LO_2	T	A	T	A	A	G
RD1.5_LO_3	T	A	T	A	A	G
RD1.5_LO_4	T	A	T	A	A	G
RD1.5_LO_5	T	A	T	A	A	G
RD1_LO_8	T	A	T	A	A	G
RD1_LO_7	T	A	T	A	A	G
RD1_LO_6	T	A	T	A	A	G
RD1_LO_5	T	A	T	A	A	G
RD1_LO_4	T	A	T	A	A	G
RD1_LO_3	T	A	T	A	A	G
RD1_LO_2	T	A	T	A	A	G
RD1_LO_1	T	A	T	A	A	G
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	T	A	T	A	A	G

	1750	1760	1770	1780	1790	1800
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	C	A	A	T	A	A
RD1.5_LO_2	C	A	A	T	A	A
RD1.5_LO_3	C	A	A	T	A	A
RD1.5_LO_4	C	A	A	T	A	A
RD1.5_LO_5	C	A	A	T	A	A
RD1_LO_8	C	A	A	T	A	A
RD1_LO_7	C	A	A	T	A	A
RD1_LO_6	C	A	A	T	A	A
RD1_LO_5	C	A	A	T	A	A
RD1_LO_4	C	A	A	T	A	A
RD1_LO_3	C	A	A	T	A	A
RD1_LO_2	C	A	A	T	A	A
RD1_LO_1	C	A	A	T	A	A
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	C	A	A	T	A	A

	1810	1820	1830	1840	1850	1860
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	T	A	C	C	G	T
RD1.5_LO_2	T	A	C	T	G	T
RD1.5_LO_3	T	A	C	T	G	T
RD1.5_LO_4	T	A	C	C	G	T
RD1.5_LO_5	T	A	C	T	G	T
RD1_LO_8	T	A	C	T	G	T
RD1_LO_7	T	A	C	T	G	T
RD1_LO_6	T	A	C	T	G	T
RD1_LO_5	T	A	C	T	G	T
RD1_LO_4	T	A	C	T	G	T
RD1_LO_3	T	A	C	T	G	T
RD1_LO_2	T	A	C	T	G	T
RD1_LO_1	T	A	C	T	G	T
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	T	A	C	T	G	T

	1870	1880	1890	1900	1910	1920
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	TCCTA					
RD1.5_LO_2	TCCTA - - -					
RD1.5_LO_3	TCCTA - - -					
RD1.5_LO_4	TCCTAGC - -					
RD1.5_LO_5	TCCTAGCAGTATTTTTAAAAACACCATtCTCAATTACTGAGTATtCCATTAACCTATTtAtT					
RD1_LO_8	TCCTAGCAGTATTTTTAAAAACACCATtCTCAATTACTGAGTATTCCATTAACCTATTTATT					
RD1_LO_7	TCCTAGCAGTATTTTTAAAAACACCA - TCTCAATTACTGAGTA - TCCATTAACCTA - TTA - T					
RD1_LO_6	TCCTAGCAGTATTTTTAAAAACACCA - TCTCAATTACTGAGTA - TCCATTAACCTA - TTA - T					
RD1_LO_5	TCCTAGCAGTATTTTT - AAACACCA - TCTCAATTACTGAGTA - TCCATTAACCTA - TTA - T					
RD1_LO_4	TCCTAGCAGTATTTTTAAAAACACCGTTCTCAATTACTGAGTA - TCCATTAACCTA - TTA - T					
RD1_LO_3	TCCTAGCAGTATTTTTAAAAACACCATtCTCAATTACTGAGTATTCCATTAACCTATTTATT					
RD1_LO_2	TCCTAGCAGTATTTTTAAAAACACCA - TCTCAATTACTGAGTA - TCCATTAACCTA - TTA - T					
RD1_LO_1	TCCTAGCAGTATTTTTAAAAACACCATtCTCAATTACTGAGTATTCCATTAACCTATTTATT					
S. bullata CRIB	TCCTAGCAGTATTTTTAAAAACACCATtCTCAATTACTGAGTATTCCATTAACCTATTTATT					
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	TCCTAGCAGTATTTTTAAAAACACCATtCTCAATTACTGAGTATTCCATTAACCTATTTATT					

	1930	1940	1950	1960	1970	1980
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	C	a	A	C	A	A
RD1_LO_8	C	A	A	C	A	A
RD1_LO_7	C	-	A	C	A	A
RD1_LO_6	C	-	A	C	A	A
RD1_LO_5	C	-	A	C	A	A
RD1_LO_4	C	-	A	C	A	A
RD1_LO_3	C	A	A	C	A	A
RD1_LO_2	C	-	A	C	A	A
RD1_LO_1	C	A	A	C	A	A
S. bullata CRIB	C	A	A	C	A	A
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	C	A	A	C	A	A

	2050	2060	2070	2080	2090	2100
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	C	A	C	A	A	T
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	C	A	C	A	A	T

	2110	2120	2130	2140	2150	2160
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CR1B	C	A	T	C	T	T
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	C	A	T	C	T	T

	2170	2180	2190	2200	2210	2220
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	-	-	-	-	-	-
RD3_LO_2	-	-	-	-	-	-
RD3_LO_1	-	-	-	-	-	-
RD3.5_2	-	-	-	-	-	-
RD3.5_1	-	-	-	-	-	-
RD3.5_4	-	-	-	-	-	-
RD2_LO_3						
RD2_LO_1						
RD2_LO_2						
RD1_LO_11						
RD1_LO_10						
RD1_LO_9						
RD1.5_LO_1						
RD1.5_LO_2						
RD1.5_LO_3						
RD1.5_LO_4						
RD1.5_LO_5	-	-	-	-	-	-
RD1_LO_8						
RD1_LO_7						
RD1_LO_6	-	-	-	-	-	-
RD1_LO_5	-	-	-	-	-	-
RD1_LO_4	-	-	-	-	-	-
RD1_LO_3	-	-	-	-	-	-
RD1_LO_2	-	-	-	-	-	-
RD1_LO_1	-	-	-	-	-	-
S. bullata CRIB	T	G	A	A	T	T
RD1_RO_1	-	-	-	-	-	-
RD1_RO_2	-	-	-	-	-	-
RD1_RO_3	-	-	-	-	-	-
RD1_RO_4	-	-	-	-	-	-
RD1_RO_5	-	-	-	-	-	-
RD1_RO_6	-	-	-	-	-	-
RD1_RO_7	-	-	-	-	-	-
RD1_RO_8	-	-	-	-	-	-
RD1_RO_9	-	-	-	-	-	-
RD1_RO_10	-	-	-	-	-	-
RD1_RO_11	-	-	-	-	-	-
RD1_RO_12	-	-	-	-	-	-
RD1_RO_13	-	-	-	-	-	-
RD1_RO_14	-	-	-	-	-	-
RD1_RO_15	-	-	-	-	-	-
RD1_RO_16	-	-	-	-	-	-
RD1_RO_17	-	-	-	-	-	-
RD1_RO_18	-	-	-	-	-	-
RD2_RO_1	-	-	-	-	-	-
RD2_RO_2	-	-	-	-	-	-
RD2_RO_3	-	-	-	-	-	-
RD2_RO_4	-	-	-	-	-	-
S. bullata consensus'	T	G	A	A	T	T

	2230	2240	2250	2260	2270	2280
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	T	A	T	T	G	A
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	T	A	T	T	G	A

	2290	2300	2310	2320	2330	2340
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	T	C	A	A	C	T
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	T	C	A	A	C	T

	2350	2360	2370	2380	2390	2400
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	G	C	A	G	T	G
RD1_RO_1	G	C	A	G	T	G
RD1_RO_2	G	C	A	G	T	G
RD1_RO_3	G	C	A	G	T	G
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	G	C	A	G	T	G
RD1_RO_6	G	C	A	G	T	G
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	G	C	A	G	T	G
RD1_RO_10	G	C	A	G	T	G
RD1_RO_11	G	C	A	G	T	G
RD1_RO_12	G	C	A	G	T	G
RD1_RO_13	G	C	A	G	T	G
RD1_RO_14	G	C	A	G	T	G
RD1_RO_15	G	C	A	G	T	G
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	G	C	A	G	T	G
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	G	C	A	G	T	G

	2410	2420	2430	2440	2450	2460
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB						
RD1_RO_1	ACAGGGGAAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- ATAAATGATCTCCCTTCTG				
RD1_RO_2	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- ATAAATGATCTTCCTTCTG				
RD1_RO_3	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- - - - -				
RD1_RO_4		- - - - - TCTC - - - - -				
RD1_RO_5	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- ATAAATGATCTCCCTTCTG				
RD1_RO_6	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- ATAAATGATCTCCCTTCTG				
RD1_RO_7	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- ATAAATGATCTCCTTCTG				
RD1_RO_8	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTTTATAAATGAAC	TCCCTTCTG				
RD1_RO_9	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- ATAAATGATCTCCCTTCTG				
RD1_RO_10	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTTG	- ATAA				
RD1_RO_11	ACAGGGGAAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- ATAAATGATCTCCCTTCTG				
RD1_RO_12	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- ATAAATGATCTCCCTTCTG				
RD1_RO_13	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- ATAAATGATCTCCCTTCTG				
RD1_RO_14	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- ATAAATGATCTCCCTTCTG				
RD1_RO_15	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- ATAAATGATCTCCCTTCTG				
RD1_RO_16	- - - - -					
RD1_RO_17	- - - - -					
RD1_RO_18	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- ATAAATGATCTCCCTTCTG				
RD2_RO_1	- - - - -					
RD2_RO_2	- - - - -					
RD2_RO_3	- - - - -					
RD2_RO_4	- - - - -					
S. bullata consensus'	ACAGGGTAGTCATCTTGGGCCGCTCCTATTTACTCTTTTT	- ATAAATGATCTCCCTTCTG				

	2470	2480	2490	2500	2510	2520
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB						
RD1_RO_1	T	T	A	T	C	A
RD1_RO_2	T	T	A	T	C	A
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	T	T	A	T	C	A
RD1_RO_6	T	T	A	T	C	A
RD1_RO_7	T	T	A	T	C	A
RD1_RO_8	T	T	A	T	C	A
RD1_RO_9	T	T	A	T	C	A
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	T	T	A	T	C	A
RD1_RO_12	T	T	A	T	C	A
RD1_RO_13	T	T	A	T	C	A
RD1_RO_14	T	T	A	T	C	A
RD1_RO_15	T	T	A	T	C	A
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	T	T	A	T	C	A
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	T	T	A	T	C	A

	2530	2540	2550	2560	2570	2580
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	-	-	-	-	-	-
RD3_LO_2	-	-	-	-	-	-
RD3_LO_1	-	-	-	-	-	-
RD3.5_2	-	-	-	-	-	-
RD3.5_1	-	-	-	-	-	-
RD3.5_4	-	-	-	-	-	-
RD2_LO_3						
RD2_LO_1						
RD2_LO_2						
RD1_LO_11						
RD1_LO_10						
RD1_LO_9						
RD1.5_LO_1						
RD1.5_LO_2						
RD1.5_LO_3						
RD1.5_LO_4						
RD1.5_LO_5						
RD1_LO_8						
RD1_LO_7						
RD1_LO_6						
RD1_LO_5						
RD1_LO_4						
RD1_LO_3						
RD1_LO_2						
RD1_LO_1						
S. bullata CRIB						
RD1_RO_1	ATAACATTGAGGAGCAAGTACTTTATACAAGATGATATTAACAATTTAACA	-	CTTGGTGTA			
RD1_RO_2	ATAACATTGAGGAGCAAGTACTTTATACAAGATGATATTAACAATTTAACA	ATCTTGGTGTA				
RD1_RO_3	-	-	-	-	-	-
RD1_RO_4	-	-	-	-	-	-
RD1_RO_5	ATAACATTGAGGAGCAAGTACTTTATACAAGATGATATTAACAATTTAACA	ATCTTGGTGTA				
RD1_RO_6	-	-	-	-	-	-
RD1_RO_7	ATAACATTGAGGAGCAAGTACTTTATACAAGATGATATTAACAATTTAACA	ATCTTGGTGTA				
RD1_RO_8	ATAACATTGAGGAGCAAGTACTTTGTACAAGATGATATTAACAATTTAAC	-	-	-	-	-
RD1_RO_9	ATAACATTGAGGAGCAAGTACTTTATACAAGATGATATTAACAATTTAACA	ATCTTGGTGTA				
RD1_RO_10	-	-	-	-	-	-
RD1_RO_11	ATAACATTGAGGAGCAAGTACTTTATACAAGATGATATTAACAATTTAACA	ATCTTGGTGTA				
RD1_RO_12	ATAACATTGAGGAGCAAGTACTTTATACAAGATGATATTAACAATTTAACA	ATCTTGGTGTA				
RD1_RO_13	ATAACATTGAGGAGCAAGTACTTTATACAAGATGATATTAACAATTTAACA	ATCTTGGTGTA				
RD1_RO_14	ATAACATTGAGGAGCAAGTACTTTATACAAGATGATATTAACAATTTAACA	ATCTTGGTGTA				
RD1_RO_15	ATAACATTGAGGAGCAAGTACTTTATACAAGATGATATTAACAATTTAACA	ATCTTGGTGTA				
RD1_RO_16	-	-	-	-	-	-
RD1_RO_17	-	-	-	-	-	-
RD1_RO_18	ATAACATTGAGGAGCAAGTACTTTATACAAGATGATATTAACAATTTAACA	ATCTTGGTGTA				
RD2_RO_1	-	-	-	-	-	-
RD2_RO_2	-	-	-	-	-	-
RD2_RO_3	-	-	-	-	-	-
RD2_RO_4	-	-	-	-	-	-
S. bullata consensus'	ATAACATTGAGGAGCAAGTACTTTATACAAGATGATATTAACAATTTAACA	ATCTTGGTGTA				

	2590	2600	2610	2620	2630	2640
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	-	-	-	-	-	-
RD3_LO_2	-	-	-	-	-	-
RD3_LO_1	-	-	-	-	-	-
RD3.5_2	-	-	-	-	-	-
RD3.5_1	-	-	-	-	-	-
RD3.5_4	-	-	-	-	-	-
RD2_LO_3						
RD2_LO_1						
RD2_LO_2						
RD1_LO_11						
RD1_LO_10						
RD1_LO_9						
RD1.5_LO_1						
RD1.5_LO_2						
RD1.5_LO_3						
RD1.5_LO_4						
RD1.5_LO_5						
RD1_LO_8						
RD1_LO_7						
RD1_LO_6						
RD1_LO_5						
RD1_LO_4						
RD1_LO_3						
RD1_LO_2						
RD1_LO_1						
S. bullata CRIB						
RD1_RO_1	G T A - -					
RD1_RO_2	G T A					
RD1_RO_3						
RD1_RO_4	- - - - -					
RD1_RO_5	G T A C					
RD1_RO_6	- - - - -					
RD1_RO_7	G T A C					
RD1_RO_8	- - - - -					
RD1_RO_9	G T A C					
RD1_RO_10						
RD1_RO_11	G T A C					
RD1_RO_12	G T A C					
RD1_RO_13	G T A C T A A T T T A A T G G A G C T G A A T G T T G G A A A A T G T A A A T A T A T G T G C C T C A C T A G A T C A T					
RD1_RO_14	G T A C T A A T T T A A T G G A G C T G A A T G T T A G A A A A T G T A A A T A T A T G T G C T T C A C T A G A T C A T					
RD1_RO_15	G T A C T A A T T T A A T G G A G C T G A A T G T T A G A A A A T G T A A A T A T A T G T G C T T C A C T A G A T C A T					
RD1_RO_16	- - - - - G T A A A T A T A T G T G C T T C A C T A G A T C A T					
RD1_RO_17	G T A C T A A T T T A A T G G A G C T G A A T G T T A G A A A A T G T A A A T A T A T G T G C T T C A C T A G A T C A T					
RD1_RO_18	G T A C T A A T T T A A T G G A G C T G A A T G T T A G A A A A T G T A A A T A T A T G T G C T T C A C T A G A T C A T					
RD2_RO_1	- - - - -					
RD2_RO_2	- - - - -					
RD2_RO_3	- - - - -					
RD2_RO_4	- - - - -					
S. bullata consensus'	G T A C C A A T T T A A T G G A G C T G A A T G T T A G A A A A T G T A A A T A T A T G T G C T T C A C T A G A T C A T					

	2650	2660	2670	2680	2690	2700
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB						
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	CTCCAACCAATGGATTTTATAAAATGAATGGTGCTGTTCTTGAACAAGTTAATACCTTTA					
RD1_RO_14	CTCCAACCAATGGATTTTATAAAATGAATGGTGCTGTTCTTGAACAAGTTAATACCTTTA					
RD1_RO_15	CTCCAACCAATGGATTTTAT - AAATGAATGGTGCTGTTCTTGAACAAGTTAATACCTTTA					
RD1_RO_16	CTCCAACCAATGGATTTTAT - AAATGAATGGTGCTGTTCTTGAACAAGTTAATACCTTTA					
RD1_RO_17	CTCCAACCAATGGATTTTATAAAATGAATGGTGCTGTTCTTGAACAAGTTAATACCTTTA					
RD1_RO_18	CTCCAACCAATGGATTTTAT - AAATGAATGGTGCTGTTCTTGAACAAGTTAATACCTTTA					
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	CTCCAACCAATGGATTTTATAAAATGAATGGTGCTGTTCTTGAACAAGTTAATACCTTTA					

	2710	2720	2730	2740	2750	2760
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB						
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	ACGATTTAGGAATAATTTTCGATTGTAAATTGGACTTCAGAAATCATATTACAACAAC	CTG				
RD1_RO_14	ACGATTTAGGAATAATTTTCGATTGTAAATTGGACTTCAGAAATCATATTACAACAAC	CTG				
RD1_RO_15	ACGATTTAGGAATAATTTTCGATTGTGAATTGGACTTCAGAAATCATATTACAACAAC	CTG				
RD1_RO_16	ACGATTTAGGAATAATTTTCGATTGTGAATTGGACTTCAGAAATCATATTACAACAAC	CTG				
RD1_RO_17	ACGATTTAGGAATAATTTTCGATTGTAAATTGGACTTCAGAAATCATATTACATCAAC	CTG				
RD1_RO_18	ACGATTTAGGAATAATTTTCGATTGTGAATTGGACTTCAGAAATCATATTACAACAAC	CTG				
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	ACGATTTAGGAATAATTTTCGATTGTAAATTGGACTTCAGAAATCATATTACAACAAC	CTG				

	2770	2780	2790	2800	2810	2820
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB						
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	T	T	A	G	C	A
RD1_RO_14	T	T	A	G	C	A
RD1_RO_15	T	T	A	G	C	A
RD1_RO_16	T	T	A	G	C	A
RD1_RO_17	T	T	A	G	C	A
RD1_RO_18	T	T	A	G	C	A
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	T	T	A	G	C	A

	2830	2840	2850	2860	2870	2880
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB						
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	C	T	T	A	T	G
RD1_RO_14	C	T	T	A	T	G
RD1_RO_15	C	T	T	A	T	G
RD1_RO_16	C	T	T	A	T	G
RD1_RO_17	C	T	T	A	T	G
RD1_RO_18	C	T	T	A	T	G
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	C	T	T	A	T	G

	2890	2900	2910	2920	2930	2940
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	T	A	A	C	A	T
RD1_RO_14	T	A	A	T	A	T
RD1_RO_15	T	A	A	T	A	T
RD1_RO_16	T	A	A	T	A	T
RD1_RO_17	T	A	A	T	A	T
RD1_RO_18	T	A	A	T	A	T
RD2_RO_1	.	.	.	.	.	.
RD2_RO_2	.	.	.	.	.	.
RD2_RO_3	.	.	.	.	.	.
RD2_RO_4	.	.	.	.	.	.
S. bullata consensus'	T	A	A	T	A	T

	2950	2960	2970	2980	2990	3000
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	-	-	-	-	-	-
RD3_LO_2	-	-	-	-	-	-
RD3_LO_1	-	-	-	-	-	-
RD3.5_2	-	-	-	-	-	-
RD3.5_1	-	-	-	-	-	-
RD3.5_4	-	-	-	-	-	-
RD2_LO_3						
RD2_LO_1						
RD2_LO_2						
RD1_LO_11						
RD1_LO_10						
RD1_LO_9						
RD1.5_LO_1						
RD1.5_LO_2						
RD1.5_LO_3						
RD1.5_LO_4						
RD1.5_LO_5						
RD1_LO_8						
RD1_LO_7						
RD1_LO_6						
RD1_LO_5						
RD1_LO_4						
RD1_LO_3						
RD1_LO_2						
RD1_LO_1						
S. bullata CRIB						
RD1_RO_1						
RD1_RO_2						
RD1_RO_3						
RD1_RO_4						
RD1_RO_5						
RD1_RO_6						
RD1_RO_7						
RD1_RO_8						
RD1_RO_9						
RD1_RO_10						
RD1_RO_11						
RD1_RO_12						
RD1_RO_13	-	-	-	-	-	-
RD1_RO_14	T	C	T	T	A	T
RD1_RO_15	T	C	T	T	A	T
RD1_RO_16	T	C	T	T	A	T
RD1_RO_17	T	C	T	T	A	T
RD1_RO_18	T	C	T	T	A	T
RD2_RO_1	-	-	-	-	-	-
RD2_RO_2	-	-	-	-	-	-
RD2_RO_3	-	-	-	-	-	-
RD2_RO_4	-	-	-	-	-	-
S. bullata consensus'	T	C	T	T	A	T

	3010	3020	3030	3040	3050	3060
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB						
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	A	A	A	A	A	A
RD1_RO_15	A	A	A	A	A	A
RD1_RO_16	A	A	A	A	A	A
RD1_RO_17	A	A	A	A	A	A
RD1_RO_18	A	A	A	A	A	A
RD2_RO_1	A	A	A	A	A	A
RD2_RO_2	A	A	A	A	A	A
RD2_RO_3	A	A	A	A	A	A
RD2_RO_4	A	A	A	A	A	A
S. bullata consensus'	A	A	A	A	A	A

	3070	3080	3090	3100	3110	3120
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB	.	.	.	.	.	.
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	CTGTC	TTTCTCCTGAAGCTGATTAATGGTGTTATCAACGCTCAATTTCTTCTGGAAAAAC				
RD2_RO_2	CTGTC	TTTCTCCTGAAGCTGATTAATGGTGTTATCAACTCTCAATTTCTTCTGGAAAAAC				
RD2_RO_3	CTGTC	TTTCTCCTGAAGCTGATTAATGGTGTTATCAACTCTCAATTTCTTCTGGAAAAAC				
RD2_RO_4	CTGTC	TTTCTCCTGAAGCTGATTAATGGTGTTATCAACGCTCAATTTCTTCTGGAAAAAC				
S. bullata consensus'	CTGTC	TTTCTCCTGAAGCTGATTAATGGTGTTATCAACKCTCAATTTCTTCTGGAAAAAC				

	3130	3140	3150	3160	3170	3180
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB						
RD1_RO_1						
RD1_RO_2						
RD1_RO_3						
RD1_RO_4						
RD1_RO_5						
RD1_RO_6						
RD1_RO_7						
RD1_RO_8						
RD1_RO_9						
RD1_RO_10						
RD1_RO_11						
RD1_RO_12						
RD1_RO_13						
RD1_RO_14						
RD1_RO_15						
RD1_RO_16						
RD1_RO_17						
RD1_RO_18						
RD2_RO_1	T	T	T	A	C	A
RD2_RO_2	T	T	T	A	C	A
RD2_RO_3	T	T	T	A	C	A
RD2_RO_4	T	T	T	A	C	A
S. bullata consensus'	T	T	T	A	C	A

	3190	3200	3210	3220	3230	3240
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB						
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	A	C	G	C	A	A
RD2_RO_2	A	C	G	C	A	A
RD2_RO_3	A	C	G	C	A	A
RD2_RO_4	A	C	G	C	A	A
S. bullata consensus'	A	C	G	C	A	A

	3250	3260	3270	3280	3290	3300
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB						
RD1_RO_1						
RD1_RO_2						
RD1_RO_3						
RD1_RO_4						
RD1_RO_5						
RD1_RO_6						
RD1_RO_7						
RD1_RO_8						
RD1_RO_9						
RD1_RO_10						
RD1_RO_11						
RD1_RO_12						
RD1_RO_13						
RD1_RO_14						
RD1_RO_15						
RD1_RO_16						
RD1_RO_17						
RD1_RO_18						
RD2_RO_1	T	C	T	A	C	T
RD2_RO_2	T	C	T	A	C	T
RD2_RO_3	T	C	T	A	C	T
RD2_RO_4	T	C	T	A	C	T
S. bullata consensus'	T	C	T	A	C	T

	3310	3320	3330	3340	3350	3360
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB						
RD1_RO_1	.	.	.	.	.	.
RD1_RO_2	.	.	.	.	.	.
RD1_RO_3	.	.	.	.	.	.
RD1_RO_4	.	.	.	.	.	.
RD1_RO_5	.	.	.	.	.	.
RD1_RO_6	.	.	.	.	.	.
RD1_RO_7	.	.	.	.	.	.
RD1_RO_8	.	.	.	.	.	.
RD1_RO_9	.	.	.	.	.	.
RD1_RO_10	.	.	.	.	.	.
RD1_RO_11	.	.	.	.	.	.
RD1_RO_12	.	.	.	.	.	.
RD1_RO_13	.	.	.	.	.	.
RD1_RO_14	.	.	.	.	.	.
RD1_RO_15	.	.	.	.	.	.
RD1_RO_16	.	.	.	.	.	.
RD1_RO_17	.	.	.	.	.	.
RD1_RO_18	.	.	.	.	.	.
RD2_RO_1	A	C	T	T	A	A
RD2_RO_2	A	C	T	T	A	A
RD2_RO_3	A	C	T	T	A	A
RD2_RO_4	A	C	T	T	A	A
S. bullata consensus'	A	C	T	T	A	A

	3370	3380	3390	3400	3410	3420
RD3_LO_5	.	.	.	.	.	.
RD3_LO_4	.	.	.	.	.	.
RD3_LO_2	.	.	.	.	.	.
RD3_LO_1	.	.	.	.	.	.
RD3.5_2	.	.	.	.	.	.
RD3.5_1	.	.	.	.	.	.
RD3.5_4	.	.	.	.	.	.
RD2_LO_3	.	.	.	.	.	.
RD2_LO_1	.	.	.	.	.	.
RD2_LO_2	.	.	.	.	.	.
RD1_LO_11	.	.	.	.	.	.
RD1_LO_10	.	.	.	.	.	.
RD1_LO_9	.	.	.	.	.	.
RD1.5_LO_1	.	.	.	.	.	.
RD1.5_LO_2	.	.	.	.	.	.
RD1.5_LO_3	.	.	.	.	.	.
RD1.5_LO_4	.	.	.	.	.	.
RD1.5_LO_5	.	.	.	.	.	.
RD1_LO_8	.	.	.	.	.	.
RD1_LO_7	.	.	.	.	.	.
RD1_LO_6	.	.	.	.	.	.
RD1_LO_5	.	.	.	.	.	.
RD1_LO_4	.	.	.	.	.	.
RD1_LO_3	.	.	.	.	.	.
RD1_LO_2	.	.	.	.	.	.
RD1_LO_1	.	.	.	.	.	.
S. bullata CRIB						
RD1_RO_1						
RD1_RO_2						
RD1_RO_3						
RD1_RO_4						
RD1_RO_5						
RD1_RO_6						
RD1_RO_7						
RD1_RO_8						
RD1_RO_9						
RD1_RO_10						
RD1_RO_11						
RD1_RO_12						
RD1_RO_13						
RD1_RO_14						
RD1_RO_15						
RD1_RO_16						
RD1_RO_17						
RD1_RO_18						
RD2_RO_1						
RD2_RO_2						
RD2_RO_3						
RD2_RO_4						
S. bullata consensus'						

RD2_RO_1	TTGTTGTTGAAATAATTGTAAGGATATAAATTGTTATAGTCTGTAAGGA
RD2_RO_2	TTGTTGTTGAAATAATTGTAAGGATATAAATTGTTATAGTCTGTAAGGA
RD2_RO_3	TTGTTGTTGAAATAATTGTAAGGATATAAATTGTTATAGTCTGTAAGGA
RD2_RO_4	TTGTTGTTGAAATAATTGTAAGGATATAAATTGTTATAGTCTGTAAGGA
S. bullata consensus'	TTGTTGTTGAAATAATTGTAAGGATATAAATTGTTATAGTCTGTAAGGA

Supplemental Figure 6 Full sequence obtained of ORF2 from *S. bullata*.