Josip Juraj Strossmayer University of Osijek

University of Dubrovnik

Ruđer Bošković Institute, Zagreb

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Martina Pavlek

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Mehanizmi uključeni u dinamiku satelitnih DNA u kompleksnim genomima

Martina Pavlek

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Mentor/i: dr. sc. Nevenka Meštrović Radan

Kratki sažetak doktorske disertacije:

Satelitne DNA su uzastopno ponovljene nekodirajuće sekvence smještene uglavnom u (peri)centromernom području. Mehanizmi njihovog nastanka, evolucije i širenja su još uvijek nedovoljno poznati i to posebice u necentromernim područjima. Analize sekvenci biblioteke satelitnih DNA u srodnom vrstama oblića roda *Meloidogyne* otkrile su jednostavnu i kompleksnu organizaciju te moguću ulogu kratkih očuvanih motiva kao promotora genomskih rearanžmana. Potraga za novim satelitnim DNA u sekvenciranom genomu kornjaša *T. castaneum* otkrila je 9 novih necentromernih satelitnih DNA, jednoliko zastupljenih u hetero i eukromatinu. Intenzivna izmjena među homolognim i nehomolognim kromosomima ukazuje na učinkovit mehanizam širenja ovih sekvenci u necentormernim regijama.

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Stručno povjerenstvo za obranu:

 dr. sc. Ivica Rubelj, viši znanstveni suradnik Instituta Ruđer Bošković u Zagrebu, predsjednik
 dr. sc. Nevenka Meštrović Radan, znanstvena suradnica Instituta Ruđer Bošković u Zagrebu, mentorica i član

3. prof. dr. sc. Vera Cesar, redovita profesorica Sveučilišta Josipa Jurja Strossmayera u Osijeku Odjela za biologiju, član

4. dr. sc. Branka Bruvo Mađarić, znanstvena suradnica Instituta Ruđer Bošković u Zagrebu, zamjena člana

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Mechanisms of satellite DNA sequence dynamics in complex genomes

Martina Pavlek

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Short abstract:

Satellite DNAs are tandemly repeated non coding sequences preferentially located in (peri)centromeric part of the genome. Mechanisms involved in their genesis, evolution and spread in complex genomes are still not well understood, especially in non-centromeric regions. Sequence analyses of satDNAs in the library of sister species from nematode genus *Meloidogyne* revealed simple and complex type (HOR) of organization and proposed short conserved motifs as possible promotors of genomic rearrangements. Genome-wide search for new satDNAs in sequenced genome of coleopteran *T. castaneum* led to identification of 9 non-centromeric satDNA families, evenly distributed within the putative heterochromatin and euchromatin. Extensive exchange between homologous and non-homologous chromosomes, suggests efficient propagation mechanism of tandem repeats in non-centromeric regions.

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Reviewers:

1. dr. sc. Ivica Rubelj, PhD, Senior Associated Researcher, Ruđer Bošković Institute, Zagreb

- 2. dr. sc. Nevenka Meštrović Radan, PhD, Associated Researcher, Ruđer Bošković Institute, Zagreb
- 3. prof. dr. sc. Vera Cesar, PhD, Josip Juraj Strossmayer University of Osijek
- 4. dr. sc. Branka Bruvo Mađarić, PhD, Associated Researcher, Ruđer Bošković Institute, Zagreb

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1. INTRODUCTION

1.1. Satellite DNA sequence features

Satellite DNAs (satDNAs) are tandemly repeated non coding DNA sequences that make a large part of almost all eukaryotic genomes, e.g. 50% of human genome is made of repetitive sequences (Lander et al. 2001) and 30% of pericentromeric satellite DNA; 20% of fruit fly (Kapitonov and Jurka 2003) and 40% of rice (Goff et al. 2002). Genomic regions extremely enriched in satDNAs are (peri)centromeric regions of chromosomes. A comprehensive bioinformatics analysis of centromeric satDNAs in a number of animal and plant species confirmed the rapid evolution of DNA sequences in these areas (Melters et al. 2013) although there are some satellite DNAs that are conserved in nucleotide sequence for long periods of time. Recent progress in genome sequencing has revealed that satDNAs also represent a substantial fraction of noncentromeric regions (Warburton et al. 2008). Absence of coding potential, extreme diversity of satDNAs and lack of direct evidence for any possible function(s) of satDNAs in a genome addresses an important question: why and how do satellite sequences accumulate in a genome?

SatDNAs are organized as long arrays of head-to-tail linked basic repeat units, monomers. Monomers are often A+T rich and can vary in size from few nucleotides only to more than 1 kb, building arrays up to 100 Mb in length. Nevertheless, monomer length between 150-180 and 300-360 bp was observed in many satellite DNAs and can be considered as evolutionarily favored. The current hypothesis links preferred monomer length and the length of DNA wrapped around 1 or 2 nucleosomes as a requirement that may facilitate regular phasing of nucleosomes in the centromere region (Zhang et al. 2013, Heslop-Harrison and Schwarzacher 2013).

Although satellite sequence can be extremely divergent, a common feature of many satDNAs is irregular distribution of sequence variability along the monomer sequence and formation of conserved sequence segments, probably because of evolution under selective constraints (Plohl et al. 2008). The most prominent examples are found in rice (Lee et al. 2006), nematodes (Meštrović et al. 2006), *Arabidopsis* and human (Hall et al. 2003). For example, short conserved motifs detected between centromeric satellite DNAs of rice and maize may represent functional elements originating from the ancestral sequence, arising about 50–70 Myr ago (Cheng et al. 2002).

However, among all detected conserved regions, the only function is assigned to the CENP-B box of alpha satDNA in human and other primates. It is a 17 bp long motif that binds

to the centromere CENP-B protein. It has been proposed that CENP-B participates in human centromere assembly (Masumoto et al. 1993). CENP-B is highly conserved protein in all mammalian centromeres, from human to marsupials (Earnshaw and Tomkiel 1992, Bulazel et al. 2006). Motifs highly similar in sequence to CENP-B box have also been found in divers mammalian (Kipling et al. 1995, Alkan et al. 2011) (Fig. 1.1.) and non-mammalian species (López and Edström 1998, Fantaccione et al. 2005) as a part of completely unrelated satellite DNAs but their functionality was not evaluated. In addition to its putative centromeric role of CENP-B protein, extensive sequence similarity of the CENP B and *pogo*-like transposases opens a speculative possibility that DNA-CENP B protein complex also promote recombination processes involved in maintenance of the satellite DNA arrays (Casola et al. 2008, Jaco et al. 2008).

Subclass	Human	C T T C G T T G G A A A C G G G A HSA	ECD	HSA	TOT
	1 1	TTTCGTCTGAGCCGGGT ECAcons70	9/9	2/8	11/17
and the second second	н I	CTTCCCAAAGAGCTGGA ECAcons71	6/9	3/8	9/17
Bearingen	- Horse	T T T C C C G G G A A A C G A G A ECAcons421+424	7/9	5/8	12/17
		CTTCTTCCAAAGGGGC ECA3cons221	7/9	5/8	12/17
	4	CTTCTTTCCAAAGGGGC ECA4cons450	7/9	5/8	12/17
		CTTCTTTCCAAAGGGGC ECA5cons451	7/9	5/8	12/17
	L Dog	CTTCATATGGAAATTCGCFAcons244+246	3/9	5/8	8/17
Hanney	Elephant	CTTTGCCGAGAACGGAGLAFcons842+936	6/9	4/8	10/17
and the second	Armadille	CTTTGCCGAGAACGGAG DNOcons1'3	6/9	4/8	10/17
Without L	Opossum	CTTTGCCGAGAACGGAG MDOcons528	6/9	4/8	10/17
644	Platypus	C T T T G C T C C C G G C C T G A OANcons144.1+144.2	5/9	3/8	8/17

Figure 1.1. CENPB box-like motifs extracted from consensus sequences. Conserved bases in the evolutionarily conserved domain (ECD) have been reported in red and conserved bases compared with human (HSA), other than the ECD domain, are reported in blue. The number of total conserved bases is reported in *last* column. On the left side is a phylogenetic tree according to Prasad et al. 2008. (figure taken from Alkan et al. 2011)

Another feature of satellite DNAs determined by their nucleotide sequence is secondary and tertiary structure, namely dyad structures and sequence- induced bent helix axis which can be involved in heterochromatin formation (Jonstrup et al. 2008) and specific recognition of DNA- binding protein components of the heterochromatin (Radic et al. 1992), respectively. Short inverted sequence segments, often detected in satellite monomers, form dyad structures and may be recognized by mechanisms related to transposition. Bent helix axis of the satellite monomer and a resulting structure of the DNA molecule composed of tandemly repeated monomers are induced by periodic distribution of nucleotides, particularly by distribution of short tracts of As and/or Ts phased with a turn of double helix (Martínez-Balbás et al. 1990).

1.2. Evolution of satellite DNA

1.2.1. Dynamic of satellite DNA evolution

As a part of non-coding genome high mutation rate is tolerated and indeed satellite DNAs are one of the most rapidly evolving DNA sequences in eukaryotic genome that show differences even among closely related species (Henikoff et al. 2001). In contrast, sequence divergence between monomers of the same family is often low, usually up to 15% (see for example King and Cummings 1997). However, the divergence can be much higher in some cases, such as in monomeric human alpha-satellite with repeating units divergence up to 30% (Rudd and Willard 2004) or lower as detected in homogenous satDNA of bees with only 1.4 % monomer divergence (Tares et al. 1993). High monomer homogeneity in satDNA family is achieved by non-independent evolution of monomers through the two-level process of molecular drive. Mutations are homogenized throughout members of a satDNA family by mechanisms of non-reciprocal sequence transfer and concomitantly fixed within a group of reproductively linked organisms as a result of random assortment of genetic material (Dover 1982, 1986). The consequence is concerted evolution of monomers with higher sequence similarity of a satellite family among the same then between different species and finally formation of species specific satellite DNAs (Fig. 1.2.1.a). Level of sequence variability in a satellite DNA is therefore equilibrium between the process of accumulation of mutations and the rate of their spread (or elimination) among satellite monomers.

Homogenization mechanisms also affect repeat organization of some satDNAs, resulting in higher-order repeats (HORs) (see section 2.3.1. Complex organization of alpha satDNAs). An important outcome of mechanisms involved in homogenization is a higher degree of sequence similarity observed among adjacent repeats than among those retrieved at random. Monomers can often be clustered into satDNA subfamilies which are usually chromosome-specific (Dover 1986, Willard and Waye 1987). Sequence divergences accumulate because of higher homogenization efficiency among adjacent monomers than among those positioned in different arrays on the same chromosome, and progressively, on homologous and heterologous chromosomes (Dover 1986).

4

Besides gradual sequence evolution of satDNAs in separate lineages, it has been also suggested that changes in the number of copies could produce species-specific satDNA as a result of a differential amplification of satDNAs which coexist in closely related species building satellite DNA library (Fig. 1.2.1.b). This model has originally been suggested by Fry and Salser (1977) analyzing a satellite DNA from the kangaroo rat, but the first experimental evidence of this concept was provided by studying satellite DNAs in insects of the genus Palorus (Meštrović et al. 1998). Study of the 4 unrelated species-specific dominant centromeric satellite DNAs revealed presence of low-copy counterparts of each of them in every examined species. Comparisons of high-copy and low-copy monomer variants of these satellites showed complete lack of any species-diagnostic mutations. Copy number changes may be accompanied by rapid change of satellite DNA profile and can explain speciesspecificity of satellite profiles even when satellite sequences remain "frozen" during long evolutionary periods (Mravinac et al. 2002). Not only distinct satellite DNAs, but also monomer variants of the single family can be distributed in genomes in the form of a library. For example, broad distribution of BIV160 satDNA indicates that library of similar variants existed in bivalve species for about 540 million years (Plohl et al. 2010). Until now, satellite DNA libraries were detected in various plant and animal taxa, probably representing the most common mode of satellite DNA evolution for example (Lin and Li 2006, del Bosque et al. 2011, Koukalova et al. 2010).



Figure 1.2.1. Schematic representation of satellite DNA evolutionary concepts. **a)** Concerted evolution. Satellite DNA is changed due to gradual accumulation of sequence divergence. **b)** Satellite DNA library concept. Variation in satellite profiles is obtained by changes in copy number. (figure taken from Plohl et al. 2012)

1.2.2. Mechanisms of satellite DNA evolution

Mechanisms by which satellite DNAs are homogenized are unequal crossover, gene conversion, rolling circle replication and transposition (Fig. 1.2.2. and Fig. 1.2.3.) (Dover 1986, Smith 1976, Stephan 1986). Unequal crossover and gene conversion have been identified as the most widespread mechanism involved in satellite DNA dynamics through recombination during meiosis when homologue chromosomes become physically linked (Mahtani and Willard 1998, Talbert and Henikoff 2010). Unequal exchange can lead to expansion of new repeat variants and/or formation of higher-order repeats, as well as eliminating variation in monomers (Fig. 1.2.3.). Subsequent unequal crossovers between pairs of tandem array blocks either tandemly duplicate or delete an integral number of blocks.



Figure 1.2.2. Unequal exchange in satellite arrays. Identical tandem satellite repeats become diversified over time by mutation. Unequal exchange results in gain or loss of tandem repeats. Repeated exchange can lead to homogenization of satellite repeats (left). If the unit of exchange consists of multiple diverged monomers, higher-order repeats are generated (right). (figure taken from Talbert and Henikoff 2010)



Figure 1.2.3. Schematic representation of **a**) gene conversion, **b**) rolling circle replication and **c**) transposition - modular structure of one transposable element and the same element with 4 tandem repeats as core elements.

Gene conversion is the nonreciprocal exchange of genetic material that is initiated by DNA double-strand breaks and repaired by copying a short (usually 2 kb or less) stretch of the homologous chromosome. Dispersion of satellite DNAs on heterologous chromosomes can be explained by other two mechanisms, rolling circle replication and transposition. The discovery of human extrachromosomal circular DNA originating from satDNA supports the idea that excision, rolling circle replication and reinsertion of eccDNA plays a significant role in the evolution of satellite repeats. Growing number of reports indicate a link between transposable elements and satDNAs in the genome suggesting that efficient dispersion of satellite sequences throughout the genome can be facilitated by mechanisms related to transposition. For example, 2-6 tandem repeats that are related in sequence and monomer length to broadly distributed BIV160 satellite family among mollusks, are found as a part of sequences resembling MITEs in clam Crassostrea virginica (Plohl et al. 2010, Gaffney et al. 2003). Also, high copy number MITE, named DTC84, is characterized in the clam Donax trunculus and one of its organization features is presence of core repeats (Šatović and Plohl 2013). More examples are found in Drosophila sp. (Miller et al. 2000) and in the cycas Zamia paucijuga (Cafasso et al. 2003) but the true nature of mechanism(s) that expand fragments of mobile or mobile- like elements into long arrays of satellite DNAs is not known. While evolution of sequence segments from mobile elements to satellite DNAs seems to be a logical scenario, the possibility that satellite DNA fragments were simply captured by mobile elements is also open (Kejnovsky et al. 2006). At this point it may be speculated that both pathways are possible and that a sequence can be repeatedly reverted from one organizational form to the other. Recent study of repetitive sequences in rice centromere also indicate that segmental duplication of large arrays of satellite repeats is primarily responsible for the amplification of satellite repeats (Ma and Jackson 2006).

1.3. Satellite DNAs and centromeres

The centromere is a chromosomal locus responsible for the faithful segregation of genetic material during cell division. The majority of eukaryotes studied in terms of centromeric DNA have monocentric chromosomes with large regional centromeres (Fig. 1.3.1.a). The centromere includes the core or functional centromere domain, a specialized locus at which microtubules attach to the complex multiprotein structure of the kinetochore in order to segregate chromosomes in mitosis and meiosis. Two classes of highly abundant repetitive sequences, satDNAs and transposable elements (TEs), represent major DNA components of many centromeric regions of monocentric chromosomes. Centromere paradox is that despite of the extreme diversity of satDNA sequences in this region, centromere function is very highly preserved throughout all eukaryotes. It is proposed that fast evolving satellite DNAs push adaptive evolution of centromeric histones (CENH3) which in turn serve as a link between fast evolving satellite DNAs and preserved kinetochores (Henikoff et al. 2001). In the absence of a universal DNA sequence, species-specific histone H3 variant CENH3 is the most prominent protein identifier of centromere function.

Centromeric regions harbor as much as megabases of satellite DNA even though much less is enough for centromere function. For example, functional part of *Drosophila* sp. centromere is 15-40 kb long satDNA array or 30-70 kb in artificial human chromosome (Okamoto et al. 2007). Generally, huge differences in copy number of satellites in (peri)centromeric regions among homologous and heterologous chromosomes are very common (Plohl et al. 2012) even between individuals (Altemose et al. 2014).



Figure 1.3.1. Assembly of kinetochores on monocentric (A) and holocentric (B) chromosomes (figure taken from Dernburg 2001)

Holocentric centromere organization, with kinetochore forming in a plate shape along the whole length of the chromosomes (Dernburg 2001) (Fig. 1.3.1.b), has arisen independently at least 13 times during species evolution (Mola and Papeschi 2006) but DNA sequences underlying these centromeres are very poorly known. However, comprehensive study of satDNA in centromeric regions of different plant and animal species show that genomic content of tandem repeats in holocentric species differs greatly (Melters et al. 2013). Centromeric function in holocentric species, based on immunodetection of CENH3 homologs, has been intensively analyzed only in the nematode *Caenorhabditis elegans* and in few other species. For example, *C. elegans* genome contains only a few tandem repeats (Hillier et al. 2007) while ChIP analysis shows that ~50 % of this genome is associated with CENH3, but CENH3 loci are not correlated with repeat density (Gassmann et al. 2013). In contrast, comprehensive characterization of holocentric *Luzula elegans* shows that 61 % of its genome is built of highly repetitive DNAs, including over 30 highly divergent satellite families, while 33 % of the genome comprises Ty1/copia LTR retrotransposons of the Angela clade (Heckmann et al. 2013).

1.3.1. Complex organization of alpha satDNAs

One of the most extensively studied repetitive DNA families is the primate specific alpha satellite DNA. Monomer of human alpha satellite is 171- bp long monomer and satellite arrays are categorized into two basic types according to their genomic organization and sequence properties: monomeric and higher order repeats (HOR). HOR fraction represent centromere core which is associated with centromere function, while monomeric arrays constitute the flanking pericentromeric heterochromatin and are not involved in centromeric activity (Fig. 1.3.2.).



Figure 1.3.2. Structural organization of human (peri)centromeric regions. A typical human chromosome is schematically delineated, emphasizing (peri)centromeric regions. Small arrows in different colors represent single monomers of alpha satellite DNA, while HOR units are indicated by large red arrows. A fraction of HORalpha satellite forms centromeric chromatin, built from subdomains of nucleosomes containing centromeric histone CENP- A (red circles) interspersed with histone H3 dimethylated at lysine 4 ($H_3K_4me_2$) (green circles). The remainder of alpha satellite DNA is assembled into heterochromatin enriched for nucleosomes containing histone H3 methylated at lysine 9 (H_3K_9me) (grey circles). (figure taken from Plohl et al. 2012 and based on Schueler and Sullivan 2006)

HORs are based on multimeric repeats with 2 to over 20 diverged monomers. Monomers within a HOR show an average pairwise sequence similarity of ~70%, until mutual HOR similarity is 97–100%. HOR arrays spread up to several megabases and in most cases appear to be chromosome specific. HOR alpha satellite associates with CENH3 and some monomers within HOR units contain the CENP- B box. Monomeric arrays are heterogeneous without any ordered periodicity and individual repeats have identity of 50-100%. These heterogeneous arrays are frequently interrupted by other satellites and interspersed repetitive elements such as LINEs, SINEs, and LTRs (Plohl et al. 2012).

Alpha satellite DNA is a widespread repetitive family within the primate lineage and it shows concerted manner of evolution (Willard and Waye 1987). All characterized primate species have a common monomer length of ~170 bp but monomer sequence and structural characteristics are very diverse among species (Fig. 1.3.3.). During evolution, at the time of the very first amplification steps, several different variants emerged (Alexandrov et al. 2001) and by their combining more complex repeating units ascended, among which the simplest are dimeric HOR units found in the genomes of Old and New World monkeys. They are also characterized by no chromosome specificity which appeared within the last 25– 35 Myr of primate evolution.



Figure 1.3.3. Structural properties of alpha satellite DNA in primates. Schematic illustration of repeating units. The form of HOR units, chromosome specificity of satellite suprachromosomal families as well as the presence of CENP- B box within the sequence is indicated. Phylogenetic relationships and approximate divergence dates are derived from the tree of living primates (Perelman et al. 2011). (figure taken from (Plohl et al. 2012)

1.4. Genome-wide analyses of satellite DNAs

Satellite DNAs are very unevenly distributed among genomes. In contrast to centromeric satDNAs which have been characterized in many plant and animal species studies of tandem repeats out of centromere regions were mainly carried out for a microand minisatellites. Since they are mostly part of repetitive heterochromatin, which generally lacks genes and other unique sequences, they are almost absent in most sequenced genomes which makes them hard to study. The repetitive nature of satDNAs makes them hard to sequence and even harder to assemble. For example, in coleopteran *Tribolium castaneum* 30% of assembled genome are repetitive sequences (Wang et al. 2008) but high copy centromeric satellite TCAST, whose abundance is experimentally estimated to as much as 35% (Feliciello et al. 2011), is highly underrepresented in assembled genome (Richards et al. 2008). However, recent development of appropriate bioinformatics algorithms and programs together with raising abundance of sequenced genomes opens a possibility for extensive and throughout analyses of whole genomes in terms of satDNA profile.

Warburton and others (2008) analyzed repetitive profile in euchromatic portion of human genome. They discovered it harbors many satellite DNAs, even 10 kb long fragments of tandemly repeated sequences (it was assumed that satellite DNAs in euchromatin are dispersed and that they don't form long arrays) which contained huge variety of monomer lenghts, from several to more than 1000 bp. In human, Satellites 2 and 3 show extreme variability in length of satellite DNA arrays, from 7 to 98 Mb, on Y chromosome among members of same population (Altemose et al. 2014). Comprehensive bioinformatics analysis of two mouse whole-genome shotgun assemblies characterized 62 newly TR families distributed on all chromosomes which make up a kind of unique chromosome bar code (Komissarov et al. 2011).

Recent studies of satDNAs in euchromatic genome region also suggest a role in modulation of gene regulation (Stam et al. 2002) in disease-associated gene mutation and acumulation the differences between closely related species which may have a phenotypic effects (Paar et al. 2011).

1. 5. Model organisms

1.5.1. Satellite DNAs in *Meloidogyne* spp

Species from genus *Meloidogyne* are root-knot plant-parasitic nematodes that cause vast damage in agriculture. The recent completion of two root-knot nematode genomes *M. incognita* (Abad et al. 2008) and *M. hapla* (Opperman et al. 2008) emphasized them as model organisms of metazoan plant parasitic species (Bird et al. 2009). In recent years extensive studies on satDNAs in many *Meloidogyne* species recovered that satellite sequence in these species evolve according to library model of evolution (Meštrović et al. 2006). Analysis of the distribution of sequence variability among three related satellite DNAs from the library revealed highly structured monomers, composed of alternating lowly variable, moderately variable and highly variable domains. Interestingly, comparison of satellite DNA sequences cloned from each species revealed that the entire monomer sequence is uniformly conserved, even in domains characterized as highly variable, although species are separated for about 45 Myr. An exceptionally complex pattern of sequence

variability was found in a family of satellite DNAs of root- knot nematode species from the genus *Meloidogyne* indicated two phases in evolution of satellites in the library (Fig. 1.5.1.).



Figure 1.5.1. The two phases in evolution of MEL172 satellites from Meloidogyne species (Meštrović et al. 2006). The first phase is formation of satDNAs in the library which are shaped and spread under selective pressure due to functional interactions. The second phase includes sequence conservation and persistence of satDNAs in the library for long time-periods.



Figure 1.5.2. Root-knot nematode most parsimonious hypothetic evolutionary scenario based on the distribution of satellite DNAs. Arrows indicate the origin and distribution of satellite DNAs in root-knot nematodes. (taken from Meštrović et al. 2009, modified)

In addition, overall analysis of satDNAs in *Meloidogyne* species revealed their distribution as an informative character that can explain some aspects of evolutionary relationships, while interspecies sequence divergence did not bear any relevant information (Meštrović et al. 2009) (Fig. 1.5.1).

Previous work showed that recently separated and reproductively isolated sister species *M. fallax* and *M. chitwoodi* share one, unique, satellite DNA from pMcCo family (Castagnone-Sereno et al. 1998) (Fig. 1.5.2.). Also, *M. chitwoodi* besides that one has another 5 satellite DNAs from the same familiy which altogether form two subfamilies, subfamily 1 (1a, 1b, 1c and 1d satDNAs) and subfamily 2 (2a and 2b satDNAs) (Castagnone-Sereno et al. 1998). Possible existence of a satellite library in these recently separated species makes them an ideal system for exploring the mechanisms involved in satellite DNA formation and spread and possible requirements on their sequences.

1.5.2. Satellite DNAs in *Tribolium* spp.

The cosmopolitan insect genus Tribolium comprises 33 species, including the major global pests of stored grain and cereal commodities for human consumption. Among them Tribolium castaneum, also known as the red flour beetle, represents a powerful model organism for studies of insect development, population genetics as well as comparative genomics. An extensive research has been done on satDNAs in many Tribolium species (Juan et al. 1993, Mravinac et al. 2004, Ugarković et al. 1996, Mravinac et al. 2005, Žinić et al. 2000, Mravinac and Plohl 2007, Mravinac and Plohl 2010). Single species-specific satellite DNAs distributed on (peri)centromeres of all chromosomes of the complement dominate in the majority of *Tribolium* species making up to 40% of the whole genomes. The genome of *T*. castaneum has recently been sequenced at sevenfold redundancy and annotated (Richards et al. 2008). The third version of the assembly (Baylor College of Medicine; Tcas 3.0) containing more than 90% of the sequenced genome has been assembled into 10 chromosomes (Kim et al. 2010). It is the first coleopteran genome that has been sequenced thus representing the largest and the most species diverse eukaryotic order. T. castaneum has a large blocks of (peri)centromeric heterochromatin uniformly distributed on all chromosomes, characterized by abundant species specific satellite DNA (TCAST satDNA) which comprise 35% of the genome (Feliciello et al. 2011). However, due to the presence and abundance of nearly identical satellite monomers T. castaneum centromeric satDNA has

been poorly represented by only 0.3% in genome sequence assembly (by RepeatScout) with the majority of sequenced pericentromeric satDNA included in unassembled reads (Wang et al. 2008). Given that the estimated genome size of 204 Mb is 44 Mb larger than the assembled genome sequence, it is likely that the centromeric portion of satellite DNA is omitted from assembly. Three complementary approaches used for de novo identification of repetitive DNA content and distribution recovered more than 30% of repetitive DNA in the assembled T. castaneum genome (Wang et al. 2008). Analysis using Tandem Repeat Finder with parameters \geq 2 copies, <500 pb of length, alignment score to report 30 and alignment parameters 2,7,7 recovered 4.9 % of total tandem repeats (2.5 % satellite DNA). Second approach using RepeatScout (≥50 bp) identified even 26% of repetitive DNA. Further, 4475 repeat families obtained by Repeat Scout were divided based on the percent of the genome that they occupy into classes: HighA, HighB, Mid and Low. Repetitive DNAs are not uniformly distributed among chromosomes: CH7 contains the least, while CH2, CH3, CH8, CH9 and CH10 contain the most (Wang et al. 2008). Distribution and density of repetitive DNA on each chromosome is shown in Figure 1.5.3. Position of putative heterochromatin (grey square under the plot for each chromosome in Fig. 1.5.3.) is determined by accumulation of HighA class repetitive families (Wang et al. 2008). Interestingly, in comparison with Drosophila genome microsatellites and minisatellites (1-6 bp and 7-100 bp per repeat unit, respectively) are less abundant in *Tribolium*. On the contrary, satellites over 100 nucleotides, which are quite rare in *Drosophila*, are prevalent in *Tribolium* genome.



Figure 1.5.3. Density and distribution of repetitive DNA on each chromosome of *T. castaneum*. The total length (kb) of repetitive DNA in each 500 kb interval along the chromosome is plotted. The 300 kb long uncaptured gaps were not included in the chromosomes. The HighA class includes the 360 bp satellite. Gene number, gap length and distribution of other repetitive classes within the 500 kb intervals are shown below the main graph for each chromosome. The combined average of HighA repeats and TE per 500 kb along the chromosome is depicted as a black line. (Figure taken from Wang et al. 2008)

2. AIMS

Key question about satellite DNA evolution concerns the nature of mechanisms that drive formation and spread of novel tandem repeats in genomes. Satellite library in recently separated *Meloidogyne* species makes them an ideal system for exploring the mechanisms involved in satellite DNA formation and possible requirements on satellite sequences. Analysis of organization, sequence features and phylogenetic relationships of monomers in five divergent satDNAs of the library shared by *M. fallax* and *M. chitwoodi* will be performed. In addition, the genome of *T. castaneum* has recently been sequenced and identification of repetitive DNA content recovered more than 30% of repetitive DNA. Genome-wide profiling of tandem repeats on assembled *T. castaneum* genome using Tandem Repeat Finder will be done. Further, localization of the most prominent satDNAs in relation to the centromeric satDNA and investigation of relationships among tandem repeats of particular satDNA family from different loci and structure of local genomic features will be performed. The expected results should expand the knowledge about the mechanisms involved in genesis and propagation of satellite sequences in complex genomes.

3. MATERIALS AND METHODS

3.1. Materials

Laboratory chemicals and material used in this study are listed in Tables 3.1. to 3.5. Commonly used buffers and solutions are listed in Table 3.1., commercial kits in Table 3.2. and enzymes in Table 3.3. Material is listed in Table 3.4. and other chemicals Table 3.5.

Molecular marker O'GeneRuler DNA Ladder Mix (Fermentas) was used for sample size estimation and Lambda DNA 50ng/ μ l was used to determine sample concentration.

Buffers and solutions	Contents
G buffer	0.1 M NaCl, 0.01 M Tris-HCl (pH 8.0), 25 mM EDTA (pH 8.0), 0.5% SDS
TE buffer	10 mM Tris-HCl (pH 8.0), 1 mM EDTA (pH 8.0)
TAE	40 mM Tris, 20 mM acetic acid, 1 mM EDTA (pH 8.0)
SSCx20	3 M NaCl, 0.3 M Na-citrat (pH 7.0)
PBS	137 mM NaCl, 2.7 mM KCl, 10.1 mM Na ₂ HPO ₄ , 1.8 mM KH ₂ PO ₄ (pH 7.4)
Southern hybridization	
solution	0.25 M Na ₂ HPO ₄ pH 7.2, 1 mM EDTA, 20% SDS, 0.5% blocking reagent
Southern buffer 1	0.1 M maleic acid, 3 M NaCl, 0.3% Tween 20 (pH 8.0)
Southern buffer 2	1% blocking reagent in buffer 1 (Southern)
Southern buffer 3	0.1 M Tris-HCl (pH 9.5), 0.1 M NaCl
Washing buffer (Southern)	20 mM Na ₂ HPO ₄ pH 7.2, 1 mM EDTA, 1% SDS)
Fixative solution FISH	acetic acid : aps. ethanol (1:3, v/v)
FISH buffer 1	5% (v/v) 1M MgCl ₂ in PBS buffer
FISH buffer 2	2.7% (v/v) 37% formaldehyde, 97.3% (v/v) FISH buffer 1
FISH denaturation solution	70% (v/v) fomamide in 2XSSC buffer
DeSO4 buffer	20% (m/v) DeSO ₄ , 50 mM NaPO ₄ (pH 7.0) in 4xSSC buffer
FISH hybridization solution	60% (v/v) formamide, 40% (v/v) DeSO₄ buffer
FISH washing buffer	50% (v/v) formamide, 50% (v/v) 2xSSC buffer
4M buffer	5% (m/v) blocking reagent in 4xSSC buffer
4T buffer	0.05% (v/v) Tween 20 in 4xSSC buffer
DAPI solution	50ng/ml DAPI in 2xSSC buffer
Antifade reagent	2.33% (m/v) DABCO, 8% (v/v) reH ₂ O, 2% (v/v) 1M Tris-HCl buffer (pH 8.0),
	90% (v/v) glycerol
NaOH 0.4 M	
KCI 0.075 M	
Na-acetate 3 M (pH 7.4)	

Table 3.1. Buffers and solutions

Table 3.2. Commercial kits

Kit	Manufacturer		
QIAquick Gel Extraction Kit	Qiagen		
QIAquick PCR Purification Kit	Qiagen		
pGEM-T Easy Vector SystemI	Promega		
GoTaq Flexi DNA			
Polymerase	Promega		
High Pure Plasmid Isolation			
Kit	Roche		
Nick Translation Mix	Roche		
Cy3 PCR Labeling Master	Jena Bioscience		
DNeasy Tissue Kit	Qiagen		

Table 3.3. Enzymes

Enzyme	Manufacturer
T4 DNA ligase	Promega
RNase A	Roche
Restriction enzymes: Hindll, Mbol, Hpall, Alul, Haelll, Hinfl, Rsal, Dral, EcoRl	Fermentas, Roche, BioLabs
Proteinase K	Roche

Table 3.4. Material

Matrials	Manufacturer		
Nylon mambranes,			
positively charged	Roche		
Röntgen film	Amersham		

Table 3.5. Other chemicals

Other chemicals	Manufacturer		
Cy3 Reactive Dye	Amersham		
Cy3-dUTP-PCR	Jena Bioscience		
Biotinylated dNTP Mixture	BioLabs		
Sodium dodecyl sulfate (SDS)	Sigma		
Agarose LE	Roche		
X-gal	Sigma		
IPTG	Invitrogene		
Blocking reagent	Roche		
CPD-Star	Roche		
Deoxynucletide Soultion Mix	BioLabs		
Elucrescent Avidin D	Vector		
	Laboratories		
Riotinulated Anti-Avidin D	Vector		
	Laboratories		
Streptavidin-AP-conjugate	Roche		
Colcemide	Roche		
Pepsine	Sigma		
Tween 20	Promega		
Fomamide	Sigma		
Formaldehyde	Sigma		
Acetic acid	Kemika		
Phenol	Sigma		
Phenol:chloroform	Sigma		
Kopleksal III (EDTA-Na ₂ x2H ₂ O)	Kemika		
Trizma base (Tris)	Sigma		
Ethanol aps.	Kemika		
Chloride acid	Kemika		
ומאט	Serva		
DAFI	Feinbiochemica		
DABCO	Sigma		
Glycerol	Kemika		
Bacto Tryptone, Bacto Yeast	Becton, Dickinson		
extract	& Co.		
Ampicilin	Sigma		
Luria Agar	Sigma		

Cloning vectors pUC18 (Fermentas) and pGEM T-Easy vector (Promega) were used to transform *Escherichia coli* Subcloning Efficiency DH5 α (Invitrogene) and XL10-Gold (Agilent Technologies) chemo competent and ultracompetent cells and ElectroMAX Stbl4 electrocompetent cells (Invitrogene). Bacteria were grown on liquid (for 1 liter: 10g tryptone, 5g yeast extract, 5g NaCl and ampicillin with final concentration of 100 µg/ml) and solid medium (15g of agar added per one liter of liquid medium).

Primers used for *Meloidogyne* species are listed in Table 3.6. and their position (except 2bL and R) is marked in Supplementary figures 4.1.2. and 4.1.3. Primers used for *T. castanuem* are listed in Table 3.7. Positions of Tcastan1 and Tcastan2 are marked in Figure 4.2.3., for R66_F and R66_R in Figure 4.2.16. and for all others in Supplementay figure 4.2.3.

Sequence name	Primer name	Sequence 5'-3'
1a satDNA	1aL	CCAAATTCAGCAAATTTCCAACGAT
	1aR	AATCCATCGACTAGTTTTTGAG
1a satDNA	1aL	CCAAATTCAGCAAATTTCCAACGAT
(HOR specific)	1a'R	GGGGAAGGAATATTTTTGAACTTTT
1b satDNA	1bL	CATATCTCTCAAAGCCTTCT
	1bR	TCGGAAGCATATTCGCTGT
1c satDNA	1cL	TCGATTCACCTCTTCATCCTC
	1cR	GGGGGGAGAATGGATACTTTG
2a satDNA	2aL	CCTCTTTCGAATGATATATGAATC
	2aR	TTCAGTAAGTTATGAGACTTGTTCC
2b satDNA	2bL	GGACTTATGAAATTGTAGGTCAGT
	2bR	GCTCTTTCGAATGATATATGAATC
U1	U1L	GGTGTAGAAGAGACAAGCCTC
	U1R	AGGGTGTTCCTTTACTCCTTC
U2	U2L	CTTGTTAGATATTTACAATTTTGG
	U2R	ATTCCCATTCTATATAGATGATG
<i>M. fallax</i> SCAR	Ff2	CCATTTCTGCTAAATGCCAAACTA
	Rf	GGACACAGTAATTCATGAGCTAG
M. chitwoodi	Fc2	GGCATTGACGTGCTCCGAGAGT
SCAR	Rc	GGTCTGAGTGAGGACAAGAGTA
 (HOR specific) 1b satDNA 1c satDNA 2a satDNA 2b satDNA U1 U2 <i>M. fallax</i> SCAR M. chitwoodi SCAR 	1a'R 1bL 1bR 1cL 1cR 2aL 2aR 2bL 2bR U1L U2R Ff2 Rf Fc2 Rc	GGGGAAGGAATATTTTTGAACTTTTCATATCTCTCAAAGCCTTCTTCGGAAGCATATTCGCTGTTCGATTCACCTCTTCATCCTCGGGGGGGAGAATGGATACTTTGCCTCTTTCGAATGATATATGAATCTTCAGTAAGTTATGAGACTTGTTCCGGACTTATGAAATTGTAGGTCAGTGCTCTTTCGAATGATATATGAATCGGTGTAGAAGAGACAAGCCTCAGGGTGTTCCTTTACTCCTTCCTTGTTAGATATTTACAATTTTGGATTCCCATTCTATATAGATGATGCCATTTCTGCTAAATGCCAAACTAGGACACAGTAATTCATGAGCTAGGGCATTGACGTGCTCCGAGAGTGGTCTGAGTGAGGACAAGACTA

Tabl	e 3.6.	Mel	loidog	yne	spp	.primers
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Sequence name	Primer name	Sequence 5'-3'
Cluster 1 (Cl1)	kl1_F	AAGTCGGCTACGACTAACCGTTC
	kl1_R	TTGCAAATTTGGATTCCGCCCGG
Cluster 2 (Cl2)	kl2_F	TATACGCAAAATGAGCCGC
	kl2_R	AAAGTCGTAGAGCAATGCGG
Cluster 3 (Cl3)	kl3_F	CACCAAATTTGGTCGAAAATGAC
	kl3_R	CGTGTTTAAATCCTCAGAACTTGC
Cluster 4 (Cl4)	kl4_F	GTTTGTTCCAGTGAATTCTGCGG
	kl4_R	CCGTTTTGCTCTACGACTTTTAG
Cluster 5 (Cl5)	kl5_F	GGTGTTGAAAAGTCATAARTTGAGTG
	kl5_R	GAGCCGGTGTACACAACATT
Cluster 7 (Cl7)	kl7_F	CGACGCATGGGTCAATCTAAGACA
	kl7_R	ATTCGAAACTTTTCAAAAAAATTGG
Cluster 8 (Cl8)	kl8_F	GAATCGTCCGAAATAAGCCG
	kl8_R	CTGAAAACGCCTTATTCTGGC
Cluster 9 (Cl9)	kl9_F	TCATGTTCGGACAAACACC
	kl9_R	TTTTTTACAGTCGAAGGCCC
Cluster 10 (Cl10)	kl10_F	GACAGATTTGGAATCCTTAGAC
	kl10_R	CTACGATTCGTAGTTTTGGAG
TCAST	Tcastan1	TGTAGGACTAACCATAAGCG
	Tcastan2	CAATGTTTGAGACGAAGACG
plasmid primers	M13 N	GTAAAACGACGGCCAGT
	M13 R	CAGGAAACAGCTATGAC
R66-like region	R66_F	TTCATATGGCTTCTCCGTTGG
	R66_R	TATTTACTGAGGTATTGAATTTGAT

Table 3.7. T. castaneum primers

3.1.1. Animal material

The *Meloidogyne* spp. isolates used in this study were chosen from the living collection maintained at INRA, Sophia Antipolis, France. The geographic origin of both studied species was The Netherlands; Spijkenisse for *M. chitwoodi* and Baexem for *M. fallax*. Nematodes were maintained on tomatoes (*Lycopersicon esculentum* cv. Saint Pierre) grown at 20°C in a greenhouse. *Tribolium castaneum* culture (laboratory strain) used in this study was obtained from Central Science Laboratory (Sand Hutton, York, UK). Insects were maintained on flour and kept in glass jars at room temperature, in a laboratory at Ruđer Bošković Institute.

3.2. Methods

3.2.1. Sampling and DNA Isolation

Tribolium castanem genomic DNA was isolated from adults. Approximately 70 specimens were frozen in liquid air (~ -196°C), grinded, suspended in G buffer (100 mg tissue \rightarrow 1 ml G buffer) containing 0.2 mg/ml of Proteinase K and left for overnight incubation at 50°C. After two rounds of phenol and phenol:chlorophorm (1:1) extraction, upper faze (containing DNA) was transferred to 2 volumes of 100% ice-cold ethanol and 0.1 volume of sodium acetate and precipitated by centrifugation for 15 minutes. The pallet was resuspended in TE buffer. Total nematode genomic DNA was purified from 50 - 100 μ l eggs using the DNeasy Tissue Kit according to the manufacturer's instructions. RNA was removed by incubation with RNaseA, 20 μ g/ml, for 1 hour at 37°C. Quality and quantity of DNA was checked by electrophoresis on 1% agarose gel by comparison with DNA markers of known length and concentration. Concentration was also checked on BioSpec-nano Spectrophotometer in Laboratory for molecular ecotoxicology at Ruđer Bošković Institute.

3.2.2. PCR Analyses, Cloning and Sequencing

Primers listed in Tables 3.6. and 3.7. were constructed based on consensus sequence of each of the satellite families during this work and were used to amplify specific DNA fragments in polymerase chain reaction (PCR). The reaction mixture consisted of reaction buffer, 1.5 mM MgCl₂, 0.2 mM dNTPs (Biolabs), 0.5 U GoTaq DNA polymerase, 0.4 mM of each primer and 20 ng of genomic DNA. The PCR cycling parameters used were as follows: 2 min initial denaturation at 94°C, followed by 30 cycles of: 94°C for 30 sec, 58°C for 30 sec, and 72°C for 1 min. Final extension was at 72°C for 10 min. Annealing temperatures for T. castaneum satDNAs were adjusted: 48°C for Cl10, 48.8°C for Cl9, 55°C for Cl7, 58°C for Cl1 and CI5 and 60°C for clusters 2, 3, 4 and 8. PCR products were purified using QIAquick PCR Purification Kit and separated by electrophoresis on agarose gel. Fragments of interest were cut from the gel, purified by QIAquick Gel Extraction Kit and ligated in pGEM T-Easy vector with T4 DNA ligase. 3µl of ligation mixture was used to transform Escherichia coli Subcloning Efficiency DH5α Competent, XL10-Gold Ultracompetent and ElectroMAX Stbl4 electrocompetent cells. All transformations were done according to manufacturer instructions. Bacteria were grown on solid medium overnight on 37°C (chemocompetent) and 30°C (electrocompetent) and recombinant clones were selected based on blue-white selection (40 µl X-gal and IPTG was added to each plate). Specifically, clones containing plasmid vector were selected based on antibiotic resistance and clones with recombinant plasmid were recognized by their white color opposite to blue clones which had plasmids without DNA sequence of interest. White colonies were transferred to liquid medium, grown over night to amplify and to isolate plasmids of interest using High Pure Plasmid Isolation Kit. Sequence of cloned DNA segments was determinated in Macrogene sequence centers in South Korea and Netherlands.

3.2.3. Southern and Dot Blot Analyses

Based on sequences of cloned fragments, recombinant clone for each satDNA was selected to be used as mold for oligonucleotide probe construction by polymerase chain reaction (selected clones are marked in Supplementary Figure 4.2.3.). The probes were labeled with biotin-16-dUTP (nucleotide mixture was: 0.5mM dATP, 0.5mM dCTP, 0.5mM dGTP, 0.4mM dTTP, 0.1 mM biotin-16-dUTP) and primers used were plasmid primers M13 (5'GTAAAACGACGGCCAGT3' and 5'CAGGAAACAGCTATGAC3') with which 234 bp of plasmid sequence is also amplified (a part on each side of the inserted fragment). The probe for TCAST satellite was labeled with Cy3-dUTP (Cy3 Reactive Dye and Cy3-dUTP-PCR) by nick translation using Nick Translation Mix and by polymerase chain reaction using Cy3 PCR Labeling Master, according to the protocol provided by manufacturers. The mold for TCAST probe synthesis was dimer obtained after digestion of *T. castaneum* genomic DNA with Alul and cloned into the plasmid vector pUC18. Primers used in PCR reacition were specific primers Tcastan1 and Tcastan2.

For Southern blot hybridization restriction analyses were done on all investigated genomic DNAs with different restriction endonucleases (Table 3.3.), preferentially with ones that cut once in a monomer. Fragments obtained by digestion of 5 to 8 µg of *T. casteneum* and ~3 µg of nematode genomic DNA were separated by electrophoresis on agarose gel and transferred to nylon membrane by alkaline transfer in 0.4M NaOH. After overnight transfer the membrane was washed 2x5min in 2xSSC buffer, dried, fixed by baking at 120°C for 20 minutes and then incubated for 2-4 hours in Southern hybridization solution at 60-68°C (prehybridization). For hybridization, the probe was denaturated by cooking for 10 minutes and then added to fresh Southern hybridization solution for overnight hybridization at the same temperature as prehybridization. Final probe concentration was 10-20 ng/ml. Next day

the detection procedure was: 3x20 minutes in washing buffer at 2°C below hybridization temperature, 5 minutes in Southern buffer 1 at room temperature, incubation for one hour in Southern buffer 2, incubation for 30 minutes in Southern buffer 2 with added streptavidin-AP-conjugate (1:10000), 5x10 minutes washing in Southern buffer 1 and incubation 2x5 minutes in Southern buffer 3. Finally, chemiluminescent detection of the signal was carried out by adding CDP-Star reagent to the membrane and leaving it for 15 minutes to several hours or overnight to expose the Röntgen film.

The abundance of satellite DNA sequences was estimated by quantitative dot blot analysis using a series of genomic DNA dilutions. Known concentrations of satellite monomers, excised from a plasmid, were dot-blotted and used as a calibration curve.

3.2.4. Fluorescence in situ hybridization (FISH)

Two colored fluorescence in situ hybridization (FISH) was carried out on *T. castaneum* male gonads. To determine positions of new satDNAs related to (peri)centromeric regions a mixture of Cy3 TCAST probe and biotin labeled probe for each of new satDNAs was made and in order to investigate localization of CI5 repeats and their flanking regions we used mixture of monomer Cy3 probe amplified by kl5_F and kl5_R primers and flanking region biotin probe amplified by R66_F and R66_R primers. Slides were prepared by "squash,, technique. Male gonads were isolated from adults, transferred to colcemide (10 μ g/ml) for 1 hour, then to 75 mM KCl for 15 minutes (or less) to produce hypotonic shock after which they were fixed in fixative solution for 10 minutes, transferred to slide with 100 μ l of 45% acetic acid, covered with covering glass, firmly squashed, frozen in liquid air and after removing cover glass left to dry on room temperature. After drying slides can be stored on -20°C or used for hybridization right away. Pretreatment for FISH was: 5 minutes washing in preheated (37°C) 2xSSC buffer, 1 hour incubation with RNase A (20mg/ml in 2xSSC) on 37°C, 3x5 minutes washing in 2xSSC, 10 minutes incubation with pepsin (100 µg/ml in 10 mM HCl) on 37°C, 2x5 minutes washing in PBS buffer, 5 minutes washing in FISH buffer 1, 10 minutes incubation in FISH buffer 2, 5 minutes washing in PBS buffer, dehydration through series of ice cold ethanol, 70%, 90% and 100%, 3 minutes in each and then drying at room temperature. Denaturation of sample is carried out in FISH denaturation solution at 70°C for 2 minutes followed by another series of ethanol dehydration drying at room temperature. 100 ng of each probe (TCAST and one of new satellite DNAs) was mixed together and dried,

resuspended in 10 µl of FISH hybridization solution, denaturated at 75°C for 5 minutes and then applied to the sample which was left for overnight incubation at 37°C. Detection procedure was as follows: 4x5 minutes washing in FISH washing buffer at 37°C, 3x5 minutes washing in 2xSSC buffer at 37°C, 30 minutes incubation at 37°C in 4M buffer, 30 minutes incubation at 37°C in 4M buffer with fluorescent Avidin D (1:500), 3x5 minutes washing in 4T buffer, 20 minutes incubation at 37°C in 4M buffer, 20 minutes washing in 4T buffer, 5 minutes washing in 98S buffer, dehydration through series of ice cold ethanol, 70%, 90% and 100%, 5 minutes in each and then drying at room temperature. After dyeing in DAPI solution, a drop of antifade reagent was applied on the sample which was then covered with cover glass. All signals were viewed through appropriate filters for blue (DAPI), red (CY3) and green (FITC) fluorescence, using Opton Leitz microscope equipped with Pixera Pro150ES digital camera at the Division of Molecular Biology, Department of Biology, Faculty of Science in Zagreb.

3.2.5. Bioinformatics methods

Sequenced genome of Tribolium castanem was downloaded in fasta format from the web page <u>ftp://ftp.bioinformatics.ksu.edu/pub/BeetleBase/3.0/</u> in the form of 10 chromosomes and 2153 unassembled reads. Sequence of each chromosome was uploaded to Tandem repeats database (TRDB) (Gelfand et al. 2006), <u>https://tandem.bu.edu/cgi-</u> bin/trdb/trdb.exe, where it was analyzed with tandem repeats finding algorithm (TRF) (Benson 1999) for tandemly repeated sequences. Conditions that can be adjusted are alignment parameters (match, mismatch, indels) and minimum alignment score to report. The program allows the result of TRF (a series of arrays) to be filtered out for copy number (number of repeats in the array), pattern size (size of the monomer unit) and for redundant sequences. After all chromosomes have been processed with TRF and filtered out, remaining arrays have been merged in one file which was then analyzed with clustering tool. Conditions that can be adjusted are cutoff value (from 95 to 60% of similarity) and appliance of heuristical, DUST and PAM algorithm. The result of these analyses is formation of several clusters - groups of arrays that in this case represent putative satellite DNAs. Sequences of all arrays from selected clusters were downloaded in fasta format. Left and right flanking region of all clustered arrays was also downloaded, 4000 bp in length. For each of the arrays
flanking regions had to be checked for monomer residues (sometimes several full length copies) and in some cases manually adjusted. This happens because in the case of 10 to 15 bp (or more) long deletions TRF algorithm doesn't recognize the sequence after the deletion as the same array. TRF analyses were done on unassembled reads also, just to understand the rough distribution of putative satellites in them.

All *T. castaneum* downloaded and *Meloidogyne* sp. cloned sequences were blasted against NCBI GenBank Database and Repbase Update (a collection of repetitive DNAs) (Jurka et al. 2005) to check similarity with published sequences. The sequences were further analyzed in programs BioEdit 7.0.9.0. (Hall 1999) and Geneious 5.5.6. Alignments of all monomers of each of the putative satellite DNAs were done using ClustalW algorithm (Thompson et al. 1997) which also constructed consensus sequences that were used to produce specific primers for each of the putative satellite DNAs.

The same alignments (without truncated monomers from the beginning and the end of the array) were used for phylogenetic analyses. First step was to select best-fit model of nucleotide substitution for each of the alignments which was done by jModelTest 2.1.3. (Darriba et al. 2012). Obtained model and other parameters were then applied in phyML 3.0. (Guindon and Gascuel 2003) and PAUP (Swofford 2002) programs to build a phylogenetic tree for each of the alignments. The trees were adjusted and displayed in MEGA 3.1 (Kumar et al. 2004), FigTree 1.3.1. and CorelX3 programs.

Sequenced genomes of two species from the same genus as studied nematode model organisms, *Meloidogyne incognita* and *M. hapla*, were searched for specific sequence motifs.

4. RESULTS

4.1. Sequence analysis of satellite DNAs in Meloidogyne chitwoodi and M. fallax

4.1.1. Analysis of complex satDNA Arrays

Possibility of sample cross-contamination with other nematode DNA was excluded through PCR check of genomic DNAs with SCAR (sequence characterized amplified region) primers (listed in Table 3.6.) specific for *M. chitwoodi* and *M. fallax* species (Zijlstra 2000) (Fig. 4.1.1.).



Figure 4.1.1. Electrophoretic separation of PCR products obtained by amplification of *M. chitwoodi* and *M. fallax* genomic DNAs using SCAR primers for a) *M. chitwoodi* and b) *M. fallax*.

PCR search for orthologue counterparts of satellite DNAs from *M. chitwoodi* in *M. fallax* confirmed the presence of 1a, 1b, 1c, 1d and 2a families while 2b has not been isolated (Fig. 4.1.2.). Amplification with primers specific for 1a, 2a and 2b satellite DNAs produced ladder of bands based on the monomer size. Amplification with primers specific for 1b produced bands of monomeric and dimeric size together with a fragment of about 1.5 kb in length, while amplification with 1c and 1d primers revealed complex but similar profiles (shown only for 1c).



Figure 4.1.2. Electrophoretic separation of PCR products obtained by amplification of *M. chitwoodi* and *M. fallax* genomic DNAs using primers specific for 1a, 1b, 1c, 2a and 2b satellite DNAs. M is the DNA ladder marker.

For more detailed analyses of 1c satellite DNA, bands corresponding to multimeric size (i.e. \geq 500 bp) obtained by amplification from both genomes were cloned and sequenced. All sequenced clones (59 altogether) are listed in Table 4.1.1.

Eight cloned fragments are composed of alternating 1c and 1d satellite DNA monomers which together define the dimeric unit, 338 bp long (169 bp x 2), organized in homogenous arrays in both genomes. Alignment of all 8 clones ($M_{1c}fa_n$ and $M_{1c}ch_n$; Table 4.1.1.) is given in Supplementary Fig. 4.1.1. Absence of a 170 bp based ladder in PCR amplification with 1c or 1d specific primers suggests that dimeric form composed of 1c and 1d monomers is the basic repeating unit of those two satellite families. Multiple sequence alignment of another 12 fragments ($H_{1c}fa_n$ and $H_{1c}ch_n$; Table 4.1.1.) revealed complex arrays composed of satellite DNA monomers 1a, 1b, a new 1b' variant, 1c, 1d and 2a together with so far uncharacterized sequence segment named U1. No relevant sequence homology of U1 with the studied satellite DNAs or any other sequence deposited in data bases was revealed with BLAST search. The alignment of complex HOR element, with each satellite family colored in different color, is given in Supplementary Fig. 4.1.2.

Table 4.1.1. Description of cloned satellite DNA arrays. In cloned satellite fragments, letters H, M and h indicate higher-order repeats, monomeric arrays, complex fragment, respectively. Then follows primer name (first subscript), species acronym and clone number (second subscript).

primers	species	Satellite	Length (bp)
		fragments	
		H _{1c} fa ₂	1353
		$H_{1c}fa_8$	1588
		$H_{1c}fa_{17}$	1530
	M. fallax	$H_{1c}fa_{18}$	1445
		$M_{1c}fa_8$	505
		$M_{1c}fa_{11}$	505
		$M_{1c}fa_6$	505
		$M_{1c}fa_7$	505
1c satDNA		$H_{1c}ch_2$	1480
primers		$H_{1c}ch_3$	1480
(1cL and		$H_{1c}ch_4$	1480
1cR)		$H_{1c}ch_6$	1480
		$H_{1c}ch_8$	1480
	M chitwoodi	H _{1c} ch ₉	1523
	w. chilwoodi	H _{1c} ch ₁₁	1200
		$H_{1c}ch_{12}$	1533
		M _{1c} ch ₁₃	505
		$M_{1c}ch_{16}$	505
		$M_{1c}ch_{10}$	505
		$M_{1c}ch_5$	505
		H _u fa₄	1422
		Hufa₁	1419
		H _u fa ₇	1419
	M. fallax	$H_u fa_8$	1252
		Hufa₀	1253
		H _u fa ₁₀	1419
U1 primers		h _u fa ₁	750
(U1L and		h _u fa ₂	750
U1R)		h _u fa ₃	870
		H _u ch ₁₁	1264
		H _u ch ₂₁	1269
		H _u ch ₂₂	1268
	M. chitwoodi	H _u ch ₂₃	1266
		huch1	750
		h _u ch ₂	750
		h _u ch ₃	870

	anasias	Satellite	Length		
primers	species	fragments	(bp)		
		$M_{1a}fa_1$	910		
		$M_{1a}fa_2$	903		
	M fallax	$M_{1a}fa_3$	903		
	Wi. Juliux	$M_{1a}fa_4$	901		
		$M_{1a}fa_6$	902		
1a satDNA		$M_{1a}fa_7$	906		
primers		$M_{1a}ch_3$	941		
(1aL and		$M_{1a}ch_4$	586		
1aR)		$M_{1a}ch_5$	587		
	М.	$M_{1a}ch_6$	575		
	chitwoodi	$M_{1a}ch_8$	914		
		$M_{1a}ch_9$	922		
		$M_{1a}ch_{10}$	911		
		$M_{1a} ch_{13} \\$	911		
		$M_{2a}fa_3$	801		
	M fallay	$M_{2a}fa_4$	487		
za sat DNA	wi. juliux	$M_{2a}fa_5$	487		
(2al and		$M_{2a}fa_7$	487		
(202 0110 2aR)	Λ.	$M_{2a}ch_1$	487		
	chitwoodi	$M_{2a}ch_2$	487		
	cintwoodi	$M_{2a}ch_3$	801		
2b satDNA		$M_{2b}ch_1$	500		
primers	М.				
(2bL and	chitwoodi	$M_{2b} ch_2$	500		
2bR)					

In order to extend the segments of complex arrays, U1 specific PCR primers were constructed and used for amplification in both genomes. Obtained PCR products revealed fragments of expected lengths (~1200 and ~1400 bp) but also a shorter fragment of about 700 bp. Sequencing of longer fragments (H_uch_n and H_ufa_n; Table 4.1.1.) confirmed the same HOR organization and their alignment is shown together with sequences obtained with 1c primers in Supplementary Fig. 4.1.2. Schematic representation of HOR element, composed of U1, 1a, 1b, 1b', 1d, 1c and 2a units is given in Fig. 4.1.3.



Figure 4.1.3. The long-L and short-S HOR sequence. The percent identity between monomers is written on arrows above the scheme. Box 1 and Box 2 in junction regions between different monomeres are indicated. 1d* and 1c* represent truncated 1d and 1c monomers.

Interestingly, 1d and 1c units at the end of HOR are truncated with complete monomer 2a located between them (Fig. 4.1.3.). Detailed sequence analyses showed high homogeneity of HOR units - 84 to 99% of mutual sequence identity. In contrast, neighboring monomers in HORs show a wide range of relationships: from relatively high sequence identity of 86% between 1b and 1b' variants, through moderate similarity of about 60% to apparently unrelated sequences sharing only 32% identity, such as detected between 2a and 1c monomers. The similarities between satDNAs are summarized in Table 4.1.2. and illustrated in Fig. 4.1.3.

								1dHch _n ,	1cHch _n ,	2aHch _n ,	
monomer	Monomers	Group		1aHch _n ,	1aMch _n ,	1bHch _n ,	1b'Hch _n	1dHfa _n ,	1cHfa _n ,	2aHfa _n	2hMch
length	name	name		1aHfa _n	1aMfa _n	1bHfa _n	1b'Hfa _n	1dMch _n	1cMch _n ,	2aMch _n ,	ZDIVICIIn
								1dMfa _n	1cMfa _n	2aMfa _n	
170	1aHch _n ,										
170	1aHfa _n	1aH	26	94 (2.8) ^a							
169 (+5)	1aMch _n ,										
105 (15)	1aMfa _n	1aM	50	81 (1.6)	94 (2.1)						
	1bHch _n ,										
170	1bHfa _n	1bH	10	63 (1.9)	64 (0.8)	99 (0.3)					
170	1b'Hch _n										
	1b'Hfa _n	1b'H	21	64 (1.2)	66 (0.9)	86(2.9)	93 (4.7)				
	1dHch _n ,										
160	1dHfa _n ,	1dMH									
105	1dMch _n ,										
	1dMfa _n		31	64 (1.9)	63 (2.0)	57 (0.5)	56 (0.7)	98 (1.7)			
	1cHch _n ,										
169	1cHfa _n ,	1cMH									
105	1cMch _n ,	ICIVIT									
	1cMfa _n		31	56 (0.6)	53 (1.0)	52 (0.2)	51 (1.2)	62 (1.0)	99 (0.5)		
	2aHch _n ,										
190	2aHfa _n	25MH									
100	2aMch _n ,	2014111									
	2aMfa _n		37	39 (0.9)	40 (1.0)	46 (0.6)	42 (1.0)	36 (0.7)	32 (0.5)	97 (1.6)	
179	2bMch _n	2bM	10	40 (1.1)	40 (0.8)	51 (0.5)	46 (1.6)	37 (0.6)	35 (0.6)	60 (0.9)	96 (1.3)

Table 4.1.2. Mean of	percent seq	uence identity	between main	groups of	f satDNAs monomers.
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n-number of analyzed monomers

^aaverage percent identity scores for each pairwise comparison are indicated in bold, while standard deviation (SD) is indicated in bracket

In addition, HOR segments revealed two variants which differ in the presence of 1btype monomers. Long HOR variants have two consecutive monomers, 1b and 1b', that share sequence identity of 86%, while short HOR variants lack 1b monomer. Genomic DNA cut with the REs specific for 1c monomer sequence and probed with the labeled 1c monomer fragment supports the proposed HOR tandem organization (marked with asterisks on 1c part of Fig. 4.1.4.) Southern hybridization of genomic DNA with 1c indicates that long HOR variants prevail in *M. fallax* genome, while short variants seem to be more abundant in *M. chitwoodi*, as can be seen in Fig. 4.1.4.



Figure 4.1.4. Southern hybridizations of *M. chitwoodi* and *M. fallax* genomic DNAs partially digested with RE-s and probed with 1a, 1b, 1c, 2a and 2b satDNA monomers and with U1 sequence. Approximate contribution of particular sequence in the genome, estimated by dot blot, is shown as a percentage indicated below Southern blots. HORs are indicated with asterisk. M is the DNA ladder marker. ND-not detectable.

Analyses of 6 cloned sequences obtained from 700 bp-long band amplified with U1 primers ($h_u fa_n$ and $h_u ch_n$) (Table 4.1.1.) revealed one additional complex fragment common for *M. fallax* and *M. chitwoodi*. Schematic representation of this fragment is shown in Figure 4.1.5. while alignment of those sequences is shown in Supplementary Fig. 4.1.3.



Figure 4.1.5. Schematic representation of complex fragment. The red line represents the overlapping segment of 1a and 1d monomers

These fragments are composed of complete 1a and 1d monomers linked to a novel 170 bp long fragment named U2 and flanked by U1 sequences. It has to be noted that a 62 bp-long perfectly conserved fragment of U1 is also found as a part of U2 sequence (marked with green box in Supplementary Fig. 4.1.3.) Tandem organization of the 700 bp complex fragment could not be proven by additional PCR analyses using U2 specific primers (constructed for this purpose) meaning that it is probably present in both genomes as an interspersed repeat.

4.1.2. Homogenous Monomeric Arrays

Ladder-like profile produced with 1a-specific primers gave fragments corresponding to multimers of 170 bp in both genomes. Cloning and sequencing of multimeric fragments (M_{1a}fa_n and ,M_{1a}ch_n; Table 4.1.2.) revealed homogenous tandem arrays with 94% of mutual identity (Table 4.1.1.) composed of a variant of 1a satellite DNA sequence, named 1aM. Alignment of 14 1aM sequences, cut to monomers, is given in Supplementary Fig. 4.1.4. This 1a variant, 1aM, is different from the HOR variant therefore named 1aH. Average sequence identity between 1aH and 1aM variants is 81% (Table 4.1.1.) and their alignment is shown in Supplementary Fig. 4.1.5.

Southern blot with probe for 1aM-type satellite DNA confirmed tandem organization of 1aM variants (Fig. 4.1.4.). In addition, 1aH-specific primers were constructed to check if 1aH builds independent tandem arrays. PCR reaction did not reveal any ladder-like profile indicating that these variants are exclusively present as subunits of HORs.

PCR amplification with 1b primers revealed fragments whose length (~1400 bp) corresponds to HOR organization. According to primer position, fragments of monomeric and dimeric forms that appeared in the PCR reaction also originate from HORs. In support, Southern blot analysis of genomic DNAs with 1b showed hybridization signals only in bands corresponding to HOR arrays (Fig. 4.1.4.) emphasizing unique organization of 1b monomers exclusively in HORs in both genomes. PCR reaction with primers for 2a satellite confirmed its tandem organization as homogenous monomeric arrays in both genomes, as published previously (Philippe Castagnone-Sereno et al. 1998). This research revealed a new type of organization of this satellite - its presence in above analyzed HOR element in both genomes and difference in abundance with 3.5% of 2a in *M. chitwoodi* and 20% in *M. fallax* (Fig. 4.1.4.).

Examination of 2b satellite by PCR amplification and Southern blot recovered its exclusive presence in the *M. chitwoodi* genome in the form of high copy homogenous monomeric arrays (Fig. 4.1.2.). The only observed hybridization signal in *M. fallax* is the faint band which could represent a sporadic 2b sequence embedded in a longer DNA segment (Fig. 4.1.4.)

The abundance of all satDNA was estimated by quantitative dot blot analysis using a series of genomic DNA dilutions ranging from 50 to 200 ng. Satellite monomers, excised from a plasmid, were dot-blotted in the range between 0.05 and 1 ng, and used as a calibration curve. Fig. 4.1.6. shows dot blot result for 1c satDNA in *M. fallax* genomic DNA. Estimated abundance for all satDNAs is shown in Fig. 4.1.4. under Southern blot figures.



Figure 4.1.6. Dot blot for 1c satDNA in *M. fallax* genomic DNA.

4.1.3. Phylogenetic Analyzes of Monomers

All together 212 monomeric units from *M. chitwoodi* and *M. fallax* were used to examine phylogenetic relationships of all monomers, regardless to their organizational pattern and species of origin, in order to assess sequence dynamics of repetitive units in the closely related genomes. Based on multiple sequence alignment, presented in Supplementary Fig. 4.1.6., neighbor-joining phylogenetic analysis was performed which showed eight different clusters (1aH, 1aM, 1bH, 1b'H, 1cDH, 1dDH, 2aMH and 2bM; letters H, D, M indicate HOR, dimeric or monomeric organizational form, respectively) distributed in two main branches, satellite families of group 1 and group 2 (Fig 4.1.7.). Monomers within clusters could not be distinguished according to the species of origin nor was it possible to differentiate 1c, 1d and 2a monomers according to their array affiliation. As already observed, 1a satellite family splits in 1aM and 1aH according to their organizational origin while 1aH further clusters in two subgroups, based on short and long HOR forms. 1b monomers form two distinct groups, 1bH and 1b'H, related to their position in HORs.



Figure 4.1.7. The phylogenetic tree of 1a, 1b, 1b' 1c, 1d, 2a and 2b monomers. Monomers from the HORs (H), dimeric (D) and monomeric arrays (M). Phylogenetic analysis of 212 monomers was performed by neighbor-joining method with bootstrap value of 100. Numbers at nodes indicate bootstrap values (100 replicates; only values greater than 70% are shown.

Sequence comparisons between monomer groups display three different levels of similarity (Table 4.1.2.). Similarity is high within 1bH group (86%) and between 1aM and 1aH (81%) monomer variants. Similarities within other satDNAs of group 1 and within satDNAs of group 2 are moderate, ranging from 51 to 66%. Sequence comparison and phylogenetic analyses between monomers of group 1 and 2 gives negligible similarities, 32–46% (Table 4.1.2.), and it can be supposed that these two groups might represent sequences of unrelated origin.

4.1.4. Conserved Motifs and Junctions Between Monomers

In contrast to the very low overall sequence similarity between some of the monomer groups, pairwise sequence alignment of consensus sequences of all 6 satellite families showed in Figure 4.1.8.A, and sliding window analysis (Fig 4.1.7.B) of all monomer sequences identified common domains of low variability. The grey shaded domain in Figure 4.1.8.A indicates the region of low variability shared among all satellite DNAs. Part of this region, 17 bp long segment, is a conserved block named Box 1 interesting because it remains conserved among highly divergent satellite DNAs like 1c and 2a that share only 32% identity while in the same time only one change characterizes the Box 1. Interestingly, transitions from truncated 1d to 2a monomer and from 2a to truncated 1c are located exactly at the Box 1. Significant degree of similarity is noted when conserved Box 1 sequences of all 6 satellite DNAs families are compared with the human CENP-B box. The comparison is shown in Figure 4.1.8.C with 6 satellite DNAs presented as a reverse complement. Six of them have 10–12 out of 17 nucleotides conserved and if bases essential for CENP-B binding in human are considered, 4-5 out of 9 remain conserved. The lowest identity is in exclusively HORincluded elements, 1b'H and 1bH, in which sequences may represent degenerate variants of the motif. This analysis was extended with the search for related motifs in two species from the same genus whose genomes have been sequenced, M. incognita and M. hapla. Preliminary results recovered no similarity in *M. hapla* genome but found different repetitive sequences with the Box 1 in unassembled part of *M. incognita* genome (Supplementary Fig. 4.1.7.). However, none of these repeats indicated any sequence similarity with satellite DNA sequences from *M. chitwoodi* and *M. fallax*.



Figure 4.1.8. a) Consensus sequences of 1dMH, 1cMH, 1aH, 1bH, 1b'H, 1aM, 2aMH and 2bM satDNAs, determined according to the 50% majority rule. Conserved Box 1 and Box 2 are indicated within the boxed area, and shaded part represents a region of low variability. b) Identification of low variable domains by sliding window analysis by DnaSP. The average nucleotide variability P is shown by a solid line, and dashed lines represent 2-fold value of standard deviation. c) Comparison of two variants of Box 1 with the consensus of human CENP-B box. The reverse complementary sequence of Box 1 is presented. Identities between sequences are highlighted in grey, and bases considered essential to bind the CENP-B protein in human (Csink and Henikoff 1998) are highlighted in red. The number of total conserved bases is reported in brackets. d) Aligment of Box 2 sequences from HOR related monomers; positions identical to the overall consensus are shown with dots.

In HOR-related monomers of group 1 satellite DNAs (1aH, 1bH, 1b'H, 1cH and 1dH) there is another common region named Box 2, conserved between the group members. Its position is indicated by black box in Figure 4.1.8.A and in Supplementary Fig. 4.1.2. Alignment of consensus sequences of Box2, part of all satellites from group 1, is given in Figure 4.1.8.D. This region is 20 bp-long composed of T, C and A tracts and shows significant degree of mutual sequence identity with only few nucleotide changes. It is interesting that the Box 2 region is always found in HORs as a transition region between monomers from group 1. In addition, detailed analysis of the so-called complex fragment (Figure 4.1.5.) revealed that 1a monomer extends into 1d monomer in the 50 bp long overlapping region shared by both monomers. This whole segment is highly conserved, with only 6 nucleotide substitutions.

4.2. New satellite DNAs in the genome of coleopteran Tribolium castaneum

4.2.1. Identification of new satDNAs in genome of *T. castaneum*

First step in finding new satellite DNAs in sequenced genome of beetle Tribolium castaneum (Richards et al. 2008) was to analyze the genome with tandem repeats finder (TRF) algorithm (Benson 1999) that is implemented in Tandem Repeats Database (TRDB) (Gelfand et al. 2006). The genome is composed of 10 assembled chromosomes and 2153 unassembled reads (The third version of the assembly: Tcas_3.0). Their sizes are from 10 Mb of the smallest chromosome 1 (Ch1) to the 38 Mb big chromosome 3 (Ch3) (Table 4.2.1.). Each chromosome was analyzed separately while chromosome 3 had to be divided in two parts because of its large size. Alignment parameters were 2,7,7 (match, mismatch, indels) and minimum alignment score to report was 50. The result of this search was a list of arrays that were subsequently filtered out by monomer length between 100 and 500bp. This monomer size was chosen because that size is generally the most widespread and most of so far known satellites fall into that range. After that all redundant arrays (arrays with overlapping positions on chromosome) had to be removed from further analyses. They appear because program, when it is possible, offers more than one array type for the same sequence. For example, the same array can be recognized as 10 copies of 180 bp long monomers or as 5 copies of 360 bp long monomers. In those cases arrays with shorter monomer size were selected for further anylyses. 2960 arrays of tandem repeats with a total length of 3.25 Mb were obtained. They constitute 2.1% of the 156 Mb long T. castaneum assembled genome.

To explore trends of monomer length in those arrays and a possible correlation with copy number of monomers in arrays, they were divided into three classes: arrays with 2 monomers (634 arrays), 3-4 monomers (1563 arrays) and \geq 5 monomers (763 arrays). Each class was analyzed separately (Figure 4.2.1.). Arrays with only 2 repeat units are predominantly built of monomers with length between 100 and 180 bp, while number of arrays drops with increased monomer size. Arrays with 3-4 monomers are most abundant when monomer size is in a narrow range between 160 and 180 bp. This analysis also indicates an increased number of arrays in the interval between 320 and 340 bp. Further increase of number of monomers in arrays (\geq 5 monomers) shows even more prominent domination of arrays with 160-180 bp long monomers and additional enrichment in the 320-

340 bp range. Furthermore, dramatic decrease in the number of long arrays is evident when monomer length increases above 340 bp.

Table 4.2.1. Size of each of the 10 chromosomes and unassembled reads (total length, length with captured and without captured and uncaptured gaps) and number of tandem arrays on each chromosome detected by TRF before and after filtering.

chromosome name	length with captured and uncaptrued gaps in bp	length with captured gaps in bp	length without captured and uncaptured gaps in bp	number of arrays before filtering	number of arrays after filtering (>5 copies, 100- 500 bp)
Ch1	10877635	7277635	7017036	728	23
Ch2	20218415	14518415	14025453	1574	18
Ch3	38791480	28591480	27070658	5150	166
Ch4	13894384	12094384	11543342	1535	47
Ch5	19135781	14335781	13841583	1684	30
Ch6	13176827	8976827	8259034	2489	126
Ch7	20532854	15432854	14850616	1697	37
Ch8	18021898	13521898	12793837	2576	117
Ch9	21459655	15459655	14607456	2287	69
Ch10	11386040	7486040	7061652	2254	130
unassembled	41251169	22771169	20543936		
Σ	~228 Mb	~160 Mb	~151,6 Mb	21974	763

For all 10 chromosomes comparison of positions of short (<5 monomers/array) and long arrays (>5 monomers/array) in respect to regions of putative eu and heterochromatin, determined by Wang et al. (2008) according to the abundance of HighA repetitive class and TEs, was done and is shown in Figure 4.2.2. Chromosomes with highest proportion of satellite DNAs are chromosomes 3, 6, 8, 9 and 10 which is in accordance with previous study where the same chromosomes show accumulation of HighA class repetitive families obtained by ScoutRepeat approach (Wang et al. 2008). In our research distribution of short (<5 monomers) satDNA arrays (Figure 4.2.2.) showed almost uniform distribution along the whole chromosomes, including the HighA domain (putative heterochromatin). Interestingly, long arrays (≥5 monomers) showed higher tendency to reside in euchromatic regions, being less represented in HighA domains. Although observed trend of long array distribution could be due to the gaps in assembly of repetitive sequences, marked uncaptured gaps do not indicate any increased frequency in HighA domains than in chromosomal segments defined as euchromatic.



Figure 4.2.1. Correlation of monomer number in extracted TRF arrays and monomer length. Number of arrays is plotted as a function of monomer length for arrays with 2 monomers, 3-4 monomers and \geq 5 monomers.



Figure 4.2.2. Genomic distribution of arrays with studied tandem repeats are superimposed on *T. castaneum* assembled chromosomes (CH1 to CH10) drawn according to Wang et al. (2008). Blue vertical bars represent short (<5 monomers/array, upper line) and long arrays (>5 monomers/array, lower line). The actual number of arrays per chromosome is indicated above each chromosme. Red dots correspond to centromeric TCAST satDNA found in the assembled genome. Red triangles indicate assumed position of the centromere and large blocks of centromeric heterochromatin. Horizontal bar represents putative

euchromatin (white) and heterochromatin (HighA domain, grey) regions as identified in Wang et al. (2008). Locations of the 300 kb placeholders were included to define uncaptured gaps (yellow bars).

4.2.2. The largest tandemly repeated DNA families

In order to explore the most abundant satDNAs in the assembled T. castaneum genome analyses were focused on arrays with ≥ 5 monomers obtained in the TRF output. This cut off level was selected for two reasons, to avoid a noise in phylogenetic analysis that would be caused by a large number of shorter arrays, and because analysis of preferential monomer length revealed positive correlation between number of repeats in arrays and monomer size typical for satDNAs (Figure 4.2.1.). Total length of all 763 arrays with ≥ 5 monomers is 1.63 Mb that constitute 1.04% of 156 Mb (160 Mb with captured gaps) large assembled T. castaneum genome (Kim et al. 2010) which is less than 2.5 % obtained by Wang et al. but they used more relaxed TRF parametrs, as mentioned in section 2.5.1. Arrays were further clustered based on profile similarity using tool called *Clustering* which is also integrated in TRDB. Conditions were as follows: P-value excluded (set to 0), cutoff value set at 70%, heuristical and DUST algorithm excluded, PAM algorithm included with default values (0.7 and 0.3). The result was 56 clusters with altogether 371 clustered arrays. The biggest cluster had 49 while last 40 clusters had only 2 arrays. Only three arrays represented (peri)centromeric satDNA and we extracted TCAST monomers from them. Using BLAST search TCAST monomers from unassembled reads were also extracted. Alignment of all obtained monomers recovered five subfamilies of TCAST pericentromeric satDNA (two were previously described (Ugarković et al. 1996; Feliciello et al. 2011), while others are newly determined) which have mutual sequence similarity of about 70% and are characterized by monomer length variation (Fig. 4.2.3.). In contrast to conservation of monomer length within satDNA family common for the most satDNAs, these monomers show large deletions (20-50 bp) and organization in form of interspersed monomers from different families (Feliciello et al. 2011). Taking into account that TRF analysis does not tolerate repeat variants with large deletions in array it was to be expected that pericentromeric satDNA was not considerably included in our output.



Figure 4.2.3. Alignemnt of 5 TCAST subfamilies. Positions identical to the first sequence are shown with dot and deletions are indicated with dash. Positions of primers Tcastan1 and Tcastan2 are marked with arrows above alignment.

In order to define distribution of this satDNA in the assembled genome, BLAST search of extracted arrays using consensus sequences of all subfamilies as queries was performed (red spots in Figure 4.2.2.). Only 130 short arrays mainly with 1 to 2 copies, distributed randomly along chromosomes and without any detectable preference towards the HighA domain, were determined.

Based on number (>=10) and distribution of arrays (at least two arrays on one chromosome and presence of cluster on at least two chromosomes) first 10 clusters were chosen for further analyses. Criteria are defined to enable comparative studies of monomers from different arrays on particular chromosome as well as comparisons of arrays among chromosomes. Alignments of all clusters were checked and cluster 6 was excluded from further analyses because it contains total divergent sequences. After manual checking of all arrays from one cluster some have been removed from further analyses. The reasons were too long array length, for example arrays with 368, 240, 182, 170, 115 and 102 monomers that weren't confirmed in following FISH analyses, and arrays with both flanking regions made of unspecified (N) nucleotides (two arrays from cluster 5). These arrays are probably artificial and are a result of incorrect assembly process.

Structural characteristics of remaining 9 clusters are summarized in Table 4.2.2. They make up a little less than 1/3 of tandem repetitive sequences of assembled genome obtained by TRF. 7 out of 9 families have a monomer which can be grouped in the size-range of about 170bp and 300bp. Nucleotide sequences of all satellite families show high AT content (≥60%) and nucleotide diversity of monomers within family are in range from 10 to 28 %. Their abundance in assembled genome is in range from 0,006% up to 0,075% (9-

117kb). We also found that periodicity of AT tracts is prominent feature of all analyzed satDNAs. Number of monomers in obtained arrays was up to 54 copies which speaks in favor of the fact that noncentromerne regions of chromosomes are not resistant to the accumulation of long satellite DNA arrays. Similarity BLAST search against available data bases - NCBI GenBank Database and Repbase Update (Jurka et al. 2005) resulted in no significant similarity with any of so far known sequences suggesting that extracted tandem repeats are new, *T castaneum*-specific sequences. Local BLAST search of newly satDNAs with High, Mid and Low repetitive classes obtained by RepeatScout (Wang et al. 2008) recovered significant homology with Cl4 and Cl5 (Supplementary Figure 4.2.1.). Detailed analyses show high homology of 7 repetitive elements with monomers of Cl4 satDNA. These repetitive elements represent multimers with different monomer variants of the heterogenous Cl4 family (21% divergence between monomers; Table 4.2.2.) as well as part of monomer with different flanking regions. Three RepeatScout defined repetitive elements show homology with Cl5. These repeats are composed of Cl5 monomer and flanking regions. Monomers from other clusters have only homology with short AT rich tracts.

-																			-
		Number of arrays per chromosome																	
Cluster name	Number of arrays	Ch 1	Ch 2	Ch 3	Ch 4	Ch 5	Ch 6	Ch 7	Ch 8	Ch 9	Ch1 O	Max. number of monom -ers per array	Nucleotide diversity (Pi) of monomers in cluster±standard deviation	The average length of monomers (bp)	AT conten t	Number of monomers	Total repeat family lenght (kb)	Proportion of the genome (%) assembled reads	% of genome estimat ed by dot blot
Cl 1	46	0	1	13	1	1	8	3	4	10	5	31	0,20143±0,00320	166-173	66,2	489	83	0,053	>1
CI 2	42	9	1	4	5	4	4	1	10	1	3	39	0,12138±0,00303	166-172	72,3	512	87	0,056	0,5
CI 3	35	2	1	3	6	3	7	2	5	2	4	17	0,11734±0,006	205-219	74,8	230	48	0,031	0,2
CI 4	33	0	1	5	0	2	3	8	10	4	0	50	0,21765±0,00296	168-176	69,7	426	73	0,047	0,5
CI 5	30	0	1	6	3	3	5	1	7	1	3	28	0,09620±0,00182	270-338	73,1	384	117	0,075	>1
Cl 7	7	0	0	5	0	1	0	0	1	0	0	54	0,16874±0,00385	179-181	66	157	28	0,018	0,5
Cl 8	10	0	0	4	1	2	1	0	2	0	0	12	0,28310±0,00129	109-114	68,9	83	9	0,006	0,2
Cl 9	10	0	0	2	0	0	1	0	1	4	2	24	0,16321±0,00733	161-167	67,3	120	20	0,013	0,2
Cl 10	10	0	0	2	0	1	3	0	1	0	3	10	0,25299±0,00481	311-346	72,6	64	21	0,013	0,2
Σ	223	11	5	44	16	17	32	15	41	22	20						486	0.312	>4

 Table 4.2.2.
 Structural characteristics of 9 clusters obtained by TRF.

The same set of analyses was done with more relaxed parameters. Alignment score was lowered to 2, 3, 5, monomer length range was expanded to 100-2000 bp and cutoff value for clustering was set to 60%, but there was no significant change in the output data. Clusters with more than 10 arrays were the same like in more stringent analyses; the only difference was a few extra, but more diverse, arrays per cluster.

Alignments of all monomers from each of the 9 selected clusters were downloaded in fasta format and imported in bioinformatics programs BioEdit 7.0.9.0 (Hall 1999) and Geneious 5.5.6 where they were further analyzed. All gaps from the TRDB alignment were deleted and new, ClustalW alignment (Thompson et al. 1997), was performed and consensus sequence for each of the cluster was defined (Figure 4.2.4.). Complete alignments of each of the clusters are shown in Supplementary Figure 4.2.2. Since tandemly repeated segments of genomes are still poorly assembled dot blot hybridization analyses was performed for each of extracted families in order to estimate actual genome content of 9 *in silico* found satDNAs. Furthermore, in order to determine the positions of new satDNAs related to (peri)centromeric regions two colored FISH was performed and for the purpose of validating a tandem repeats profile of new satDNAs Southern blot hybridization analyses were carried out. For the purpose of creating specific probes for each of the new satDNAs primers for amplifying each of the clusters (listed in Table 3.7.) were constructed based on consensus sequences. Products of PCR reactions with those primers are shown in Figure 4.2.5. Positions of the primers are marked in Supplementary Figure 4.2.3.

Cl1 cons	AATTAATTG	10 AGIGTTTC 110 CTTGTCAA	TAACGTAG	AATGACCGGI MAAACCAAAC	40 130 130 17 T T C T T	CAAATTTO	SCAAGAAT	CAAGTOGO TTTOGGAG	TACGACT 160 TTATTTC	AACCGTTC 170 172 CTTAGGG	^{io} GGAAAA TA	⁹⁰ CGGCAA
Cl2 cons	GGAACAAAC	10 CGCATTGC 110 AAAACTTT	TCTACGAC	30 PPTTAGTTT 20 A C A PO T TGT	40 TGAGTT 130 TAAAAGT	ATGAATT ¹⁴⁰ TGGTTTT	50 TTTTTTTTT 154	GAATAAAA AATGAGCC	TTTTCCA 160 GCTGAAT	CTATAGAT 170 172 TCAATGA	attgocta	
Cl3 cons	7 IGCAATTTT 100 IGAAATTTGG 190	10 IGCAAGTTC 110 ICCGAAAAT 200	20 TGAGGATT 11 GACCAAAA 210	30 PAAACACGT 20 ATTTACOTTA 220	40 130 TCTAAG 227 227	CCAAAAA ¹⁴⁰ CGTTTAT	50 CAAGTTT 150 PCAGCAAA	MACTTAAT	70 GTTTTTA 160 TATTGCG	TTAAACTA ¹⁷⁰ CAAAATTT	© GAACGAAA/ 180 CTTAAAAA/	MANCAC IGTAAGC
Cl4 cons	AAAAAAAAA hoo	ACAGAATT ¹⁰ TTATAACT ¹¹⁰ CTACCTTA	CAAAAACTI	DA TGA CA TTA DA A A G TC G TA DA A A G TC G TA DA A A G T TA A A	40 IGAGCAA 130 AAATTA	AACGGTT	SOFTCCAG ISTTCCAG ISTTCCAG	Ö TGAATTCT AATGGTGG	GCGGCTC 150 ATGCGCC	ATTTTCCGI 170 GAATTATT	9 TATTATAC 179 TATTAT	²⁰ IACCATT
CI5 cons	1 100 100 100 100 100	10 AATCIGIG 110 IIGIGAAAT 200 ATAAAAAAA	20 ACTCAAAC 1 AAATAAAT/ 210 ATCAAACC	30 PATGACTTT 20 TACGACACA 220	40 ICAACAC 130 AACAATA	GCATTT 140 AAATGGA 230 CCATTAA		TGTACACA TGGTATCG 250	70 ACATTTT 190 CTTCCAC	AATTGEAA 170 GTTGGGCTA 290	PO TTAAATTT 150 CCGTTTGT 270 TTAAACAC	
CI7 cons	290 TTACGTCCC	AATAAATT 10 AAACCTTC 110	200 ATTTGAGT(200 CTCTACAA(1	30 30 30 30 30 30 30 30 30 30 30 30 30 3	320 PATTTAT 40 AATTGG 130	370 AGTTACT AGTCGTC 140	332 50 5 G G C T T T T 15	GTTTCI	70 TTTTTATT 160	AAATTOGG 170	80 A A T A T A G G 180	⁹⁰ ACAATAT
Cl8 cons	ITGAAAAAA AAGMAAAGA 100 GAAAGIIIII	10 ATCGTCCG 110 CTCGTCCG		30 CGTTTTCATC 121 121	CAAACT	ogtoğtt Ataacati	50 XÁATCGTT	ATGCAGCA CTTTTGAG	ATTGCCT 70 CCAGAAT	TCAT TTTT	GTAGGAĠ P TTGAGPOTO	90 TTTTAT
CI9 cons	L BBBGCAAAC 100 AAAAAAATCA	10 TTTATTT 110 TGTTCGGA	TTTTCACCO CAAACACCO	30 ACTTTATA 20 CTTGGGACC	40 130 17 TAATG	ATTTTCT 140 AATTTTT	50 TATTTT 15 AAGATTC	GCAGGAGA TTTAAGAT	70 TTAAGCO 160 TTCCCGA	CTTCGATA 160 TTTC	⁹⁰ G G G G G T T C (90 ACTGTA
CI10 cons	GTOGACCAT 100 GGCATATTT 190	10 A T T T T G T C 110 T T G A C A T A 200	20 TAA TATCT(1 AA TTTTCG 210	30 20 20 11A TTGTG7 220	IGAATOG 130 COTTGA	TAGAACA) 140 CAATTTT 230	50 X A A A T A A A 150 F T T T A T T G 240	GACAGATT GTAGGTAG 250	TGGAATC 160 GTAAGTA	CTTAGACA 170 AAAATTTT	90 ATTTTACGI 180 GACCAAGT 270	90 PCAAATA PGTTTTA 290
	TTOGGATTA 290 TCAATTTTT	ATTTGCACA	ATTTTGAC	310 TTATTATT	BAAAAT 320 TTAATT	GATTGTA	AGAAA TAG AAAA TTAA	ATAATTAA 340 AATCAAAT	TAAA TAAA	A A A G G G C T	ACAAGTOGI	TTTGA

Figure 4.2.4. Consensus sequences of all nine clusters, Cl1 to Cl10.

Fragments obtained by PCR were used to transform bacterial cells. Several clones from each of the 9 transformation experiments were sequenced and one was chosen for oligonucleotide probe construction by PCR. Alignments of all cloned fragments are given in Supplementary Figure 4.2.3. in which clones chosen for probe construction are marked by black boxes.

Results obtained by dot blot (showed only for CI5 and CI7 satDNA in Fig. 4.2.6) revealed that Cl1 and CI5 are the most abundant, each comprising about 1% the genome (Table 4.2.2.). Second category, with 0.5% abundance, are Cl2, Cl4 and Cl7. Other satDNAs comprise about 0.2% of the genome each. In summary, real abundance of all analyzed satDNAs is more than 4% of the genome which is about 10 times higher than in the assembled genome. Additional analyses of unassembled reads with TDRB, using the same parameters as for chromosomes, showed the highest proportion of Cl5, Cl7, Cl1 and Cl2 satellite DNAs in unassembled portion of the genome (Supplementary Figure 4.2.4.).



Figure 4.2.5. Electrophoretic separation of PCR products obtained by amplification of *T. castaneum* genomic DNA using primers specific for each of the new satDNAs. **a**) Primers for clusters 2, 3, 4, 10, 8 and 9; **b**) primers for cluster 7; **c**) primers for cluster 5; **d**) primers for cluster 1. M is the DNA ladder marker.



Figure. 4.2.6. Determination of the abundance of clusters 7 and 5 in total *T. castaneum* genomic DNA by dot blot hybridization.

Data obtained by dot blot are in accordance with FISH analyses, shown in Figure 4.2.7. Two colored FISH was used to determine positions of new satDNAs related to (peri)centromeric regions. TCAST satDNA has previously been characterized as the major satellite that encompasses (peri)centromeric regions of *T. castaneum* chromosomes (Ugarković et al. 1996). TCAST probe was labeled Cy3 and probes for each of the 9 clusters were biotin labeled. Because of small size of *T. castaneum* chromosomes and their condensation state which cause lower FISH sensitivity, specially in a case of low copy satDNA families, detailed mapping of newly satDNAs on chromosomes in meiotic prometaphase was not possible. For that reason chromosomes in mitotic prometaphase which enabled detection of centromere regions together with signals of newly detected satDNA were used. Signals obtained after FISH hybridization with Cl1 and Cl5 probe were significantly stronger

than for other families, as has already been shown by dot blot experiments. In general, FISH analyses showed localization of all nine satellites almost exclusively at noncentromeric chromosome regions with some overlapping signals in pericentromeric regions, especially in CI5 FISH analysis. Also, cytogenetical analyses enabled detection of Yp chromosome, two metacentric chromosomes Ch3 and Ch2, while the remaining chromosomes are mostly telocentric.

Southern blot hybridization analyses were carried out for the most prominent satDNAs, Cl1, Cl2, Cl4, Cl5 and Cl6 (Fig. 4.2.7.), which each represent 0.5% or more of the genome, to validate a tandem repeats profile of the sequence sets generated *in silico* by TRF. Other low copied satDNAs, Cl3, Cl8, Cl9 and Cl10 were below the level of detection by Southern blot hybridization because they present 0.2% of the genome or less. Genomic DNA was digested completely using restriction enzymes which cut once in the most monomer sequences and with the once with recognition sites only in some monomers. These restriction enzymes were chosen because they produce clear n-mers in tandem organized sequences. Selection of REs for particular satDNA was based on alignment of all monomers of one cluster. Hybridization analyses for the most prominent satDNAs were performed separately with probe specific for each TRF satDNA family. In addition to a strong signal of predicted monomer size typical satellite ladder-like pattern showing individual n-mers units was observed in all hybridization analyses. No intermediate bands are observed in any of the ladders indicating a tandem arrangement of monomers in all detected families.



Figure 4.2.7. Fluorescence in situ hybridization of centromeric TCAST satDNA and satDNAs determined in this work by TRF analysis. Chromosomes are counter-stained with DAPI. The bar represents 1 μm. **a)** FISH showing centromeric TCAST satDNA (red signals) on *T. castaneum* chromosomes in meiotic prometaphase. Arrows point to chromosomes Ch2, Ch3, Ch4 and Yp. Two-colored FISH performed on chromosomes in mitotic prometaphase show localization of new satDNAs (green): **b)** Cluster 1, **c)** Cluster 2; **d)** Cluster 3; **e)** Cluster 4; **f)** Cluster 5; **g)** Cluster 7; **h)** Cluster 8; **i)** Cluster 9; **j)** Cluster 10. Aside to chromosome spreads Southern blot analyses of genomic DNA digested with restriction enzymes and hybridized with specific probes: Cl1 with Hinfl and HaeIII (**b**), Cl2 with EcoRI and HaeIII (**c**), Cl4 with HaeIII and Hinfl (**e**), Cl 5 with Rsal and Dral (**f**) and Cl7 with HaeIII and Hinfl (**g**) are shown. Only satDNAs >1% of genomic DNA are presented.

4.2.2. Phylogenetic relationships among newly defined satDNAs

For revealing evolutionary trends of dominant non-centromeric satellite sequences in *T. castaneum* genome phylogenetic relationships between monomers from 9 extracted clusters were examined. Maximum likelihood (ML) trees based on Clustal W alignments (Supplementary Figure 4.2.2.) were obtained with the PhyML 3.0. software (Guindon and Gascuel 2003) using best-fit models calculated by the jModelTest 2.1.3. (Darriba et al. 2012). Truncated monomers from the beginning and from the end of the array were removed from alignments. Monomers were annotated with respect to chromosome of origin (1 to 10) and the original position of array on that chromosome. Trees are displayed and adjusted in FigTree 1.3.1. and CorelX3 softwares. Annotations and branches of all monomers from one chromosome are colored in the same color, identical for all trees. Trees for all clusters, with monomer annotations, are shown in Figures 4.2.8., 4.2.9., 4.2.10. and 4.2.11. Simplified tree forms, without monomer names and with added symbols for specific kind of distribution, defined further in the text, are shown in Figures 4.2.13., 4.2.14. and 4.2.15. for 6 selected clusters.

Colored arches and other symbols indicate: dominant chromosome-specific clusters of neighboring arrays (beige arches), chromosome specific clusters of arrays on distant position (lilac arches), clusters with arrays which come from non-homologous chromosomes (recent exchange, green arches) and dispersed monomers (diverse symbols). The tree topologies generally show strong clustering of repeats from the same array but the exception are dispersed short arrays (5-7 monomers) which is particularly evident in the Cl3 which is dominated by that kind of arrays.



Figure 4.2.8. ML trees of Clusters 1 and 2. Arrays from one chromosome are colored in the same color.



Figure 4.2.9. ML trees of Clusters 3 and 4. Arrays from one chromosome are colored in the same color.



Figure 4.2.10. ML trees of Clusters 5 and 7. Arrays from one chromosome are colored in the same color.



Figure 4.2.11. ML trees of Clusters 5 and 7. Arrays from one chromosome are colored in the same color.

Cluster 1

It is obvious that divergent Cl1 family (20%) is represented by both short and long arrays which is confirmed by FISH results (Fig. 4.2.7. b). However, the longest arrays are not represented in the assembled genome. The relationships are very diverse. Monomers from some long arrays tend to be clustered together while from others are very distant. There are 3 chromosome specific groups of distant arrays, 3 groups of arrays from different chromosomes while short arrays show scattered distribution. The cluster is distributed on every chromosome except Ch1 (sex chromosome) showing significant exchange between non-homologous and on chromosomes 2, 4 and 5 is present with only one, not to homogenous array.

Cluster 2

Low divergence between monomers (12%) is characteristic of this cluster. ML tree displays significant and relatively recent (short branches) dispersion of arrays between non-homologous chromosomes visible in two stages (indicated with two green arches). There is only one chromosome-specific cluster (Ch1=X chromosome) with mixed monomers (originated from tree arrays) located on distant chromosome positions. Cl2 tree shows exchange between sex-chromosome (Ch1=X) and autosomes.

Cluster 3

This family is also characterized by the low monomer divergence (11%) and short arrays, mainly comprising from 5 to 7 monomers. Cl3 tree displays clustering of monomers from long arrays while monomers derived from short arrays show scattered formation (see symbols on the tree). Cl3 tree also shows dynamic exchange of arrays between non homologous chromosomes.

Cluster 4

This family has a significant monomer divergence (21%) even within arrays, which is evident from the long branches. Tree mainly consists of long arrays whose monomers tend to be clustered together. There are two examples of chromosome specific clustering: arrays located close to each other (up to 20 kb) which are probably homogenized together (beige arches) and distant arrays that show intra chromosomal exchange (lilac arches). This family also shows significant exchange between non homologous chromosomes.

Cluster 5

Despite of the lowest overall divergence among monomers (9%) this cluster shows strong grouping of monomers from the same array (the average array length is about 15 monomers). Arrays from the same chromosome show slight tendency to group together even in the case when arrays are on distant locations (lilac arches). The tree also shows one recent interchromosomal exchange in a fraction of monomers.

Cluster 7

Tree from cluster 7 shows long arrays dominantly located on chromosome 3 and significant intrachromosomal exchange ("bar code" for Ch3). This almost exclusive localization of Cl7 family to Ch3 is confirmed by FISH experiments with Cl7 monomer as a probe on meiotic prometaphase chromosomes (Figure 4.2.12.). There are only two more arrays of this cluster (also visible as green dots on Figure 4.2.12), each one on distinct chromosome, deeply divided from one another and from arrays from Ch3, as can be seen from ML tree.



Figure 4.2.12. Overlapping of DAPI stained nucleus and hybridization with biotin labeled probe (green signal) for CI7 monomer. Accumulation of CI7 arrays is clearly visible on chromosome 3.

Trees for Cl8, Cl9 and Cl10 trees are shown only on Figure 4.2.11. because they follow similar evolutionary trends as described for other clusters and additional new features were not noted.



Figure 4.2.13. ML trees of clusters 1 and 2 with marked symbols for different types of distribution of satellite monomers. Arrays from one chromosome are colored in same color.



Figure 4.2.14. ML trees of clusters 3 and 4 with marked symbols for different types of distribution of satellite monomers. Arrays from one chromosome are colored in same color.



Figure 4.2.15. ML trees of clusters 5 and 7 with marked symbols for different types of distribution of satellite monomers. Arrays from one chromosome are colored in same color.
Summarized, the presented tree topologies show clustering of repeats from the same array which is particular characteristic of monomers belonging to long arrays. Short arrays generally do not show consistent clustering. Such patterns suggest homogenization mechanisms that occur at the array level and have a more dominant effect on long arrays until short ones probably have a limited homogenization possibility. General observation in all extracted satDNA families is that arrays (monomers) from the same chromosome are not clustered with significantly higher frequency with respect to arrays located at nonhomologous chromosomes, especially taking into account that some grouped arrays from homologous chromosomes are located very near to each other on the chromosome that could imply the same homogenization effect. Interestingly, dominant clusters in Cl2, Cl3, Cl4 and CI5 which include arrays from all non-homologous chromosomes, suggest extensive exchanges between non-homologous chromosomes in almost all analyzed satDNAs. Presence of several mixed clusters (heterologous chromosomes) in almost each analysed tree, allows a prediction of satDNA spread through several rounds of interchromosomal exchange and subsequent amplification. Those genome-wide expansion events, within an evolutionary short period of time, imply efficient mechanism of propagation of tandem repeats in non-centromeric genome regions, especially in cluster 5.

4.2.3. Mechanisms of propagation

In order to investigate putative mechanisms of satDNA propagation in noncentromeric part flanking regions of every array in all clusters were analysed. The hypothesis was if satDNAs are just passively carried by expansion of other DNA segments in the genome flanking regions, at least in some of them, should be mutually homologous. The 4kb of both (left and right) flanking region of all arrays were extracted and compared for each cluster separately. Flanking regions built predominantly of unspecified nucleotides (N) were excluded them from analyzes. Also, because of unspecified nucleotides on the distal side some flankings were shorter than 4kb but they were included in analyzes. This comparison showed no similarity in clusters flanking regions except for the clusters 2 and 5. Cluster 2 showed homology only in a small number of left flanking regions (7 out of 36 arrays) until the vast majority of Cluster 5 arrays (22 out of 28) could be grouped according to homologies in left and in right flanking regions. Flanking regions of Cl5 show high similarity with R66 and R140 repeated sequences from sequenced *T. castaneum* genome (class HighA) obtained by Repeat Scout analyses in Wang et al. 2008 (Supplementary Figure 4.2.1.). Detailed analyses of previously extracted repeated sequences R66 and R140 recovered that they are composed of a part of Cl5 monomer together with part of flanking region. Alignments of R66-like and R140-like flanking regions are presented in Figure 4.2.16. and Figure 4.2.17. R66-like flanking regions show homology in the sequence length of about 1 kb while R140-like flanking regions have homology in 2kb (1kb is homologous in all while last 1kb stays homologous only in part of the sequences). Search analyses of RepBase with R66-R140-like flanking regions as query showed strech of 140 bp with a high homology (84%) to non-autonomous Tc1/Mariner transposon defined in *T. castaneum* thus indicates putative transposon nature of Cluster 5 flanking regions.



Figure 4.2.16. Alignment of R66-like sequences from flanking regions of cluster 5 with R=66|TRF=0.034|NSEG=0.471|HighA sequence from Wang et al. 2008. Positions identical to the first sequence are shown in gray, differences are shown in color and deletions are indicated with dash. Positions of R66_F and R66_R primers are marked.



Figure 4.2.17. Alignment of R140-like sequences from flanking regions of cluster 5 with R R=140|TRF=0.000|NSEG=0.215|Mid and R=1877|TRF=0.000|NSEG=0.261|Mid sequence from Wang et al. 2008. Positions identical to the first sequence are shown in gray, differences are shown in color and deletions are indicated with dash.



Figure 4.2.18. Schematic representation of different types of flanking regions and monomer arrays of cluster 5. Pink square is R140-like and gray square is R66-like region. Complete monomers are marked with orange and truncated monomers with lilac arrows (numbers inside truncated arrows mark their length). Direction of arrow is according to the consensus sequence direction. Numbers above dashed line indicates how many monomers are in that array. Strait line between array and R140-like or R566-like region marks unspecified unique sequence. N marks unspecified nucleotides. Left side is 5' and right 3' in the genome.



Figure 4.2.19. Two colour FISH with R66 biotin (green signal) and CI5 monomer Cy3 (red signal) probe. Overlapping positions are yellow. On the left the same nucleus is counter-stained with DAPI.

Significant variations in the sequence length of junction regions were detected in both left and right flanking regions. Schematic representation of flanking regions with arrays of CI5 family with respect to 5'-3' genome direction, monomer orientation and composition in arrays is presented in Figure 4.2.18. This figure shows the same orientation of monomers with respect to flanking regions in all arrays while elements (flanking+arrays) extend in both directions (5' - 3' and 3' - 5') in the genome.

Double FISH with CI5 monomer and centromeric satDNA (Figure 4.2.6.) showed extreme expansion of the CI5 family throughout the genome in comparison to all other families. In order to investigate the genomic location of CI5 repeats within flanking regions we also performed double FISH experiments with probes from R66-like flanking regions (primers R66_F and R66_R) and CI5 monomer (Figure 4.2.19.). Results obtained on meiotic promethaphase chromosome spreads produced mainly co-localizing hybridization signals although individual signals of flanking regions and satellites also can be seen. This is in accordance with bioinformatics analysis of arrays where some arrays have different flanking regions.

Diversity of flanking regions in other satDNAs indicates mechanism of selfpropagation by insertion of satDNA repeats into different genome environment. For the purpose of checking if there is some part of the monomer sequence that is the preferential site of array insertion we extracted 30pb from the beginning and from the end of each array and assembled them with consensus sequence. We found no preferential site of array insertion for any of the clusters, as can be seen from the Supplementary Figures 4.2.5.-4.2.13. AT tracts can be noticed in the insertion position of several monomers but since these sequences (9 new satellite DNAs) are generally AT rich (Table 4.2.2.) we can't say that high AT composition of these positions is really significant.

5. DISCUSSION

With this study the existence of satellite DNA library, made of five divergent satDNAs (1a, 1b, 1c, 1d, and 2a), in two recently separated species of root-knot nematodes M. chitwoodi and M. fallax (van der Beek and Karssen 1997, van Megen et al. 2009) was confirmed and a comprehensive analyses of all of them were performed. 2b satDNA being present only in the *M. chitwoodi* genome is a distinctive element of this satDNA library. This is in agreement with the theory that the presence of novel satDNAs in the library is accompanying the speciation processes (Meštrović et al. 2009). A search for 1a, 1b, 1c, 1d, 2a and 2b counterparts in other congeneric *Meloidogyne* species didn't give any results thus indicating that satDNAs described in this work are specific for *M. chitwoodi* and *M. fallax*. The remarkable characteristic of studied satDNAs is complex organization of repeat units in a form of simple arrays and higher order repeats (HOR). Simple arrays, composed of monomers or dimers, are highly homogenous with the dimers built of two highly divergent monomers. Comparable dimeric organization based on monomers of low sequence similarity (50–60%) was reported in the marmoset (New World monkeys) and it represents an ancient dimeric structure of alphoid sequences (Cellamare et al. 2009). In this work, complex HORs are formed of monomers of divergent satDNAs that range from ones sharing up to 86% sequence identity to apparently unrelated sequences (32% identity). While the first group can be considered as variants of a single satDNA, such as the 1b'H-1bH monomer pair, possible common evolutionary origin of the most divergent monomers is not clear. Such a complex organization of monomers is characteristic for alpha satDNA of human and great apes (Cellamare et al. 2009, Alkan et al. 2007). Alpha satDNA HORs are composed of monomers with relatively high mutual sequence similarity (75–88%) (Rudd and Willard 2004) as opposed to characterized nematode satDNAs. A major difference in organization of simple arrays can be also observed; while alpha satDNA exhibit sequence similarity comparable to that of monomers in alpha HORs (Rudd and Willard 2004), simple arrays of M. fallax and M. chitwoodi are highly homogenous (94–97% sequence similarity). Phylogenetic analyses of alpha satDNA monomers in primates and human categorized HOR and monomeric forms as phylogenetically distinct and suggested evolution of both forms from ancestral arrays of monomeric repeats (Rudd et al. 2006). Similar analysis in M. chitwoodi and *M. fallax* revealed clustering of HOR units with those from simple arrays, indicating continuous shuffling of monomers between HORs and simple arrays. The only exception is grouping of 1aH and 1aM monomers, in accordance with array affiliation. This result suggests that mechanisms in addition to unequal crossover over and gene conversion (Dover 1986, Talbert and Henikoff 2010) are probably involved in formation of HORs (see below).

In spite to generally low level of sequence identity (32–64%) among studied satDNAs and in no relation to the organizational pattern in which they are found, examined monomers share two conserved segments, named Box 1 and Box 2. Box 1 is a conserved 17 bp- long segment characteristic for all analyzed satDNAs. This particular motif is observed even in the divergent 2b satDNA, found only in homogeneous monomeric arrays of M. chitwoodi. One single deleted nucleotide was found in Box 1 of 1bH and 1b'H monomers which, curiously, appear exclusively as HOR- included elements. This raises the speculative possibility that conserved Box 1 participates in the formation of homogenous simple arrays. It was already proposed that abundant satDNAs may have been selected for amplification because of their ability to bind nuclear proteins (Csink and Henikoff 1998). Interestingly, conserved Box 1 shows significant homology with the human CENP-B box, with identity in 10–12 out of 17 nucleotides. The CENP-B box is a well-described sequence motif of human alpha satDNA which represents a binding site for the CENP-B protein in a subset of alpha satellite HORs (Masumoto et al. 1993). It has been proposed that the CENP-B protein participates in human centromere assembly (Masumoto et al. 1993) but normal chromosome segregation in a mouse CENP-B protein null mutant and absence of CENP-B binding sites at the centromeres of human and mouse Y chromosome make its exact function unclear (Earnshaw et al. 1991, Fowler et al. 2000). DNA sequence motifs similar to the CENP-B box were found in diverse mammalian species, although their satDNA sequences are completely unrelated among themselves and with the alpha satDNA (Kipling et al. 1995, Alkan et al. 2011). For example, seven divergent horse satDNAs exibit CENP B box variants with identity in 9–12 out of 17 nucleotide of human CENP B box (Alkan et al. 2011). Presence of motifs similar to the CENP-B box has also been detected in a number of satDNAs from diverse species outside mammals (López and Edström 1998). In examined nematode species, homology of Box 1 with the human CENP-B box is in the same range found for the CENP-B box in diverse mammalian species (Alkan et al. 2011, Fantaccione et al. 2005). Exceptional feature of the nematode CENP-B box-like motif is significant conservation in the six divergent satDNAs which emphasized it as the most prominent example of the CENP-B boxlike sequence out of mammals.

Mechanisms of genetic exchange of satDNAs are hard to study because of repetitive nature of satDNAs arrays. However, our experimental system composed of complex HORs and their counterparts in simple arrays offers a convenient model in which "beginning" and "end" of monomers can be precisely defined. Detailed analyses of Meloidogyne satDNA arrays led to observation that junctions between monomers are always located in conserved motifs. Box 1 is found at sites of insertion of the complete 2a monomer into highly divergent 1d and 1c monomers, while in turn, the corresponding segment of equivalent length in 1d and 1c, limited with Box 1, has been extruded (Figure 5.1.). This rearrangement event indicates novel cut-and-paste mechanism that involves the 17 bp-long CENP-B box-like motif and, probably, is related to mechanisms of transposition. It has been already hypothesized that the CENP-B box, in addition to its putative centromeric role, might have a function in satDNA sequence rearrangements (Kipling and Warburton 1997). This assumption is based on similarity of the CENP-B protein and transposases of the pogo family (Casola et al. 2008). Accordingly, the CENP-B box might trigger illegitimate recombination in centromeric areas, in an epigenetically controlled process (Jaco et al. 2008). Highly conserved CENP-B protein homologs were detected in many mammalian species, but not in other metazoans (Casola et al. 2008). In contrast, transposase-derived proteins related to the CENP-B and with putative ability to interact with satDNAs have been detected in diverse invertebrate and vertebrate species (Casola et al. 2008).



Figure 5.1. The scheme in the frame represents outcome of the proposed cut-and-paste mechanism of 2a insertion in HOR array.

In support, a search in the genome sequence of related species M. incognita (Abad et al. 2008) allowed identification of an EST-supported gene encoding a protein with both CENP-B/Tc5 transposase DNA binding domains (Minc05185) (unpublished data) as well as the existence of different repetitive sequences that contain the CENP B box- like motif identical as that observed in this work. The conserved Box 2 is a sequence motif composed of A/T/C tracts, found as a 20 bp- long transition region of all group 1 monomers in HORs. This indicates that homopolymeric tracts which have been found as a common feature of many satellites (Plohl et al. 2008), participate in sequence recombination events in Meloidogyne. Since divergent monomers are involved, a mechanism of illegitimate recombination mediated by Box 2 can be assumed. Illegitimate recombination was previously proposed as a mechanism responsible for interspersion of long arrays generating abrupt switches between nonhomologous satDNAs in Drosophila (Kuhn et al. 2009). While switches between unrelated arrays in Drosophila were detected as relatively rare events, our results nominate Box 2 as promoter of recombination acting frequently on DNA fragments of near monomer size. The minimal observed junction length of about 20 bp in both Box 1 and Box 2 is in accordance with the length of recombination breakpoints in human alpha-satellite (Warburton et al. 1993). In support to this, the role in satDNA shuffling can be assumed by presence of different conserved regions of similar length, as observed in the MEL 172 satDNA family identified in several Meloidogyne species (Meštrović et al. 2006) and in other, such as Arabidopsis (Hall et al. 2005).

Genome-wide annotation and study of satellite-rich regions from reference assemblies of complex genomes is a challange. Due to the long arrays composed of nearly identical monomer units, satellite DNA remain the most poorly mapped areas of the genomes. However, satDNA annotation, especially in euchromatin regions, is important not only for filling gaps in assembled genomes but also for performing evolutionary studies and studying mechanisms involved in emergence and expansion of these sequences in order to better understand the impact of abundant satDNAs on genome organization and expression. Satellite-rich whole-genome assembly of coleopteran *Tribolium castaneum* based on whole genome shotgun (WGS) reads as well as Fosmid and BAC end sequences offers an exceptional platform for genome-wide analyses of satellite DNA repeats.

To build a database of putative satDNAs TRF algorithm on assembled chromosomes of the *T. castaneum* genome assembly was first applied. Further, arrays with repeats in the

range of 100-500 bp and with monomer number equal or higher than 5 were selected. The total amount of those arrays was 1.63 Mb, which constitutes about 1.04 % of the assembled genome. Arrays are not uniformly distributed between chromosomes showing higher density in five chromosomes, the result being in agreement with the previous report obtained on analysis of overall repeat fraction (HighA and TE classes) (Wang et al 2008). It is important to note that even arrays defined here as long (≥5 copies) are dispersed in non-centromeric and thus potentially euchromatic region on each chromosome.

Long gaps in the assembled genome projects are likely to represent regions of highly repetitive DNA that may have not been sequenced or assembled. In support to this, FISH and quantitative analysis of newly characterized satDNAs (Cluster 1 to Cluster 10) found in the assembled genome recovered existence of significantly higher amounts of these noncentromeric satDNAs. This is particularly obvious in Cluster 1 FISH analysis, where highly abundant signals suggest presence of long unassembled arrays. Presence of only dispersed arrays with few copies of TCAST centromeric satDNA in the assembled genome indicates complete lack of centromeric region. Although anomalies in sequencing and/or assembly coverage between heterochromatic and euchromatic regions can results in discrepancy of the distribution profiles, our results definitively indicate presence of a significant portion of long arrays of tandem repeats out of centromeric regions in the genome.

Chromosomal distribution of (Cluster 1 to Cluster 10) satDNAs is clearly distinct from that of centromeric TCAST satDNA. Based on bioinformatic and FISH analyses, all centromeric TCAST subfamilies are almost exclusively located in centromeric regions. Previous data also revealed only few short arrays of TCAST-like elements embedded in euchromatic genome portions and some of them were identified within a complex unit that resembles a DNA transposon (Brajković et al. 2012). Similar distribution profiles with large blocks of tandem repeats in the pericentromeric regions and short arrays of up to 6 or 12 monomers located in the euchromatin were defined for 1.688 (Kuhn et al. 2012) and *Rsp* satDNA (Larracuente 2014), respectively, in the *Drosophila melanogaster* genome. Authors suggest that limited number of 1.688 satDNA repeats in euchromatic arrays could be selectively constrained by their possible role as gene regulators (Kuhn et al. 2012). In humans, besides alpha satDNA, prominent arrays of classical satDNAs (e.g. satII, satIII, gamma) are exclusively located in pericentromeric regions of many chromosomes (Warburton et al. 2008, Lee et al. 2000). Distribution profile of satDNAs in *T. castaneum* suggest *certain kind of* chromosome compartmentation with limited transfer of satDNA between the centromeric region and euchromatin.

Structural analysis of tandem repeats in assembled T. castaneum genome revealed correlation between the monomer number in arrays and the monomer length. There is an obvious tendency of predominance of 170 and 360 bp long monomers if number of monomers in an array increases. In accordance, in this range are monomer lengths of satDNAs (Cluster 1 to Cluster 9) detected as the most abundant genome components in noncentromeric regions, as well as monomer length in all 5 subfamilies of centromeric TCAST satDNA. Recent data on human and plants revealed the periodicity of CenH3 nucleosomes to be exactly the same as the monomer length of the satDNA, which is therefore in phase with the sequence (Hasson et al. 2013; Zhang et al. 2013). Current understanding of this phenomenon is given by the hypothesis that links preferred monomer length in centromeric satDNAs and the length of DNA wrapped around 1 or 2 nucleosomes as a requirement that may facilitate regular phasing of nucleosomes in the centromere (Heslop-Harrison and Schwarzacher 2013). Further structural analysis of 9 non-centromeric satDNAs revealed periodical distribution of A or T >4 tracts, in the same manner as observed in TCAST and centromeric satDNAs in several other Tribolium species (Mravinac et al. 2004). In this regard, periodically distributed tracts of As and/or Ts, present in many centromeric satDNAs of tenebrionid beetles, define the sequence-induced curvature of DNA helix axis and could facilitate the tight packing of DNA in centromeric heterochromatin (Barceló et al. 1998). Results obtained in this study did not suggest any differences in structural features as monomer lengths preferences and nucleotide pattern between centromeric and noncentromeric satDNAs. We hypothesize that similarly as in the centromeric region, monomer length and A or T >4 tracts could be equally important for expansion of tandem repeats in non-centromeric parts and formation of putative micro-heterochromatic regions within euchromatin. It has been proposed that the satellite monomer length longer of two nucleosomes is rare because longer sequences are unlikely for nucleosome stabilizing. Overall analysis of TR in T. castaneum assembled genome is also in accordance with this, showing that proportion of arrays with over 380 bp long monomers dramatically decreases. As already known T. castaneum has a higher prevalence of satellite DNA in the genome in comparison with Drosophila sp. and our results confirm a presence a long arrays in

euchromatic regions. In this sense, it can be hypothesized that *T. castaneum* genome is more flexible with respect to accumulation of satellite DNA in euchromatic regions.

Within this study, the most prominent non-centromeric satDNAs in T. castaneum genome assembly were further analysed in detail in order to define evolutionary trends of repeats and mechanisms of dispersion through the genome. It was done by combining bioinformatics and experimental approach. To address these issues the availability of wholegenome assembly of *T. castaneum* genome was the most important step in making possible the examination of repeat sequence evolution at the chromosomal and at the repeat-array level. Phylogenetic analyses of monomers show similar evolutionary scheme for all analyzed families. Clustering of repeats from the same array is observed mainly for long arrays while monomers that originate from shorter arrays (5-7 monomers) often show dispersed formation in phylogenetic trees. These data suggest that homogenization mechanisms are more effective on long arrays than on short ones. In addition, phylogenetic analyses recovered extensive exchanges between non-homologous chromosomes in almost all analyzed satDNAs. This trend is particularly significant in Cl2, Cl3, Cl4 and Cl5 families where the dominant groups include arrays from all chromosomes. Presence of several mixed groups (non homologous chromosomes) in almost each analyzed tree allows a prediction of satDNA spread through several rounds of interchromosomal exchange and subsequent amplification. Those genome-wide expansion events within an evolutionary short period of time imply efficient mechanism of propagation of tandem repeats in non-centromeric genome regions, especially in Cluster 5. Previous studies that were dealing with the evolutionary trends of satellite sequences in the genome are mostly made on centromeric DNA. The conclusion drawn from these analyzes is that intrahomologous exchange is more frequent than interchromosomal. The most prominent example is the human alpha satellite DNA whose higher order (HOR) units show difference in their monomer composition and length, what makes them chromosome-specific (Rudd and Willard 2004). Further, in order to recover the mechanism involved in expansion of satDNAs thought the T. castaneum genome we analyzed flanking regions of arrays. We recovered homologous left and right flanking regions in extremely dispearsed satDNA family Cl5. Search analyses of RepBase database with flanking regions as query showed a partial homology with putative non-autonomous Tc1/Mariner. This implies that repeat sequences of Cl5 were distributed by a certain transposition activity over various chromosomal locations. Interspersed repeats are mainly represented by transposable elements (TEs), until satDNAs usually reside in centromeric compartments of genome. TEs have effective mechanisms of proliferation and movement throughout the genome. A recent study in which internal tandem repeats were found in some TEs provokes a hypothesis that onset and spread of tandem repeats can be linked to processes of transposition (Šatović and Plohl 2013). In plants, a hypervariable region of one LTR-retrotransposon was found expanded into tandem repeats of a satDNA in the pea (*Pisum sativum*) genome (Macas et al. 2009). Similarly, *Zea mays* centromeres became enriched in tandem repeats derived from LTRs and untranslated regions of two unrelated centromere-specific retrotransposons, what probably happened in two independent evolutionary events (Sharma et al. 2013). In contrast, diversity of flanking regions in other satDNAs indicates mechanism of self-propagation by insertion of satDNA repeats into different genome environment.

In summary, satDNA annotation and characterization specially in noncentromeric/euchromatin regions is important not only for filling gaps in assembled genomes but also for understanding of evolutionary trends and mechanisms involved in emergence and expansion of these sequences. Importantly, the suggested approach may help to overall understanding of composition, organization and sequences dynamic in complex genomes.

6. CONCLUSIONS

Our analysis of evolutionary trends of satDNAs in recently separated *Meloidogyne* species revealed:

- Complex organization of monomers in two *Meloidogyne* species, characterized by highly homogenous simple arrays and by higher order repeats (HORs), composed of highly divergent monomers were disclosed.
- 2. Despite sequence differences in five analysed satDNAs, two conserved motifs were recovered. Box 1 turned out to be highly similar to the CENP-B box of human alpha satDNA.
- 3. The onset of this organizational pattern was mediated by conserved Box 1 and Box 2 sequence motifs and the two mechanisms are envisaged in this process: satDNA transposition and illegitimate recombination.
- 4. HORs can represent a template from which monomers with conserved CENP-B box-like segments can be amplified and form high copy number arrays.

Genome-wide analyses of satellite DNAs in assembled *T. castaneum* genome offered important insights into the evolutionary trends of tandems repeats from a whole-genome perspective:

- In contrast of previous findings in genus *Drosophila* our analyzes showed that noncentromeric regions of the genome contain significant portion of tandem repeats organized in long arrays.
- Presence of several mixed clusters (non homologous chromosomes) in almost each analyzed phylogenetic tree allows a prediction of satDNA spread through several rounds of interchromosomal exchange and subsequent amplification.
- 3. Those genome-wide expansion events within an evolutionary short period of time imply efficient mechanism of propagation of tandem repeats in non-centromeric genome regions.

4. The finding of homologous flanking regions with transposable elements feature in extremely dispersed satDNA family imply a putative role of these regions in expansion of tandem repeats through the genome.

In summary, this PhD thesis represents the comprehensive characterization of satellite DNAs in different model organisms combining bioinformatical and experimental approaches and provides important insights into mechanisms involved in the genesis, evolution and spread of satellite DNAs in complex genomes.

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8. SUMMARY

Tandemly arrayed non-coding sequences or satellite DNAs (satDNAs) are rapidly evolving segments of eukaryotic genomes, preferentially located on centromeres. However, the mechanisms involved in the genesis, evolution and spread of satellite DNAs in complex genomes are only partially elucidate. In order to better understand mechanisms related to evolutionary trends of satellite DNA model organisms nematode *Meloidogyne* spp and beetle *Tribolim castaneum* were selected. The specific aims of this study were: (i) to characterize of satDNAs library shared by recently separated nematode species *M. fallax* and *M. chitwoodi* (ii) to performe structural, organizational and phylogenetic analyzes of sequences in the common satDNA library of *Meloidogyne* species in order to investigate mechanisms of satDNA genesis (iii) to analyse of the structure and distribution of satDNAs in the recently sequenced genome of *T. castaneum* (iv) to perform extensive bioinformatics and experimental analyses of non centromeric satDNAs in *T. castaneum* genome and reveal the evolutionary forces that govern the distribution and dynamics of non-centromeric satellite.

Structural sequence analyses of satDNAs in the library of *Meloidogyne* species disclosed complex organization patterns of monomers in the form of simple and higherorder repeat (HOR) arrays. Despite sequence differences between five satDNAs, two conserved motifs were recovered. One of them turned out to be highly similar to the CENP-B box of human alpha satDNA, identical in 10–12 out of 17 nucleotides. Analyses of monomer junction regions in complex HORs highlighted the role of short motifs in rearrangements, even among highly divergent sequences. Two mechanisms are proposed to be involved in this process, i.e., putative transposition-related cut-and-paste insertions and/or illegitimate recombination.

In addition, genome-wide identification of new satDNAs in *T. castaneum* by Tandem Repeat Finder and double Fluorescence in situ hybridization cofirmed their non-centromeric localization. Characterized satDNA arrays are almost evenly distributed within the putative heterochromatic and euchromatic regions of chromosomes. Phylogenetic studies of monomers in newly defined satDNAs showed extensive exchange between homologous as well as non-homologous chromosomes suggesting efficient propagation mechanism of tandem repeats in non-centromeric regions. The finding of homologous flanking regions with transposable elements feature in extremely dispersed satDNA family imply a putative role of these regions in expansion of tandem repeats through the genome.

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9. SAŽETAK

Uzastopno ponovljene nekodirajuće sekvence, odnosno satelitne DNA (satDNA), su brzo evoluirajući dio eukariotskog genoma, preferencijalno smještene u području centromere. Mehanizmi njihovog nastanka, evolucije i širenja u kompleksnim genomima još uvijek nisu potpuno razjašnjeni. Kako su satDNA glavne komponente peri/centromernih područja kromosoma najveći je broj studija napravljen upravo na ovoj frakciji satelitnih DNA. Iako je centromerna funkcija vrlo konzervirana, satDNA iznimno variraju u sekvenci i udjelu u genomu već i među blisko srodnim vrstama. Na osnovu komparativnih studija centromernih DNA te mapiranja centromernih regija nekih modelnih organizama zaključeno je da centromerna funkcija nije uvjetovana određenom sekvencom, ali da ovo područje preferira uzastopno ponovljene DNA. Smatra se da satDNA sudjeluju u organizaciji i evoluciji centromernog područja te da njihova varijabilnost stimulira reproduktivnu izolaciju pa tako i specijaciju. Sekvenciranje velikog broja genoma i nedavni razvoj novih bioinformatičkih platformi za analizu ponavljajućih sekvenci omogućio je analize satDNA profila na razini cijelog genoma ukazujući na prisutnost ovih regija i u eukromatinu. Nedavne studije satDNA u ovim područjima pokazale su njihovu ulogu u moduliranju genske regulacije, vezu s nekim genskim bolestima te ulogu u akumulaciji razlika koje mogu imati za posljedicu promjenu fenotipa. Na osnovu gore navedenog razvidno je da satDNA ne oblikuju samo centromerno područje nego i ostale djelove genoma tako da studije satDNA i u necentromernim područjima predstavljaju važan korak naprijed u razumijevanju organizacije i funkcioniranja genoma u cjelini.

U svrhu boljeg razumijevanja evolucijskih trendova i mehanizama formiranja te širenja satelitnih DNA razmatranih u ovom radu, odabrani su sljedeći modelni i organizmi: dvije vrste oblića iz roda *Meloidogyne* i kornjaš *Tribolium castaneum*. Postojanje satelitne biblioteke u genomima nedavno odvojenih vrsta roda *Meloidogyne* predstavlja idealan sustav za istraživanje mehanizama formiranja satDNA te otkrivanja evolucijski preferiranih oblika sekvenci. S druge strane model organizam *T. castaneum*, čiji je sekvencirani genom javno dostupan, nudi mogućnost ekstenzivnog istraživanja satDNA na razini cijelog genoma te tako i mogućnost istraživanja mehanizama uključenih u širenje ovih sekvenci u genomu. Specifični ciljevi ovog istraživanja su: **i**) karakterizacija biblioteke satelitnih DNA koju dijele nedavno odvojene vrste oblića *M. chitwoodi* i *M. fallax* **ii**) strukturna, organizacijska i filogenetska analiza sekvenci satelitnih DNA iz zajedničke biblioteke vrsta *M. chitwoodi* i *M. fallax* u svrhu otkrivanja mehanizama nastanka satelitnih DNA **iii**) analiza strukture i

distribucije satelitnih DNA u sekvenciranom genomu kornjaša *T. castanaum* iv) temeljite bioinformatičke i eksperimentalne analize ne-centromernih satelitnih DNA u vrsti *T. castaneum* u svrhu otkrivanja evolucijskih trendova koje upravljaju širenjem i dinamikom ne-centromernih satelitnih DNA.

Analiza sekvenci i strukturnih obilježja 5 satelitnih DNA u biblioteci vrsta Meloidogyne chitwoodi i M. fallax otkrila je njihovu nisku međusobnu sličnost (32–64%) te kompleksnu organizaciju satelitnih monomera iz biblioteke u obliku jednostavnih nizova i jedinica višeg stupnja organizacije, tzv. HOR-ova (od engl. higher-order repeat), usporedivu s organizacijom alfa satelita kod ljudi i ostalih primata. Za razliku od alfa satelita, filogenetska analiza satelitnih DNA kod oblića je pokazala grupiranje monomera iz jednostavnih nizova i iz jedinica višeg stupnja organizacije što ukazuje na stalnu izmjenu monomera između ova dva tipa organizacije. Unatoč činjenici da je pet proučavanih satelitnih DNA međusobno različito, pronađena su dva dijela sekvence (motiva) očuvana kod svih. Jedan od njih, nazvan Box 1, pokazuje visoku sličnost sa 17 parova baza dugim CENP-box-om humanog alfa satelita, konkretno u 10 do 12 parova baza. Dodatna zanimljiva činjenica je da je prijelaz između različitih monomera unutar HOR jedinice točno na mjestu tog motiva, tj. Box-a 1. Drugi 20 parova baza dug očuvani motiv, nazvan Box 2, nalazi se također prelasku između monomera podgrupe 1. Ova opažanja naglašavaju važnost kratkih konzerviranih odsječaka DNA u procesima genomskih rearanžmana, čak i među divergentnim sekvencama. Predložena su dva organizma odgovorna za uočene rearanžmane; cut and paste insercija povezana s mehanizmom transpozicije i/ili ilegitimna rekombinacija. Mogućnost sudjelovanja CENP-B box-u sličnih motiva kod oblića u transpozicijskim procesima i dokazana sličnost humanog CENP-B proteina s transpozazom pogo porodice ukazuje na moguću novu ulogu CENP-B boxa u sekvenci DNA osim već dokazane u vezivanju centromernih proteina.

Pretraživanjem cijelog sekvenciranog genoma (sastavljenog od 10 kromosoma i nesastavljenih dijelova) kornjaša *T. castaneum* i identifikacijom novih satelitnih DNA uz pomoć algoritma Tandem Repeat Finder-a i dvobojne flourescencijske hibridizacije *in situ* pronađeno je 9 novih, do sada neopisanih, satelitnih DNA. Usporedbom njihove lokalizacije u odnosu na od prije poznati centormerni satelit TCAST, koji čini čak 35% genima, pokazana je ne-centromerna lokalizacija svake od njih. Opisani nizovi satelitnih DNA skoro su jednakomjerno raspoređeni u heterokromatinskom i eukromatinskom području pojedinih kromosoma. Najviše ih ima na kromosomima 3, 6, 8, 9 i 10 što je u skladu s radom iz 2008

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(Wang et al. 2008) u kojem je RepeatScout metodom otkriveno da je čak 26% genoma sastavljeno od uzastopnih ponavljanja. Našom analizom ustanovljeno je da 9 opisanih satelitnih DNA čine preko 4% genoma s tim da su pojedine porodice zastupljene od ispod 0.2 pa do preko 1%. Dužina monomera novo otkrivenih satelitnih DNA je oko 170 pb što je u skladu s veličinom monomera kod većine do sada opisanih centromernih satelita. Ovaj se trend objašnjava činjenicom da se dužina poklapa s duljinom nukleosomalne DNA te ukazuje na slične strukturne karakteristike centomernih i ne-centromernih satDNA. Filogenetske analize monomera pojedinačnih novoopisanih satDNA ukazuju na značajnu izmjenu sekvenci među homolognim, ali i ne-homolognim kromosomima, ukazujući na učinkovite mehanizme širenja uzastopno ponovljenih sekvenci u ne-centromernom području, pogotovo kod nekih porodica. Proces homogenizacije učinkovitiji je kod dugih nizova dok je za kratke (5 do 7 monomera) karakteristično raspršenost po filogenetskom stablu. Postojanje homolognih rubnih regija sličnih transponirajučim elementima kod iznimno raširene porodice satelitne DNA ukazuje na moguću ulogu ovih regija u širenju uzastopnih ponavljanja po genomu.

10. CURRICULUM VITAE
EUROPEAN CURRICULUM VITAE FORMAT



PERSONAL INFORMATION

Surname(s) /	<pre>/ First name(signal content of the second seco</pre>
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Telephone(s)
Fax(es)
E-mail(s), Web address(s)
Nationality(-ies)
Date of birth
Identification number from Records of Scientific Workers

First name(s)	Pavlek / Martina
Address(es)	Laboratory for structure and function of heteochromatin, Ruđer Bošković Institute, Bijenička 54, 10002 Zagreb
Telephone(s)	+ 385 1 457 1322
Fax(es)	+ 385 1 4561 177
b address(s)	mpavlek@irb.hr
tionality(-ies)	Croatian
Date of birth	October 6 th, 1981
rom Records tific Workers	315522

WORK EXPERIENCE	
 Dates (from – to) 	08. 05. 2009 present
Name and address of employer	Ruđer Bošković Institute, Bijenička 54, 10000 Zagreb
Type of business or sector	Scientific research
Occupation or position held	Doctoral student, assistant
Main activities and responsibilities	Scientific research in natural science: biology; molecular biology; molecular
	genetics; structure, organization, function and evolution of repetitive sequences

EDUCATION

Date	2010 present
cation	Zagreb
sation cation	Ph.D. studies in Molecular Biosciences (University of Osijek, University of Dubrovnik and Rudjer Boskovic Institute)
arded	
Date	2000-2006
ation	Zagreb
ation ation	Faculty of Science, University of Zagreb
arded	B.Sc., ecology

Place of education Name and type of organisation providing education Title or qualification awarded

PERSONAL SKILLS AND COMPETENCIES

Croatian

Understandir	ng	Speaking	Writing		
Listening	Reading	Spoken interaction	Spoken production		
C2	C2	C1	C1		C1
A2	B2	A2	A1		A2

(*) Common European Framework of Reference (CEF) level

Mother tongue Other language(s) Self-assessment European level ^(?)

English German

PARTICIPATION IN SCIENTIFIC AND SPECIALIZED PROJECTS	Adris Foundation "Development of DNA markers for identifying commercially important mollusk species Ruditapes decussatus in the Adriatic Sea" (team member), 2013-2014.	
	Ministry of Science, Education and Sports "Evolution, properties and functional interactions of satellite DNA sequences" (team member), 2009-2013.	
	"Biodiversity of subterranean fauna of Karlovac County" financed by European Union through PHARE 2006 Program, 2009.	
	"Conservation of Eunapius subterraneus, the only subterranean freshwater sponge in the world", 2003-2008.	
	"KEC – Karst Ecosystem Conservation Project", 2003-2007.	
	"Dinaric Alps rare habitats and species conservation project Croatia", 2003-2006.	
	"Conservation of the Croatian subterranean fauna through inventarisation, mapping, education and popularisation", 2000. – 2010.	
	"Subterranean conservation of the lost cave systems of the Dinaric Arc", 2011-2012	
_		
PARTICIPATION IN SCIENTIFIC	2014. The 28th European Congress of Arachnology, Torino, Italy, poster	
MEETINGS	Čukušić A. & Kolundžić E.: A lot or not? A review of 200 years of spider	
	research in Croatia	
	2012. 21st International Conference on Subterranean Biology, Košice, Slovakia,	
	poster presentation: Cukušić A, Pavlek M, Ozimec R: Diversity and	
	distribution of cave dwelling spiders of the families Nesticidae and	
	2011 SIEEC2222 - Symposium internationale entomofaunisticum Europae	
	centralis, Varaždin, oral presentation: M. Pavlek, M. Plohl, N. Meštrović:	
	Highly repeated non-coding DNA in Tribolium castaneum (Coleoptera)	
	genome	
	2011. SIEEC2222 Symposium internationale entomofaunisticum Europae	
	centralis, Varaždin, poster presentation: Cukušić, Anđela; Pavlek, Martina.	
	Faunistics, ecology and biogeography of the cave-dwelling spiders of the families Nesticidae and Agelepidae (Arapese) in Croatia	
	2011, 18th International Chromosome Conference, Manchester, UK, poster	
	presentation: Pavlek, M., Plohl, M., Mestrovic, N.: Highly repeated non-	
	coding DNA in Tribolium castaneum (Coleoptera) genome	
	2010. Society for Experimental Biology Annual Main Meeting; oral presentation:	
	Meštrović, N., Castagnone-Sereno, P., Pavlek, M., Car, A., Plohl, M.: How	
	Satellite DINAS In the library are created?	
	interactions: poster presentation: Meštrović, N. Castagnone-Sereno, P	
	Pavlek, M., Car, A., Plohl, M.: Complex organization of satellite DNA library	
	in the root-knot nematodes Meloidogyne chitwoodi and M. fallax.	
	2009. First student Phd symposium "The Architecture of Life"; poster presentation:	
	Mestrović, N., Pavlek, M., Zižek, M., Plohl, M.: Analysis of satellite DANs in	
	the sequenced genome of Tribolium castaneum (Coleoptera)	
	Pavlek M Žižek M Plohl M Analysis of satellite DANs in the sequenced	
	genome of Tribolium castaneum (Coleoptera)	
	2009. Embo young scientists forum; poster presentation: Meštrović, N., Pavlek, M.,	
	Žižek, M., Plohl, M.: Analysis of satellite DANs in the sequenced genome of	
	I ribolium castaneum (Coleoptera)	
	2000. Du years of molecular biology in Croatia; poster presentation: Mestrović, N.,	
	genome of Tribolium castaneum (Coleontera)	
	2008. ESF Exploratory Workshop on Heterochromatin structure and function from	
	repetitive DNA sequences to epigenetics	

TECHNICAL SKILLS AND COMPETENCIES	 2014. 3rd Workshop on the Application of Next Generation Sequencing to Repetitive DNA Analysis in Plants, České Budějovice, Czech Republic 2011. Methodological Course in Molecular Biology and Medicine "Molecular Phylogeny", Zagreb, 2011. One month training at INRA institute in Antibes, France 2009. Practical Course "Introduction to Bioinformatics", Zagreb Expirience in field work, specially in research of caves and underground fauna, specialist for cave spiders taxonomy Nucleic acids characterization; electrophoretic techniques; hybridization techniques (Southern), molecular cloning, library screening, PCR techniques, molecular cytogenetic techniques (multicolored FISH, PRINS), computer analyses of DNA sequences (phylogenetic analyses, structure predictions, sequence assembly)
PUBLICATIONS	Meštrović, Pavlek, Car, Castagnone-Sereno, Abad, Plohl (2013) Conserved DNA Motifs, Including the CENP-B Box-like, Are Possible Promoters of Satellite DNA
	Array Rearrangements in Nematodes. PLoS ONE. 8(6): e6732 Jalžić, Branko; Bedek, Jana; Bilandžija, Helena; Bregović, Petra; Cvitanović, Hrvoje; Čuković, Tamara; Ćukušić, Anđela; Dražina, Tvrtko; Đud, Lana; Gottstein, Sanja; Hmura, Dajana; Kljaković-Gašpić, Fanica; Komerički, Ana; Kutleša, Petra; Lukić, Marko; Malenica, Marta; Miculinić, Kazimir; Ozimec, Roman; Pavlek, Martina; Raguž, Nikolina; Slapnik, Rajko; Štamol, Vesna. 2013: The cave type
	localities Atlas of Croatian fauna, Volume 2. Zagreb. Marguš, Drago; Barišić, Teo; Bedek, Jana; Dražina, Tvrtko; Gracin, Joso; Hamidović, Daniela; Jalžić, Branko; Komerički, Ana; Lukić, Marko; Marguš, Marija; Menđušić, M.; Miculinić, Kazimir; Mihelčić, G.; Ozimec, Roman; Pavlek, Martina. 2012: Tajne podzemlja. Šibenik.
	Jalžić, B.; Bedek, J., Bilandžija, H.; Cvitanović, H.; Dražina, T.; Gottstein, S.; Kljaković Gašpić, F.; Lukić, M.; Ozimec, R.; Pavlek, M.; Slapnik, R.; Štamol, V. 2010: The cave type localities Atlas of Croatian fauna, Volume 1. Zagreb. Ozimec, R.; Bedek, J.; Gottstein, S.; Jalžić, B.; Slapnik, R.; Štamol, V.; Bilandžija, H.; Dražina, T.; Kletečki, E.; Komerički, A.; Lukić, M.; Pavlek, M. 2009: Red book of cave fauna of Croatia. Zagreb: Ministry of Culture of the Republic of Croatia, The State Institute for Nature Protection.
	Pavlek, M. et Ozimec, R. 2009: New cave-dwelling species of genus Troglohyphantes (Araneae, Linyphiidae) for Croatian fauna. Natura Croatica 18 (1), 29-37.
CURRENT RESEARCH INTEREST	Mapping and analyzes of satellite DNAs in <i>Tribolium castaneum</i> (Coleoptera, Tenebrionidae) and root-knot nematodes of the genus <i>Meloidogine</i> (Nematode). Biology, ecology, phylogeny, taxonomy and evolution of Dinaric cave spiders. Research and protection of cave fauna and cave habitats in general.
N	
MEMBERSHIP IN SOCIETIES	2003 on Groatian Biospeleological Society 2003 on Croatian Mountaineering Society "Željezničar", Department of Speleology 2010 on Society for Experimental Biology (London) 2014 on European Society of Arachnology

11. SUPPLEMENTARY MATERIAL

Supplementary Figure 4.1.1. Alignment of nucleotide sequences obtained by random cloning of trimer after PCR amplification of *M. fallax* and *M. chitwoodi* genome with primers specific for 1c satellite DNA. Satellite trimers from *M. fallax* are marked fa(n) and from *M. chitwoodi* ch(n). All trimers are compared to the first sequence. Positions identical to the first sequence are shown with dot and deletions are indicated with dash.

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	TATG	120 . TTCCGG7	 <mark>\CCCT</mark> (130 . <mark>3TTTCT</mark>	. <mark>Саааа</mark> л	140 ACTAGT	 CATAC	150 	TTGA	160 ATTTC <i>I</i>	. <mark>\TAGC</mark>	170 . ACATT	. <mark>CGAT#</mark>	180 . ACAGCI	 CTTI	19(<mark>'AAGCI</mark>) <mark>.</mark> CTTT	20 CGAA	00 . IGATA	2 . CTAAF	210 . ATTCAG	220 . TATACTT
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		230	1	240		250		260		270		280	1	290	1	300)	1	310	I	320	330
	TCTC.	AGAGGGZ			CTTCA	ATTTAA	TAAAA				AATT	TCTAT	GTTC	ATGAAC	CTGT	TTCT	CGAGT	TCTG	rctgt	AAGTT	GCTTG	• • • • • ATTTCAA • • • • • • • •
	· · · · · · · · · · · · · ·	· · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·	· · · · · · · ·	· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·			· · · · · · · ·	· · · · · · · ·	· · · · · · · · · · · · · · · · · · ·	· · · · · · ·	· · · · · · · ·	· · · · ·	· · · · · ·	· · · · · · · · · · · · · · · · · · ·	· · · · · ·	 	· · · · · · ·		· · · · · · · · · · · · · · · · · · ·
		340 . TTGTTCC	 <mark>Gattci</mark>	350 . ACCTCT	. TCATCO	360 <mark>CTCTTT</mark>	 'CGAA'I	370 		380 <mark>CTCATC</mark>	. <mark>Cata</mark>	390 . <mark>ACTTA</mark>	. <mark>CCTAC</mark>	400 . <mark>CAGAAT</mark>	 TTTT	41() \AAAA	42 <mark>.CTCA2</mark>	20 . <mark>AAGTA</mark>	2 . TCCAJ	130 . TCTCC	440 <mark>CCCCAAA</mark>
	 	c	· · · · · · · · · · · · · · · · · · ·	 	· · · · · · ·	 	· · · · · · · · · · · · · · · · · · ·			· · · · · · · ·	· · · · · · ·	· · · · · · · · · · · · · · · · · · ·	· · · · · ·			· · · · · ·	· · · · · · ·	· · · · · ·	· · · · · · · · · · · · · · · · · · ·	· · · · · ·		· · · · · · · · · · · · · · · · · · ·
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Kons	 <mark>AAAT</mark>	450 . TTCTATC) <mark>3TTCC(</mark>	460 . <mark>3GACCC</mark>	.	470 <mark>CTCAAA</mark>		480	ACGAT	490 	. Jaatt	500 . <mark>TCATA</mark>	 <mark>GAA</mark>									
$M_{1c}fa_6$ $M_{1c}fa_7$ $M_{1c}ch_{16}$ $M_{1c}ch_5$	 	· · · · · · · · · · · · · · · · · · ·		· · · · · · · · · · · · · · · · · · ·	· · · · · · · ·	· · · · · · · ·	· · · · · · ·	· · · · · · · · · · · · · · · · · · ·	· · · · · · ·		· · · · · ·	 	.c.			4						
$M_{1c}fa_8$ $M_{1c}fa_{11}$ $M_{1c}ch_{13}$ $M_{1c}ch_{10}$	 		 	· · · · · · · ·			· · · · · ·		·····	 			 			IC			1			

Supplementary Fig. 4.1.2. Alignment of HORs from *M. fallax* (clone names in blue) and *M. chitwoodi* (clone names in green). H1cfa(n) and H1cch(n) represent fragments amplified with 1c primers. Hufa(n) and Huch(n) are amplified with primers specific for U1 sequence. All primer positions are marked above sequences and primers are listed in Table 3.6. SatDNA monomers are indicated in different colors; 1c, 1d, 2a, 1a, 1b and 1b'. Unlabeled part of the HOR is U1 sequence. Red boxes indicate Box 1, and black boxes represent Box 2.

	1cL	>																		
	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200
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Hlcfa2	TTCGATTCACC	TCTTCATCCTCI	TTCGAATGAGA	TATGACTCATC	AATAACTTAC	CTACAGAATO	JTTTTTTAAAAA	ACTCAAAGTAI	CCATTCTCC	CCCCAAAAAA	TTTCT	ATGTTCCGGACCO	TGTTTCTCA	AAAACTAGTC	ATACGATTTT	TGAATTTCATA	GCACATTCG.	ATTCAGCTTTCA	AGCTCTT	TCGAATG
Hlcfa8	NN		•••••	• • • • • • • • • • • •	с	· · · · · N · · · · 1	r		•••••	NN	••• <mark>•</mark> •••	N	• • • • • • • • • • •	• • • • • • • • • • •			.NN	• • • • • • • • • • • • •	• • <mark>• • • • • •</mark>	•••••
Hlcfal7	T		•••••	• • • • • • • • • • • •	с	1	r		c		• • • • • •		• • • • • • • • • • •	• • • • • • • • • • •				• • • • • • • • • • • • •	• • <mark>• • • • • •</mark>	• • • • • • • •
H1cfa18			•••••	• • • • • • • • • • • •	с	1	r				• • • • • •		• • • • • • • • • • •	• • • • • • • • • • •				• • • • • • • • • • • • •	• • <mark>• • • • • •</mark>	• • • • • • • •
Hlcch2			• • • • • • • • • • • •	• • • • • • • • • • • •	с	.T	r 		•••••		• • • • • •		• • • • • • • • • • •		T			• • • • • • • • • • • • •	• • <mark>•</mark> • • • • •	
Hlcch3	T		• • • • • • • • • • • •	• • • • • • • • • • • •	с	.T	r 		•••••		• • • • • •		• • • • • • • • • • •					• • • • • • • • • • • • •	• • <mark>•</mark> • • • • •	
Hlcch4			•••••	• • • • • • • • • • • •	c	. T 1	r				• • •							• • • • • • • • • • • • •	· · · <mark>· · · · · ·</mark>	
Hlcch6			•••••	• • • • • • • • • • • •	c	. T 1	r				• • •							• • • • • • • • • • • • •	· · · <mark>· · · · · ·</mark>	
Hlcch8			•••••	• • • • • • • • • • • •	c	. T 1	r				• • •							• • • • • • • • • • • • •	<mark>.</mark>	
Hlcch9			•••••	• • • • • • • • • • • •	c	. T 1	r				• • •							• • • • • • • • • • • • •	· · · <mark>· · · · · ·</mark>	
Hlcch12					c	тт	r													<mark>.</mark>
Hlcch11					c	1	r 													<mark>.</mark>
Huch21																			<mark>.</mark>	
Huch22																			<mark>.</mark>	
Huch23																			<mark>.</mark>	
Huch11																			<mark>.</mark>	
Hufa4																			<mark>.</mark>	
Hufal																			· <mark></mark>	
Hufa5																			· <mark></mark>	
HufaP8																				
Huch9																				
Hufa10																				

	210	220 2	30 2	240 250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400
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H1cfa2	ATATATGAATCATAT	AGAAATATTTTGTC	GATAATAAGI	TTAGCCGCGGTTGAACC	TCCCAAATTA	TTTTTTCGG	AACAAGTCTGAA	ATTTTCGGAA	CAAGTCTCAT	AACTTACTG	AATTTTCTT-	CAAAAAATA	TTCATTCCA	GCTTCAATAT	ATTCAGAATT?	AAATCCTCT	TTCGAATGATA	TATGACTCAT	ACGAAAC
H1cfa8																			
Hlcfal7																			
H1cfa18																			
Hlcch2																			
H1cch3																			
H1cch4																			
Hlcch6																			
H1cch8																			
Hicch9					G														
Hloch12																			
Wloch11													•••••						
Hugh 21																			
Huch22																			
Huch22																			
Huch11																			
Huchili Hufa4																			
Hulay Thefal																			
Hurai																			
Huras																			
Huch9																			
Huchy																			
Huraro																			
																		-	
	410	420 4	30 4	440 450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600
	410 ••••• •••••	420 4	30 4	440 450 	460	470	480 .	490 •••• •••• •	500 .	510 .	520 • • • • • • • •	530 	540 	550 	560 • •••• ••••	570 .	580	590 • • • • • • •	600 • • • • •
Hlcfa2	410 -TTACCTACAGATTT	420 4	30 4	440 450	460 	470 	480 . Igcaacttttga	490 . ACTGTTCTGTT	500 .	510 .	520 • • • • • • • • гтаадаатда	530 	540 AATGAGAAT	550 . Сатаатаааа	560 • •••• •••• Gaaaaaatti	570 . Igaagaaat	580 	590 .	600 . TAAATTT
Hlcfa2 Hlcfa8	410 	420 4 	30 4	440 450	460 	470 	480 . IGCAACTTTTGA	490 . ACTGTTCTGTT	500 . AAAAGTTGAT	510 . CAATTTTTGCT	520 Itaagaatga	530 Agaatatag;	540 AATGAGAAT(N	550 . Сатаатаааа .N	560 . GAAAAAATTT	570 . IGAAGAAAT	580 ACCATAGAAAT	590 . AAAAAGTTAA	600 . TAAATTT
Hlcfa2 Hlcfa8 Hlcfa17	410 	420 4 TTTTTACAAAAATT .N	30 4	440 450	460 	470 	480 . IGCAACTTTTGA	490 . ACTGTTCTGTT	500 . AAAAGTTGAT	510 . AATTTTTGCT	520 Itaagaatga	530 AGAATATAG	540 AATGAGAAT(N	550 . CATAATAAAA .N	560 . GAAAAAAATTT	570 	580 Accatagaaat	590 . AAAAAGTTAA	600 . TAAATTT
Hlcfa2 Hlcfa8 Hlcfa17 Hlcfa18	410 	420 4 TTTTTACAAAAATT .N	30 4	440 450	460 	470 	480 . IGCAACTTTTGA	490 . ACTGTTCTGTT	500 . AAAAGTTGAT	510 . XAATTTTTGC1	520 Itaagaatga	530 AGAATATAG	540 AATGAGAAT(N	550 . .n	560 . Gaaaaaatti 	570 . . IGAAGAAAT	580 	590 . אאאאאקדדאא	600 . TAAATTT
Hlcfa2 Hlcfa8 Hlcfa17 Hlcfa18 Hlcch2	410 	420 4 TTTTTACAAAAATT .N	30 4	440 450	460	470 	480 . Igcaactittiga	490 . ACTGTTCTGTT	500 . AAAAGTTGAT	510 . AATTTTTGCT	520 ГТААДААТДА	530 AGAATATAG	540 AATGAGAAT 	550 . САТААТАААА .N	560 . GAAAAAATTT	570 . . IGAAGAAAT	580 	590 . אאאאאקדדאא	600 . TAAATTT
Hlcfa2 Hlcfa8 Hlcfa17 Hlcfa18 Hlcch2 Hlcch3	410 	420 4 	30 4	440 450	460 	470 	480 . Igcaactittga	490 . ACTGTTCTGTT	500 . AAAAGTTGAT G	510 XAATTTTTGCT	520 ITAAGAATGA	530 Agaatatag;	540 AATGAGAAT N	550 . CATAATAAAA .N	560 . GAAAAAAATTT	570 . . IGAAGAAAT	580 	590 . AAAAAGTTAA	600 . TAAATTT
Hlcfa2 Hlcfa8 Hlcfa17 Hlcfa18 Hlcch2 Hlcch3 Hlcch4	410 	420 4 	30 4	140 450	460 	470	480 . IGCAACTTTTGA	490 . ACTGTTCTGTT	500 . AAAAGTTGAT G G	510 XAATTTTTGCT	520 Itaagaatga	530 AGAATATAG2	540 AATGAGAAT(N	550 . CATAATAAAA .N	560 . GAAAAAATTT	570 . IGAAGAAAT;	580 	590 . AAAAAGTTAA	600 . TAAATTT
Hlcfa2 Hlcfa8 Hlcfa17 Hlcfa18 Hlcch2 Hlcch3 Hlcch4 Hlcch6	410	420 4	30 4	440 450 CATTCTCCCCCAAAAAA	460 	470 	480 . IGCAACTTTTGA	490 	500 . AAAAGTTGAT G. G. G.	510 , :AATTTTTGC	520 TTAAGAATGA	530 AGAATATAG; 	540 AATGAGAAT 	550 CATAATAAAA .N	560 . GAAAAAAATTI	570 . rgaagaaat;	580 	590 . AAAAAGTTAA	600 . TAAATTT
Hlcfa2 Hlcfa8 Hlcfa17 Hlcfa18 Hlcch2 Hlcch4 Hlcch6 Hlcch6	410 	420 4 	30 4	440 450	460 	470	480 . IGCAACTTTTGA	490 	500 . AAAAGTTGAT G. G. G. G.	510 . xatttttgct	520 TTAAGAATGA	530 AGAATATAG	540 AATGAGAAT(N	550 . CATAATAAAA .N	560 . . Gaaaaaatti	570 . .	580 	590 . AAAAAGTTAA	600 . TAAATTT
Hlcfa2 Hlcfa17 Hlcfa18 Hlcch2 Hlcch3 Hlcch4 Hlcch6 Hlcch8 Hlcch9	410 	420 4 	30 4	440 450 CATTCTCCCCCAAAAAA	460 	470	480 IGCAACTTTTGA	490 	500 	510 xatttttgc7	520 TTAAGAATGA	530 AGAATATAG	540 . AATGAGGAAT N.	550 . Сатаатаааа .N	560 . GAAAAAAATT?	570 . GAAGAAAT	580 	590 . . AAAAAGTTAA	600 . TAAATTT
Hlofa2 Hlofa8 Hlofa17 Hlofa18 Hloch3 Hloch4 Hloch6 Hloch6 Hloch9 Hloch12	410 	420 4	30 4	440 450	460 	470 	480 . rgcaacttttga	490 . 	500 	510 . .aattttttgc2	520 TTAAGAATGA	530 AGAATATAG	540	550 . CATAATAAAA .N	560 . GAAAAAAATTT	570 . . 	580 	590 . AAAAAGTTAA	600 . TAAATTT
Hlcfa2 Hlcfa8 Hlcfa17 Hlcch2 Hlcch3 Hlcch4 Hlcch6 Hlcch6 Hlcch8 Hlcch12 Hlcch12	410 	420 4 ,	30 4	440 450	460 TTTCTATGTT	470	480 - rgcaactittga	490 	500 	510 	520 TAAGAATGA	530 AGAATATAG	540 . AATGAGAAT(N	550 . . 	560 . GAAAAAAATTY	570 . GAAGAAATZ	580 	590 . AAAAAGTTAA	600
Hlcfa2 Hlcfa8 Hlcfa17 Hlcfa18 Hlcch2 Hlcch4 Hlcch6 Hlcch8 Hlcch9 Hlcch11 Huch21	410 	420 4 	30 4	440 450	460 	470 	480 Igcaacttttga	490 . ACTGTTCTGTT	500 . AAAAGTTGAT 	510 	520 TTAAGAATGA	530 	540 AATGAGAAT(N	550 . CATAATAAAA N	560 . GAAAAAAATTT	570 - гдалдалат:	580 	590 . AAAAAGTTAA	600 . TAAATTT
Hlcfa2 Hlcfa8 Hlcfa17 Hlcch3 Hlcch4 Hlcch6 Hlcch6 Hlcch9 Hlcch12 Hlcch11 Huch21 Huch21	410 	420 4 ,, TTTTACAAAATT N	130 4	440 450	460 	470	480 RGCAACTITTGA	490 	500 	510 	520 	530 agaatatag: 	540 AATGAGAAT(N	550 . CATAATAAAA .N	560 . GAAAAAAATTT	570 	580 	590 . AAAAAGTTAA	600 . TAAATTT
Hlcfa2 Hlcfa17 Hlcfa17 Hlcfa17 Hlcch2 Hlcch4 Hlcch6 Hlcch8 Hlcch9 Hlcch12 Hlcch11 Huch21 Huch23	410 	420 4	30 4	440 450	460 	470	480 . rgcaacttttga	490 	500 	510 . 	520 	530 AGAATATAG: 	540 AATGAGAAT 	550 . САТААТАААА .N.	560 . GAAAAAAATTT	570 . rgaagaaat.	580 	590 . AAAAAGTTAA	600 . TAAATT
Hlcfa2 Hlcfa8 Hlcfa17 Hlcfa18 Hlcch2 Hlcch3 Hlcch6 Hlcch6 Hlcch12 Hlcch12 Hlcch11 Huch21 Huch23 Huch11	410 	420 4 ,, TTTTACAAAAATT N	130 4	440 450	460	470	480 RGCAACTITTGA	490 	500 AAAAGTTGAT 	510 AATTTTTGC?	520 TTAAGAATGA	530 	540 AATGAGAAT(.N	550 CATAATAAAA N.	560 . GAAAAAAATTT	570 . rgaagaaat.	580 	590 . AAAAAGTTAA	600 . TAAATTT
Hlofa2 Hlofa8 Hlofa17 Hlofa18 Hloch2 Hloch3 Hloch4 Hloch6 Hloch9 Hloch11 Huch21 Huch21 Huch23 Huch13 Hufa4	410 	420 4	130 4	440 450	460	470 	480 . rgcaacttttga 	490 	500 	510 . AATTTTTGC7	520 TTAAGAATGA	530 	540 AATGAGAAT N	550 CATAATAAAA N.	560 .] GAAAAAAATTT 	570 	580 	590 . AAAAAGITAA	600 . TAAATTT
Hlcfa2 Hlcfa8 Hlcfa17 Hlcfa18 Hlcch2 Hlcch3 Hlcch6 Hlcch6 Hlcch6 Hlcch12 Hlcch11 Huch21 Huch21 Huch23 Huch11 Hufa4 Hufa1	410 	420 4 ,,,, TITTACAAAAATT .N,,,,,,,	130 4	440 450	460	470 	480 IGCAACTTTTGA	490 	500 . 	510 . MATTITIGCI	520 ТТААДААТСА	530 	540 AATGAGAAT N	550 	560 	570 IGAAGAAAT	580 	590 	600 . TAAATTT
Hlcfa2 Hlcfa8 Hlcfa17 Hlcfa18 Hlcch2 Hlcch3 Hlcch6 Hlcch6 Hlcch9 Hlcch11 Huch22 Huch21 Huch21 Huch13 Huch11 Hufa4 Hufa5	410 	420 4	130 4	440 450	460 	470 cAGGAACT?	480 . rgcaacttttga 	490 	500 	510 . AATTTTTGC	520 TTAAGAATGA	530 	540 AATGAGAAT 	550 	560] GAAAAAAATTT	570 	580 	590 	600 . TAAATTT
Hlcfa2 Hlcfa17 Hlcfa17 Hlcfa18 Hlcch2 Hlcch3 Hlcch4 Hlcch6 Hlcch9 Hlcch12 Hlcch11 Huch21 Huch21 Huch23 Huch13 Hufa4 Hufa5 Hufa5 Hufa78	410 	420 4	130 4	440 450		470 	480 . GGAACTTTTGA	490 . CTGTTCTGTT 3.	500 . 	510 . MATTTTGC	520 TTAAGAATGA	530 	540 ААТGAGAAT N	550 2373373337 N.	560 	570 ГGЛАДЛАЛТ.	580 	590 	600 . TAAATTT

Hufa10



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H1cfa2	AGCTCATT	CGATTCA	GTTTTTCG	AGCTCTACAA	ATGATA	CAAATTAC	AGCGAATAT	GATTCGGAG	GAAATTTTT	T-ATCGAAG	TTTTAAAT.	TTCCTTC	CCCCAAAAA	ATTO	CAATGT	TCATGGAG	TTGGTT	TCAAA	AACTAGT	CATACGA	TTTTTGA	ATA						4
H1cfa8										.т				· · · .	N	IN.					.N	TTCA	TAGNTCA	TTCGAT	ACAGCTCTTI	TAANCT	CTTTCGA	АТ
H1cfa17										.т				· · · .								T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
H1cfa18								.gc		.т				· · · .					.T	TAA.	TT	TA.AAA	TAGCTCA	TTCGAT	ACAGCTTTTC	CATGCT	CTTTCGA	АТ
Hlcch2								.gc		.т				· · · .								T.TTA-	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
Hlcch3								.cc		.т				· · · .	G							T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
Hlcch4								.cc		.т				· · · .	G							T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
Hlcch6								.cc		.т				· · · .	G							T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
Hlcch8								.cc	c	.т				· · · .								T.CT-A	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
Hlcch9								.cc		.т		N		.c								T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
H1cch12								.cc		.т	т				G							T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTT	TAAGCT	CTTTCGA	АТ
Hlcch11								.cc		.т				· · · .								TTCA	TAGCA	ATCGAA	т			4
Huch21								.cc		.т		т		· · · .	G							T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
Huch22								.cc	G	.т				· · · .	G							T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
Huch23										.т				· · · .								T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
Huch11										.т				· · · .	G							T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
HufaN4										.т				· · · .								T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
HufaP1										.т				· · · .								T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
HufaP4										.т				· · · .								T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTTI	TAAGCT	CTTTCGA	АТ
HufaP8								.cc	G	.т									.т	TAA.	TT	TA.AAA	TAGCTCA	TTCGAT	ACAGCTTTTC	CATGCT	CTTTCGA	АТ
HuchP9								.cc	G	.т									.т	TAA.	TT	TA.AAA	TAGCTCA	TTCGAT	ACAGCTTTTC	CATGCT	CTTTCGA	AT
HufaP10										.т												T.TTCA	TAGCTCA	TTCGAT	ACAGCTCTTT	AGCT	CTTTCGA	AT
					_									_														_

	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560	1570	1580	1590	1600
	····					· • ••+••••	+ • • • • • • • • • • • • • • • • • • •										+ + • • • • • • • •			
Hlcfa2																				
H1cfa8	NATACTAAANTC	GTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ANTTTTTC	CCCCAAAAAAN	NTTNTAT	GTTCATGAAC	TGTNTCTCG	AGTTCTGTCNG	TAAGTTGCTNG.	ATNTCAATAG	GTTGTTCGA	TTCACCTNTTC	TCTCTTT	CGAATGAG	TANGANTCAT	CNTAACTTA	CCAA
Hlcfal7	GATACTAAATTC	GTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTC	CCCCAAAAAAA	TTTCTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAA	A						
H1cfa18	GATACTAAATTC	GTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTC	CCCCAAAAAAA	TTTCTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTCC	TCTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CCTACAGA
Hlcch2	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT CTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TCTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CCTACAGA
Hlcch3	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT CTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TCTCTTT	CGAATGAG	GATGACTCAT	CATAACTTA	CTTACAGA
Hlcch4	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT CTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TCTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CTTACAGA
Hlcch6	GATACTAAATTC	AGTATACTCTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT CTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGCTCGA	TTCACCTCTTC	TCTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CCTACAGA
Hlcch8	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT CTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TCTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CTTACAGA
Hlcch9	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAA-TTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTTCTGT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TCTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CCTACAGA
Hlcch12	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT CTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TC CTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CTTACAGA
H1cch11																				
Huch21	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT CTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TCTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CTTACAGA
Huch22	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT CTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TCTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CCTACAGA
Huch23	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT CTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TCTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CCTACAGA
Huch11	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT <mark>CTAT</mark>	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TC CTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CTTACAGA
HufaN4	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTC	CCCCAAAAAAA	TTTCTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TC CTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CCTACAGA
HufaP1	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTC	CCCCAAAAAAA	TTTCTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TC CTCTTT	CTAATGAG2	TATGACTCAT	CATAACTTA	CCTACAGA
HufaP4	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT CTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TCTCTTT	CTAATGAG2	TATGACTCAT	CATAACTTA	CCTACAGA
HufaP8	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT CTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TCTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CCTACAGA
HuchP9	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT <mark>CTAT</mark>	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG.	ATTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TC CTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CCTACAGA
HufaP10	GATACTAAATTC	AGTATACTTTCT	CAGAGGGAAAA	AAAATTTCTI	CAATTTAAAAA	ATTTTTTC	CCCCAAAAAAA	TTT CTAT	GTTCATGAAC	TGTTTCTCG	AGTTCTGTCTG	TAAGTTGCTTG	GTTTCAATAG	CTTGTTCGA	TTCACCTCTTC	TCTCTTT	CGAATGAG	TATGACTCAT	CATAACTTA	CCTACAGA

	- 10	<u>cR</u>				_	2aL	>				
	1610 1620	1630 1640	1650 1660 16	70 1680 16	90 1700 1710	1720	1730 1740	1750	1760 1770	1780	1790 1	.800
W1cfa2	•••••	· · · · · · · · · · · · · · · · · · ·	·····	•••••	•••••	••• •••• •••• •••	· · · · · · · · · · · · · · · · · · ·	•• •••• •••• •	••••	• • • • • • • • • •	••••	
W1ofa8												
Hicfal7												
H1cfa18	ATTTTTTTTAAAAAACTCA											
Hlcch2	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCC										
H1cch3	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCC										
Hlcch4	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCC										
Hlcch6	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCC										4
Hlcch8	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCC										4
Hlcch9	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCC										4
Hlcch12	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCC										4
Hlcch11												Æ.,
Huch21	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCCAAAAAATTT	CTATGTTCCGGACCCTGTTTCTC	AAAAACTAGTCATACGA-TT	TTTGAATTTCATAGCTCATTCO	ATTCAGCTTTCAAAG	TCTTTCGAATGATA	TATGAATCATATAG	AAATATTTTGTCGATAA	TAAGTTAGCCGCG	GTTGAACCTCCCA	A
Huch22	ATTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCCAAAAAATTT	CTATGTTCCGGACCCTGTTTCTC	AAAAACTAGTCATACGA-TT	TTTGAATTTCATAGCTCATTCO	JATTCAGCTTTCAAAG	TCTTTCGAATGATA	TATGAATCATATAG	AAATATTTTGTCGATAA	TAAGTTAGCCGCG	GTTGAACCTCCCA	A
Huch23	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCCAAAAAATTT	CTATGTTCCGGACCCTGTTTCTC	AAAAACTAGTCATACGA-TT	TTTGAATTTCATAGCTCATTCO	ATTCAGCTTTCAAAG	TCTTTCGAATGATA	TATGAATCATATAG	AAATATTTTTGTCGATAA	TAAGTTAGCCGCG	GTTGAACCTCCCA	A
Huch11	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCCAAAAAATTT	CTATGTTCCGGACCCTGTTTCTC	AAAAACTAGTCATACGA-TT	TTTGAATTTCATAGCTCATTCO	BATTCAGCTTTCAAAGO	TCTTTCGAATGATA	TATGAATCATATAG	AAATATTTTTGTCGATAA	TAAGTTAGCCGCG	GTTGAACCTCCCA	A
HufaN4	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCCAAAAAATTT	CTATGTTCCGGACCCTGTTTCTC	AAAAACTAGTCATACGA-TT	TTTGAATTTCATAGCTCATTCO	BATTCAGCTTTCAAAG	TCTTTCGAATGATA	TATGAATCATATAG	AAATATTTTGTCGATAA	TAAGTTAGCCGCG	GTTGAACCTCCCA	A
HufaP1	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCCAAAAAATTT	CTATGTTCCGGACCCTGTTTCTC	AAAAACTAGTCATACGA-TT	TTTGAATTTCATAGCTCATTCO	BATTCAGCTTTCAAAGO	TCTTTCGAATGATA	TATGAATCATATAG	AAATATTTTTGTCGATAA	TAAGTTAGCCGCG	GTTGAACCTCCCA	A
HufaP4	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCCAAAAAATTT	CTATGTTCCGGACCCTGTTTCTC	AAAAACTAGTCATACGA-TT	TTTGAATTTCATAGCTCATTCO	BATTCAGCTTTCAAAG	TCTTTCGAATGATA	TATGAATCATATAG	AAATATTTTTGTCGATAA	TAAGTTAGCCGCG	GTTGAACCTCCCA	A
HufaP8	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCCAAAAAATTT	CTATGTTCCGGACCCTGTTTCTC	AAAAACTAGTCATACGA-TT	TTTGAATTTCATAGCTCATTCO	BATTCAGCTTTCAAAG	TCTTTCGAATGATA	TATGAATCATATAG	AAATATTTTTGTCGATAA	TAAGTTAGCCGCG	GTTGAACCTCCCA	A
HuchP9	ATTTTTTTTAAAAAACTCAAAGTATCCA	TTCTCCCCCCAAAAAATTT	CTATGTTCCGGACCCTGTTTCTC	AAAAACTAGTCATACGATTT	TTTGAATTTCATAGCTCATTCO	BATTCAGCTTTCAAAG	TCTTTCGAATGATA	TATGAATCATATAG	AAATATTTTTGTCGATAA	TAAGTTAGCCGCG	GTTGAACCTCCCA	A
HufaP10	ATTTTTTTTAAAAAACTCAAAGTATCC	TTCTCCCCCAAAAAATTT	CTATGTTCCGGACCCTGTTTCTC	AAAAACTAGTCATACGA-TT	TTTGAATTTCATAGCTCATTCC	ATTCAGCTTTCAAAG	TCTTTCGAATGATA	TATGAATCATATAC	AAATATTTTGTCGATAA	PAAGTTAGCCGCG	TTGAACCTCCCA	A

	<u> 2aR</u>	
	1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 20	000
W1ofa2		
Hlcfa8		
H1cfa17		
H1cfa18		
Hlcch2		
Hlcch3		
Hlcch4		
Hlcch8		
Hicch9		
Hicch12		
HICCh5		
Hicchill Buch 21		
Hugh22		
Huch23		
Huch11	ATTATTTTTTCGGAACAAGTCTGAAAATTTCGGAACAAGTCTCCATACGAACTAACT	
HufaN4	ATTATTTTTTCGGAACAAGTCTGAAATTTCGGAACAAGTCTCATAACTTACTGAAATTTCCTCAAAAAATATTCCTCATCATATATTCCAGAATTAAATCCGAATTAAATC	
HufaP1	ATTATTTTTTCGGAACAAGTCTGAAAATTTTCGGAACAAGTCTACCGAAACAATTTCCTAAAAAATATTCCTCATAAAATTCCATCCCCCAAAAAA	
HufaP4	ATTATTTTTTCGGAACAAGTCTGAAAATTTTCGGAACAAGTCTCATAACTTACTGAAAATAATTCCATTCCAGCTTCAAAAAATATTCCAGCATTAAATCCTCATAACGAATGAAT	
HufaP8	ATTATTTTTCGGAACAAGTCTGAAAATTTCCGGAACAAGTCTCAAAAATTTTCTTCCAAAAAATATTCCATCCA	
HuchP9	ATTATTTTTCGGAACAAGTCTGAAATTTTCGGAACAAGTCTCATAACTTACTGAAATATTTCATCCAAAAAATATTCCAGGCTTCAAAAAATATTCCAGGAATTAAATC	
HufaP10	ATTATTTTTCGGGACAAGTCTGAAAATTTTCGGAACAAGTCTCATAACTAAATTTCCAGAATTTCCAGCTTCCAATATATAT	

	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
							
H1cfa2																				
Hlcfa8																				
Hlcfal7																				
H1cfa18																				
Hlcch2																				
H1cch3																				
Hlcch4																				
H1cch8																				
H1cch9																				
H1cch12																				
H1cch5																				
Wloch11																				
Hugh 21	TTCACCAR	TTTCC & CTTT	TGACTGTTCT	GTTA A ACCTT	2272277777777	CTTAACAATC		ATCACAAT			GAAGAAATA	CCARACARA	TAAAAACTTA		TCCCCCATC	COOTTTTTAC		3300033007	CTCCAAACT	CANGTOCOTTO
Hugh22	TTCAGCAAC	CTTCCAACTTT	TGACTGTTCT	GTTA A ACCTTO	IATA ATTTTTC	CTTAAGAATC	AAGAATATAG	AATGAGAAT			GAAGAAATA	CCAAAGAAA	TAAAAAGIIA	TAAATTTGT	TCCCCCCATC	CCCTTTTTAC	ACCCAGCCAA	AACCCAAGCI	CTCCAAAGT	GAAGIGGCIIG
Hugh 23	NTCAGCAAC	CTTCCAACTTT	TGACTGTTCT	GTTA A ACCTTO	IATA ATTTTTC	CTTAAGAATC	AAGAATATAG	AATGAGAAT			GAAGAAATA	CCAAAGAAA	TAAAAAGIIA	TAAATTTGT	TCCCCCCATC	CCCTTTTTAC	ACCCAGCCAA	AACCCAAGCI	CTCCAAAGT	GAAGIGGCIIG
Hugh11	TTCAGCAAC	CTTCCAACTTT	TGACTGTTCT	GTTA A ACCTTO	IATA ATTTTTC	CTTAAGAATC	AAGAATATAG	AATGAGAAT			GAAGAAATA	CCAAAGAAA	TAAAAAGIIA	TAAATTTGT	TCCCCCCATC	CCCTTTTTAC	ACCCAGCCAA	AACCCAAGCI	CTCCAAAGT	GAAGIGGCIIG
HufeN4	TTCAGCAAC	CTIGCAACIII CTTCCAACTTT	TGACIGIICI	GITAAAGGIIC		CITANGAAIC	AAGAAIAIAG	AAIGAGAAIG	37733733333		CARCANATA	CCARAGAAA.	TAAAAAGIIA	17777777777777777	TOCCCCCATC	CCCTTTTTAC	ACCCAGCCAA	AACCCAAGCI	CICCANAGI	JOANGIGGCIIG
Hulan4	TICAGCAAC		TGACIATICI		ATAATTTTTG	CITAAGAATO	AAGAAIAIAG	AAIGAGAAIG			GAAGAAAIA	CCATAGAAA.	IAAAAAGIIA		TCCCCCCATC	CCCTTTTTAC.	ACCCAGCCAA	AACCCAAGCI		JGAAGIGGCIIG
Hurapi	TTCAGCAAC		TGACIGITCI	GTTAAAAGTTO		CITAAGAATO		AATGAGAATG			GAAGAAATA	CCATAGAAA.		ATAAATTIGI	TCCCCCCATC	CCCTTTTTAC.	ACCCAGCCAA	AACCCAAGCI	CICCAAAGIC	GAAGIGGCIIG
HuraP4	TTCAGCAAC	CTTGCAACTTT	TGACTGTTCT	GITAAAAGTTO	JATAATTTTTG	CITAAGAATO	AAGAATATAG	AATGAGAATG		AAAAAAAATTT	GAAGAAATA	CCATAGAAA	TAAAAAGTTA	ATAAATTTGT	TCCCCCCATCI	CCCTTTTTAC	ACCCAGCCAA	AACCCCAAGCI	CICCAAAGT	JGAAGIGGCTTG
HUTAPS	TTCAGCAAC	CTTGCAACTTT	TGACTGTTCT	GTTAAAGGTTC	JATAATTTTTG	CTTAAGAATO	JAAGAATATAG	AATGAGAATG	ATAATAAAAG	AAAAAAA1"1"	GAAGAAATA	CCAAAGAAA	TAAAAAGTTA	ATAAATTTGT	TCCCCCCCATC	CCCTTTTTAC.	ACCCAGCCAA	AACCCAAGCI	CTCCAAAGT	JGAAGTGGCTTG
HUCNP9	TTCAGCAA	CTTGCAACTTT	TGACTGTTCT	GTTAAAGGTTO	JATAATTTTTG	CTTAAGAATO	JAAGAATATAG	AATGAGAAT	ATAATAAAA	AAAAAAATTI	GAAGAAATA	CCAAAGAAA	TAAAAAGTTA	ATAAATTTGT	TCCCCCCATCI	CCCTTTTTAC.	ACCCAGCCAA	AACCCAAGCI	CTCCAAAGT	JGAAGTGGCTTG
HutaP10	TTCAGCAA	CTTGCAACTTT	TGACTGTTCT	GTTAAAAGTTO	JATAATTTTTG	CTTAAGAATO	JAAGAATATAG	BAATGAGAAT	CATAATAAAA	JAAAAAAATTT	IGAAGAAATA	CCATAGAAA'	TAAAAAGTTA	ATAAATTTGT	TCCCCCCATCI	ICCCTTTTTAC.	ACCCAGCCAA	AACCCAAGCI	CTCCAAAGT	JGAAGTGGCTTG

	2210 2220
Hlcfa2	
Hlcfa8	
Hlcfal7	
H1cfa18	
Hlcch2	
Hlcch3	
Hlcch4	
Hlcch6	
Hlcch8	
Hlcch9	
Hlcch12	
Hlcch11	
Huch21	TCTCTTCTACACCAATCACTAGTG-
Huch22	TCTCTTCTACACCAATCACTAGTG-
Huch23	TCTCTTCTACACCAATCACTAGTG
Huch11	TCTCTTCTACACCAATCACTAGTG
HufaN4	TCTCTTCTACACC
HufaP1	TCTCTTCTACACC
HufaP4	TCTCTTCTACACC
HufaP8	TCTCTTCTACACC
HuchP9	TCTCTTCTACACC
HufaP10	TCTCTTCTACACC

Supplementary Fig. 4.1.3. Alignment of complex fragments from *M. fallax* (clone names in blue) and *M. chitwoodi* (clone names in green) amplified with primers specific for U1 sequence. Sequences are indicated in different colors: 1a monomer (green), 1d monomer (grey) and U2 sequence (yellow). Unlabeled part belongs to U1 sequence. Blue box represents overlapping region of 1a and 1d monomers. Box 1 is indicated in red and Box 2 in black square. Green boxes represent perfectly conserved fragment common for U1 and U2 sequences. Primer positions for U2 are indicated above sequences.



Supplementary Fig. 4.1.4. Alignment of 14 1aM sequences obtained cut to monomers.

	20	30	40	50	60	70	80 	90 -	100	110	120		140	150	160	170
the second se	CAAAAATTTTTT	Т-СТСАААА	CTAGTC A		ATTACATAGO	TCATTCCATT	CAGCTTAT	SAGCTCTTC	CANTGATACC	-AAATTCAGCAA	ATTTCCAACG	A TCC A A ATT	የማማጥጥልማርር ል	ልር ምምምር ልልምባ	'A TTCCCCTCAA	ссссааатт
TTTTCAAAATTT	CAAAAATTTTTT	T-CTCAAAA	ACTAGTCGA	TAGATTTTAA	ATTTCAAAGC	TCATTCGATT	AGCTTAT	GAGCTCTTTC	CGAATGATACC	AAATTCAGCAA	ATTTCCAACG	ATAGAAATT	TTTTTATCGA	ACTTTGAATT	ATTCCTTCAA	CCCCAAATTI
TTTTCAAAATTT	CAAAAATTTTTT	T CTCAAAA	ACTAGTCGA	TAGATTTTAA	ATTTCANAGC	TCATTCGATT	CAGCTTAT	GAGCTCTTTC	CG AATG ATACA	AAATTCAGCAA	ATTTCCAACG	TIGGAAATT	TTTTTATCGA	ACTTTGAATT	ATTCCTTCAA	CCCCAAATTI
TTT	CAAAAATTTTTT	T-CTCAAAA	CTAGTORA	TAGATTTTAA	ATTACATAGC	TCATTCGATT	CAGCTTAT	GAGCTCTTTC	CG AATG ATACC	AAATTCAGCAA	ATTTCCAACG	ATAGAAATT	TTTTTATCGA	ACTTTGAATT	ATTCCGTCAA	CCCCAAAT
TTT	CAAAAATTTTTT	T CTCAAAA	ACTAGTCGA	TAGATTTTTAA	ATTTCATAGC	TCATTCGATT	CAGCTTATC	GAGCTCTTTC	CG AATG ATACC	AAATTCAGCAA	ATTTCCAACG	ATAGAAATT	TTTTTATCGA	ACTTTGAATT	ATTCCTTCA	CCCCAAATTI
TTT	CAAAAATTTTTT	T-CTCAAAA	CTAGTONA	TAGATTTTAA	ATTACATAGC	TCATTCGATT	CAGCTTAT	GAGCTCTTTC	CG AATG ATACC	AAATTCAGCAA	ATTTCCAACG	ATGGAAATT	TTTTTATCGA	ACTTTGAATT	TATTCCGTCAA	CCCCAAATTI
TTTCAAATTT:	CAAAAATTTTTT	T-CTCAAAA	ACTAGTCGA	TAGATTTTAA	ATTTCANAGC	TCATTCGATT	AGCTTAT	GAGCTCTTTC	CGAATGATACC	AAATTCAGCAA	ATTTCCAAOG	AT <mark>A</mark> GAAATT'	TTTTTATCGA	ACTTTGAATT	ATTCCTTCAA	CCCCAAATT
TTTTCAAAATTT	CAAAAATTTTTT	T CTCAAAA	ACTAGTCGA	TAGATTTTTAA	ATTTCAAAGC	TCATTCGATT	CAGCTTAT	GAGCTCTTTC	CG AATG ATACA	AAATTCAGCAA	ATTTCCAACG	TTGGAAATT	TTTTTATCGA	ACTTTGAATT	ATTCCTTCAA	CCCCAAATT
TTT	CAAAAATTTTTT	T-CTCAAAA	ACTAGTCGA	TAGATTTTTAA	ATTTCATAGC	TCATTCGATT	CAGCTTATC	GAGCTCTTTC	CG AATG ATACC	AAATTCAGCAA	ATTTCCAACG	ATAGAAATT	TTTTTATCGA	ACTTTG AATT	ATTCCTTCA	CCCCAAATT
TT	CAAAAATTTTT	T-CTCAAAA	TCTAGTO	TAGATTTTAA	ATTACATAGC	TCATTCGATT	CAGCTTAT	GAGCTCTTTC	CG AATG ATACC	AAATTCAGCAA	ATTTCCAAOG	ATGG AAATT	TTTTTATCGA	ACTTTG AATT	ATTCCGTCAA	CCCCAAATT
TTTTCAAAATTT	CAAAAATTTTTT	T CTCAAAA	ACTAGTCGA	TAGATTTTTAA	ATTTCAAAGC	TCATTCGATT	AGCTTAT	GAGCTCTTTC	CG AATG ATACC	AAATTCAGCAA	ATTTCCAACG	ATAGAAATT	TTTTTATCGA	ACTTTGAATT	ATTCCTTCAA	CCCCAAATI
TTTTCAAAATTT	CAAAAATTTTT	T-CTCAAAA	ACTAGTCGA	TAGATTTTAA	ATTTCARAGC	TCATTCGATT	CAGCTTAT	GAGCTCTTTC	CG AATG ATACA	AAATTCAGCAA	ATTTCCAACG	TTGG AAAT T	TTTTTATCGA	ACTTTGAATT	ATTCCTTCAA	CCCCAAAT
TTT	CAAAAATTTTTT	T-CTCAAAA	ACTAGTCGA	TAGATTTTAA	ATTTCATAGC	TCATTCGATT	CAGCTTATC	GAGCTCTTTC	CG AATG ATACC	AAATTCAGCAA	ATTTCCAACG	ATAGAAATT	TTTTTATCGA	ACTTTGAATT	ATTCCTTCA	CCCCAAAT
TTT	CAAAAATTTTTT	T CTCAAAA	CTAGTONA	TAGATTTTAA	ATTACATAGC	TCATTCGATT	CAGCTTAT	GAGCTCTTTC	CG AATG ATACC	AAATTCAGCAA	ATTTCCAACG	ATGGAAATT	TTTTTATCGA	ACTTTGAATT	ATTCCGTCAA	CCCCAAAT
TTTTCAAAATTT	CAAAAATTTTTT	T CTCAAAA	ACTAGTCGA	TAGATTTTAA	ATTTCANAGC	TCATTCGATT	AGCTTAT	GAGCTCTTTC	CG AATG ATACC	AAATTCAGCAA	ATTTCCAAOG	ATAGAAATT	TTTTTATCGA	ACTTTGAATT	ATTCCTTCAA	CCCCAAAT
TTTTCAAAATTT	CAAAAATTTTTT	T-CTCAAAA	ACTAGTCGA	TAGATTTTAA	ATTTCANAGC	TCATTCGATT	CAGCTTAT	GAGCTCTTTC	CG AATG ATACA	AAATTCAGCAA	ATTTCCAAOG	TGG AAATT	TTTTTATCGA	ACTTTGAATT	ATTCCTTCAA	CCCCAAAT
արարտ հ	CAAAAATTTTTT	- CTCAAAA	ACTAGTCGA	TAGATTTTAA	ATTTCATAGC	TCATTCGATT	CAGCTTATC	GAGCTCTTTC	CG A ATG A TACC	AAATTCAGCAA	ATTTCCAAG	ATAGAATT	TTTTTATCGA	ACTTTGAATT	ATTCCTTCA	CCCCAAAI
th theb a	CAAAAATTTTT	T-CTCAAAA	CTAGTONA	TAGATTTTAA	ATTACATAGC	TCATTCGATT	CAGCTTAT	BAGCTCTTTC	GAATGATACC	AAATTCAGCAA	ATTTCCAAGG	ATGGAAATT	TTTTTATCGA	ACTTTGAATT	ATTCCCTCAA	CCCCAAA
TTTTCAAAATTT	CAAAATTTTTT	T-CTCAAAA	ACTAGTCGA	TAGATTTTTAA	ATTTCANAGC	TCATTCGATT	AGCTTAT	GAGCTCTTTC	GAATGATACC	AAATTCAGCAA	ATTTCCAAGG	ATAGAATT	TTTTTATCGA	ACTTTGAATT	ATTCCTTCAA	CCCCAAA
TTTTCAAATTTT	CAAAAATTTTTT	T-CTCAAAA	ACTAGTOGA	TAGATTTTAA	ATTTCANAGC	TCATTCGATT	CAGCTTAT	SAGCTCTTT	GAATGATACA	AAATTCAGCAA	ATTTCCAAOG	TGGAAATT	TTTTTATCGA	ACTTTGAATT	ATTCCTTCAA	CCCCAAAT
րար	CAAAAATTTTT	- CTCAAAA	ACTAGTCG A	TAGATTTTAA	ATTTCATAGC	TCATTCGATT	CAGCTTATC	GAGCTCTTTC	GAATGATACC	AAATTCAGCAA	ATTTCCAAG	ATAGAAATT	TTTTTATCGA	ACTTTGAATT	ATTCCTTCA	CCCCAAA
di di di di	CAAAAATTTTTT	T-CTCAAAA	CTAGTONA	TAGATTTTTAA	ATTACATAGC	TCATTCGATT	CAGCTTAT	SAG CTCTTTC	GAATGATACC	-AAATTCAGCAA	ATTTCCAAOG	ATGG A A ATT	TTTTTATCG A	ACTTTGAATT	ATTCCGTCAA	CCCCAAA
TTTTCAAAATTTT	CAAAAATTTTT	T-CTCAAAA	ACTAGTCGA	TAGATTTTTAA	TTTCAAAGC	TCATTCGATT	RAGCTTAT	SAG CTCTTTC	CG A ATG A TACC	-AAATTCAGCAR	ATTTCCAAGG	ATTAGAATT	TTTTTTATCG A	ACTITGAATI	ATTCCTTCAA	CCCCAAA
TTTTCAAAATTT	CAAAAATTTTT	Т СТСАААА	ACTAGTCGA	TAGATTTTAA	ATTTCANAGC	TCATTCGATT	CAGCTTAT	BAGCTCTTTC	CGAATGATACA	AAATTCAGCAA	ATTTCCAAOG	TGGAAATT	TTTTTMICON TTTTTATCG A	ACTTTG AATT	ATTCCTTCAA	CCCCAAA
TTTTCAAAATTT	CAAAAATTTTT	TECTCAAAA	ACTAGTOG A		ATTTCA AGC	TCATTCGATT	CAGCTTAT	SAG CTCTTTC	C A ATG A TA CC	-AAATTCAGCAZ	ATTTCCAAOG	TCC A A ATT	TTTTTTTCC A	ACTTTG AATT	ATTCCCCTCAA	CCCCAAA
т. т. т. Стата ст. т. т	CAAAAA	T-CTCAAAA	ACTAGTCGA	TAGATTTTAA	ATTTCATAGC	TCATTCGATT	CAGCTTATC	BAGCTCTTT	CGAATGATACC	- A A A TTCAGCAR	ATTTCCAAG	TGG A A AT T	TTTTTTATCG A	CTTTG AATT	ATTCCTTCAA	CCCCAAA'
	CAAAAAAATTTTT	т стсалал	ACTACTOR	TACATTTTAA	ATTTCATAGC	TEATTCOATT	CACCUTATC	CACCTCNTTC	CANTCATACC	AAATTCADEAF	ATTCCAACC	ATCC A AATT	TTTTTATCOA	ACTITICAATI	ATTCCCTCAN	CCCCAAAI
1111CAAA111.	CAAAAATTTTT	T-CACADAA	ACTACTO	TACATTTTAA	ATTTCATAGC	TRATTCOATT	CAGCTTATC	CACCTCATTC	COARGATACC	- A A A TTC A DE A Z	ATTTCCAACG	A TOG A A ATT	TTTTTATCOA	ACTITICAATI	ATTCCGTCAA	CCCCAAA
th theb i		T-CTCALLA	ACTACTCA	TAG AT T T T T AA7	ATTACATAGE	TCATTCGATT	CAGCTTATC	CACCECTER CACCET	CONTRACTACC	-AAATICACAA	ATTTCCAACG		TTTTTATCOA TTTTTTATCOA	ACTIGAATI	ATTCCOTCAA	CCCCAAA
in inch i	CAAAAATTTTT	т стсаааа	ACTACTO	TAC ATTTTTA A	ATTTCATACC	TEATTCCATT	CACCTURATIO	CACCTCATTC	CANTCATACC	- A A A TTC A DE A Z	ATTTCCAACC	A TCC A A ATT	TTTTT - ATCC A	ACTITIC ANT	ATTCCTTCAA	CCCCAAA
the state of the s	CAAAAATTTTT	TCACADAA	ACTACTC	TACATTTTAA	ATTTCATAGC	TRATICGATI	CACCUTATC	CACCTCATTC	CANTCATACC	AAATICACAA	ATTTCCAAC	ATCC A AATT	TITT ATCOM	ACTITICANT I	ATTCCTTCAA	CCCCAAA!
T T T .		T CACADAA	ACTACTC	TAGATTTTAA	ATTTCATAGC	TRATICGATI	CAGCITATC	CACCTCATTC	CANTENTACC	AAATICAGCAR	ATTTCCAACG		TITIIAICGA TTTTTATCGA	ACTIGANT	ATTCC TTCAA	CCC AAA
T TT		T CTCANAA	ACTACTC	TAGALLIIIIAA TACAUUUUUAA	ATTACATAGE	TEATTCOATT	CACCUTATO	CACCECTER	COALGAIACC	AAATICAGCAP	ATTICCAROS			ACTIICAALI ACTIICAALI	IATICCTICAA	CCCCAAA
111.		T CICAAAA	ACTAGICGA	TAGALLI LIAAA	ATTACATAGC	TCATICGATI	CAGCITATC	CACCECTIC	COARIGATACC	AAATTCAGCAF	ATTICCARG	A TOG AAAT I		ACTIGARTI	ATTCCGTCAA	CCCCAAA.
I I I .	CAAAAAIIIIII	T CACAAAA	ACTAGICGA	TAGALILITAA	ATTECATAGE	TCATICGATI	CAGCITATC	CACCTCATIC	CGAAIGAIACC	AAATTCAGCAP	ATTTCCAACG	ATGG AAATT	TITIAIC	ACTIIGAATI	ATTCCGTCAA	CCCCAAA
1-1-1		T CACAAAA	ACTAGIC	TAGALLIIIAAA	ATTICATAGC	T MAIICGAII	CAGCITAIC	BAGCICMIIC	CANCATACC	AAATICAGCAR	ATTICCAROS	ATOG AAATT	TITITATCOA	ACTIICAATI	ATTCCOTCAR	CCCCAAA.
1 1 1 . m mm r	CAAAAAAIIIIII	T CHCAAAA	ACTAGIC	TAGATTTTAAA	ATTICATAGE	TEATICGATT mcammccamm	CAGCITATC	BAGCICHIIC	CG A ANG A MA CC	AAATICAGCAA	ATTICCAAG		TITTIAICGA	ACTIIGAATI	ATTCCGTCAA	CCCCAAA.
I I I .	CAAAAATTTTT	T CICAAAA	ACTAGICGA	TAGATITIAAA	ATTICATAGC	TCATICGATI Dannecoann	CAGCITAI	BAGCICITIC	C A ATG A TACC	AAATIC	ATTICCAACG	A DCC A A AUTO	TITIIGICGA	ACTIIGAATI	ATTCCTTCAA	CCCCAAA.
1.1.1.		T CICAAAA	ACTANCOM	TAGALI LITAAA	ATTICATAGE	T ATTCGATT management	CAGCILAIC	G AG CICI II (CGAAIGAIACC	AAATICAGCAA	ATTICCAACG	A IGG AAAI I	TITIIGICGA	ACTIIGAATI	ATTCCGTCAR	CCCCAAA.
111.	CAAAAATTTTTT	T CTCAAAA	ACTANTCA	TAGATTTTAA	ATTICATAGC	T ATTCGATT	CAGCITAIC	GAGCICITIC	CG A ATG A TACC	AAATTCAGCAA	ATTICCAAG	AIGG AAAI I	TITITAIGG A	ACTIIGAATI	TATICCGICAA	CCCCAAA
TTT	CAAAAATTTTTT	T CTCAAAA	ACTAGTC	TAGATTTTAA	ATTTCATAGC	T ATTCGATT means and means	CAGCTTATC	L AG CTCTTTC	LG AATG ATACC	AAATTCAGCAA	ATTTCCAAG	ATGG AAAT T	TTTTTAT <mark>G</mark> G A	ACTITGAATI	ATTCCTTCAA	CCCCAAA
1 1 1	CAAAAAA	T CTCAAAA	ACTAGTCGA	TAGATITTAA	ATTICATAGC	TCATG GATT	CAGCATAT	SAGCICITIC	GAAIGAIACC	AAATICAGCAA	ATTTCCAAG	AIGMAAAII	TITITATCG A	ACTIIGAATI	ATTCCGTCAA	CCCCAAA
TTT	CAAAAATTTTT	TCACAAAA	ACTAGTC	TAGATTTTAA	ATTTCATAGC	TMATTCGATT	CAGCTTATC	GAGCTCMTTC	GAATGATACC	AAATTCATTAA	ATTTCCAACG	ATGG AAAT T	TTTTTATCG A	ACTITGAATI	TATTCCGTCAA	CCCCAAA
TIT	CAAAAAATTTTT	TECTCAAAA	ACTAGTCGA	TAGATTTTTAA	ATTTCATAGC	TCATG	CAGCATAT	5 AG CTCTTTC	LG AATG ATACC	AAATTCAGCAA	ATTTCCAACG	ATGAAATT	TTTTTATCGA	ACTITGAATI	TATTCCTTCAA	CCAAA
TTT	CAAGAAATTTTT	TCTCAAAA	ACTAGTCGA	TAGATTTTTAA	ATTTCATAGC	TCATTCGATT	CAGCTTATC	GAGCTCTTTC	CGAATGATACC	AAATTCAGCAA	ATTTCCAAG	TGGAAATT	TTTTTATCGA	ACTTTG AATT	ATTCCTTC -	CCCCAAA
TTT	CAAAA	TECTCAAAA	ACTAGTCGA	TAGATTTTTAA	ATTTCA-AGC	TCATTCGATT	CAGCTTATC	IS AG CTCTTTC	GAATGATACC	AAATTCAGCAA	ATTTCCAAG	ATGG AAATT	TTTTTATG A	ACTTIGATI	TATTCCTTCAA	CCCCAAA
TTT	CAAAA	TUTCAAAA	ACTAGTCGA	TAGATTTTAA	ATTTCATAGC	TCATTCGATT	CAGCTTATC	L AG CTCTTTC	CGAATGATAMC	AAATTCAGCAA	ATTTCCAACG	ATGG AAATT	TTTTTATG A	ACTTTGAATT	TATTCCGTCAA	CCCCAAA!
TTTTCAAAATTT	CAAAAATTTTTT	TECTCAAAA	ACTAGTCGA	TAGATTTTAA	ATTTCAMAGC	TCATTCGATT	CAGCTTAT	5 AG CTCTTTC	GAATGATACC	AAATTCAGCAA	ATTTCCAACG	TGG AAATT	TTTTTATCGA	ACTTTGAATT	ATTCCGTCAA	CCCCAAAI
TTTTCAAAATTT	CAAAAAATTTTT	T CTCAAAA	ACTAGTCGA	TAGATTTTAA	ATTTCATAGC	TCATTCGATT	CAGCTTATC	LAG CTCTTTC	LG AATG ATACC	AAATTCAGCAA	ATTTCCAAOG	TGG AAATT	TTTTTATCGA	GCTTTGAAT1	TATTCCTTCAA	CCCCAAAI
TTT	CAAAAAAATTTT	T-CTCAAAA	ACTAGTC	TAG ATTTTTAA	ATTTCATAGC	THATTCGATT	CAGCTTATC	LAG CTCATTC	LG AATG ATACC	AAATTCATTAA	ATTCCAACG	ATGG AAATT	TTTTTATCGA	ACTTTGAATT	ATTCCGTCAA	CCCCCAAAT
TTT	CAAAAATTTTTT	T-CACAAAA	ACTAGTCA	TAGATTTTAAA	ATTTCATAGC	TMATTCGATT	CAGCTTATC	IS AG CTCATTO	IG AATG ATACC	AAATTCATTAA	ATTTCCAACG	ATGG AAATT	TTTTTTCGA	ACTTTGAATT	CATTCCGTCAA	CCCCAAA

Supplementary Fig. 4.1.5. Alignment of 1aM and 1aH sequences. 1aH marked with black box.

	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180
Consensus	-TTTTCAAAATTTT	CAAAAATTTTT	TTTCTCAAAA	AACTAGTCGAT	AGATTTTTAA	ATTTACATA	GCTCATTCGATT	CAGCTTATCO	GAGCTCTTTC	GAATGATACC	CAAATTCAGCAA	ATTTCCAACGA	TGGAAATTTT	TTTAT-CG	AACTTTGA	ATATATTCCT	TCAACCCCAAF	ATTTTTAAA
Mlafa-1b				.T		A		T								G		
Mlafa-lc Mlafa-ld		• • • • • • • • • • • •	••==•••••	• • • • • • • • • • • •		A.	• • • • • • • • • • • • •	TT.				· · · · · · · · · · · · · · · · · · ·	.A			••=•••••		
Mlafa-le				.T				T					.A.			G		.CGA
Mlafa-2a													.A				T	
Mlafa-2b Mlafa-2c				.TT		A		T.		• • • • • • • • • • • •			Δ			· · - · · · · · · · · · · · · G		
Mlafa-2d						A.		T		A		T	· • • • • • • • • • • • • • • • • • • •			· · · · · · · · · · · · · · · · · · ·		
Mlafa-3a													.A				T	
Mlafa-3b				.TT		A		T	• • • • • • • • • • • •	• • • • • • • • • • •	• • • • • • • • • • • •	• • • • • • • • • • • •			• • • • • • • • •	· · - · · · · · · · G		
Mlafa-3d	-					- A		T		A		T						
Mlafa-4a													.A				T	
Mlafa-4b	······································			.T		A		T								G		
Mlafa-4C				• • • • • • • • • • • •		- A		тт	• • • • • • • • • • •	Α		· · · · · · · · · · · · · · · · · · ·	·A		*******	••=•••••		
Mlafa-6a													.A				T	
Mlafa-6b				.T		A		T								G		
Mlafa-6c Mlafa-6d				•••••		- A		TT. T		A		· · · · · · · · · · · · · · · · · · ·	.A		• • • • • • • • •			Δ -
Mlafa-7a													.A.			· · - · · · · · · · · ·	T	
Mlafa-7b	······································		=	.T		A		T								G		
Mlafa-7c Mlafa-7d		********		• • • • • • • • • • • •		A.		TT.	• • • • • • • • • • • •		• • • • • • • • • • • •		. A					
Mlach-13a						A.		T				T				G		
Mlach-13b	······································	A										T			.G			
Mlach-13c		AA		T			T		A	• • • • • • • • • • •	TT	C	• • • • • • • • • • •		• • • • • • • •	· · - · · · · · · · · · · · · · · · · ·		
Mlach-10a		T							A					-GC				
Mlach-10b				T			T		A									
Mlach-10c		********	A	T			T		A	*********					******	· · - · · · · · · G		
Mlach-9a		T				A-			· · · · · · · A · · ·				· A · · · · · · · · ·	-GC		G		
Mlach-9b						A			A					C		G		
Mlach-9c			A	T			T		A		•••••					G		
Mlach-9d Mlach-8a							T	т	A		т.		.A	G		-		
Mlach-8b				TT.			T							G		G		
Mlach-8c				TT	********		T				• • • • • • • • • • • •			G.	*******	G		
Mlach-8d Mlach-4a		Α		T			GT	АТ	• • • • • • • • • • • •	• • • • • • • • • • •			A	G.				
Mlach-4b			A	T			T											
Mlach-5a		A					GT	AT					A			–	A	
Mlach-6a																–		
Mlach-6b		T								T . •				GC		. – G		
Mlach-3a					• • • • • • • • • •	A.		T			• • • • • • • • • • • •	T		••••		G		
Mlach-3D Mlach-3c		A		т.			т.		А						.G	G		
Mlach-3d			A	. T			T		A		T T					G		
H1cfa2-1aH			• • - • • • • • • •		GG.	••••		CT.T	AC	AT	A	.A		-AT	GCA.	.A		CTTC
HICTA8-IAH H1cfa17-1aH					GG.			CT T	AC	АТ Д Т	– A –	Δ		-AT	G CA	.A		CTTC
H1cfa18-1aH		A			GG.	-T		CT.T	A	AT				AA	G.CA.	.A	A	CTTC
H1cch2-1aH		A		T G.	TT	T.AA.T.A.		TAAT	ATC	A <u>T</u>			<u>c</u>	AA	GCA.	.A	CA	CTTC
HICCh3-laH					GG. G. G.		· · · · · · · · · · · · · · · · · · ·	TAAT 1	А АТС	T	• • • • • • • • • • • •	• • • • • • • • • • • •	· · · · · · · · · · · ·	AA AA	GCA.	.A	CA	CTTC
H1cch6-1aH					GG.	-T		TAAT	ATC	AT				AA	T.CA.			CTTC
H1cch8-1aH		–			GG.	· · · · - <u>·</u> · · · ·		CT.T	A	ATTT			T	- AA	GCA.	.A	CA	CTTC
Hlcch9-1aH			•••••	• • • • • • • • • • • •	GG.	T	• • • • • • • • • • • • • •	TAAT /		AT	• • • • • • • • • • • •	• • • • • • • • • • • •	• • • • • • • • • • •		GCA.	.A		CTT(
Huch11-1aH		A			GTT	AA.T.A.			ATC	AT			с	AA		A		CTTC
Huch21-1aH					GG.	- T		TAAT	ATC	AT				- AA	T CA.			CTTC
Huch22-1aH					GG.	T		TAAT	ATC	AT			• • • • • • • • • • •	AA	TCA.			CTTC
161 = C \$10000		A	=		17					- · · · · · · · · · · · · · · · · · · ·	A			AA	17 LA			Contraction of the second s

Supplementary Fig. 4.1.6. Alignment of 1a, 1b, 1b', 1c, 1d, 2a and 2b monomers from *M. fallax* and *M. chitwoodi*. Monomers are extracted from monomeric and HOR arrays using KSA algorithm (Rosandić et al. 2003). All monomers are compared with first sequence and positions identical to the first sequence are shown with dot. Monomer group are indicated on the right side. Box 1 is shaded with yellow. Detail descriptions of satellite monomers are indicated below:

1cHch_n-1c monomers from chitwoodi HOR arrays (H_{1c}ch_n, H_uch_n) 1cHfa_n -1c monomers from fallax HOR arrays (H_{1c}fa_n, H_ufa_n) 1cMch_n-1c monomers from chitwoodi monomeric arrays (M_{1c}ch_n) 1cMfa_n -1c monomers from fallax monomeric arrays (M_{1c}fa_n) 1dHch_n-1d monomers from chitwoodi HOR arrays (H_{1c}ch_n, H_uch_n) 1dHfa_n -1d monomers from fallax HOR arrays (H_{1c}fa_n, H_ufa_n) 1dMch_n-1d monomers from chitwoodi monomeric arrays (M_{1c}ch_n) $1dMfa_n$ -1d monomers from fallax monomeric arrays ($M_{1c}fa_n$) 1aHch_n-1a monomers from chitwoodi HOR arrays (H_{1c}ch_n, H_uch_n) 1aHfa_n -1a monomers from fallax HOR arrays (H₁, fa_n, H₁, fa_n) 1aMch_n-1a monomers from chitwoodi monomeric arrays (M_{1a} ch_n) 1aMfa_n-1a monomers from fallax monomeric arrays (M_{1a} fa_n) 1bHch_n-1b monomers from chitwoodi HOR arrays (H_{1c}ch_n, H_uch_n) 1bHfa_n -1b monomers from fallax HOR arrays (H_{1c}fa_n, H_ufa_n) 1b'Hch_n-1b monomers from chitwoodi HOR arrays (H_{1c}ch_n, H_uch_n) $1b'Hfa_n - 1b$ monomers from fallax HOR arrays ($H_{1c}fa_n$, $H_{u}fa_n$) 2aHch_n-2a monomers from chitwoodi HOR arrays (H_{1c}ch_n, H_uch_n) 2aHfa_n -2a monomers from fallax HOR arrays (H_{1c}fa_n, H_ufa_n) $2aMch_n$ -2a monomers from chitwoodi monomeric arrays ($M_{2a}ch_n$) $2aMfa_n$ -2a monomers from fallax monomeric arrays ($M_{2a}fa_n$) 2bMch_n-2b monomers from chitwoodi monomeric arrays (M_{2b} ch_n)

	10 20 30 40 50 60 70 80	90 100 110 120 130 140 150 160 170 180 190 200
ldHch2	CAGTGTTCATGAACCTGTTT-TCTCAAAAACTAGTCATACGATTTTTGAT-TTTA-TAGCTCATTCGATACAGCTCTTTA	AGCTCTTTCGARTGATGATC-ANATTCAGT-ATACTTTCTCCAGAGGAAAAAAATTTCTTCAATTAAAA-AATTTTTCCCCCAAAAAAAA
1dHch3		······································
1dHch4 1dHch6	ACACA	
1dHch8		
1dHch9		······································
1dHch12 1dHch21	A	
1dHch22	CA	
1dHch23	A	······································
1dHch11 1dHfaN4	A	
1dHfaP1	A	
1dHfaP4	CA	······································
1dHfaP8 1dHchP9	AT	1dHI
1dHfaP10		
ldHch13a	AACAA.	······································
ldMch13b	A	
1dMfa16a	A	
1dMfa16b	A	······································
ldMfalla ldMfallb	ACAA	
1dMfallc		
1dMfa2a	ACAA.	
1dMfa2b		
1dMch3a		
ldMch3b	AACAA.	······································
1dMch3c	A	
1cHch3	TACGCG.GTTGTCTGA.T.GCC.ATGT.G.	TCAG., GATG.CTCCACACTTACATTTTTAAAAC.CG-TCCACC
1cHch4	TACGCG.GTTGTCTGA.T.GCC.ATGTGTC.	ТС
lcHch6	TACGCG.GTTGTCTGA.T.GCC.ATGCT.CC.	$\begin{array}{cccc} \mathbf{G}_{\mathbf{C}} & \mathbf{G}_{\mathbf{C}} \mathbf{T} \mathbf{A}^{-} \mathbf{G}_{\mathbf{C}} \mathbf{G}_{\mathbf{C}} \mathbf{C} \mathbf{C} \mathbf{C} \mathbf{C} \mathbf{C} \mathbf{C} C$
1cHch9	TACGCG.GTTGTCTGA.T.GCC.ATGTCC.	TCAAAC.CCCCCCCC.
1cHch12	TACGCG.GTTGTCTGA.T.GCC.ATGTGTC.	ТС
1cHch21	TACGCG.GTTGTCTGA.T.GCC.ATGT.CC.	TCG.TA-TG.CTCCAC.ACTTACATTTTT.AAAA.C.CG-T.CCA.CC.
1cHch23	TACGCG.GTTGTCTGA.T.GCC.ATGTCC.	TCAAAC.CCCCCCCC.
1cHch11	TACGCG.GTTGTCTGA.T.GCC.ATGTGTC.	ТС
1cHfaN4	TACGCG.GTTGTCTGA.T.GCC.ATGT.GT.CC.	TCG.TA-TG.CTCCAC.AC.TACATTTTTAAAA.C.C.CG-T.CCACC.
1cHfaP4	TACGCG.GTTGTCTGA.T.GCC.ATGTCC.	Тт
1cHfaP8	TACGCTG.GTTGTCTGA.T.GCC.ATGTGTCC.	TCG.TA-TG.CTCCAC.AC.TACATTTTTAAAAC.CG-TCCACC
1cHchP9	TACGCG.GTTGTCTGA.T.GCC.ATGT.GT.CC.	TCG.TA-TG.CTCCAC.AC.TACATTTTTAAAA.C.CG-T.CCA.CC
1cMch13a	TACGCG.GTTGTCTGA.T.GCC.ATGT.GCC.	TCAAAC.CCCCCCCC.
1cMch13b	TACGCG.GTTGTCTGA.T.GCC.ATGCT.CC.	ТСТG. ^Т А-ТБ.СТССАС.АС.ТАСАТТТТТААААС.СG-ТССАССС.
lcMchl3c lcMfal6a	TACGCG.GTTGTCTGA.T.GCC.ATGTCC.	$ \begin{array}{cccc} \mathbf{G}_{\mathbf{C}} \mathbf{T} \mathbf{A} - \mathbf{G}_{\mathbf{C}} \mathbf{C} \mathbf{C} \mathbf{A} \mathbf{C} \cdot \mathbf{A} \mathbf{C} \cdot \mathbf{A} \mathbf{C} \mathbf{C} \mathbf{A} \mathbf{C} \mathbf{C} \mathbf{A} \mathbf{C} \mathbf{C} \mathbf{C} \mathbf{C} \mathbf{C} \mathbf{C} \mathbf{C} C$
1cMfa16b	TACGCG.GTTGTCTGA.T.GCC.ATGT.G.	TCTG.TA-TG.CTCCAC.IAC.ICTTTTTAAAAC.CG-TCCACC
1cMfalla	TACGCG.GTTGTCTGA.T.GCC.ATGCTCC.	TCG.TA-TG.CTCAAC.AC.TACATTTTTAAAA.C.C.CG-TCCACC.
1cMfallb	TACGCG.GTTGTCTGA.T.GCC.ATGTCC.	TCG.TA-TG.CTCCAC.AC.TACATTTTTAAAA.C.CG-T.CCA.CC
1cMfa2a	TACGCT.CG.GTTGTCTGA.T.GCC.ATGCT.CC.	TCG.TA-TG.CTCCAC.AC.TACATTTTTAAAA.C.CG-TCCACC.
1cMfa2b	TACGCTG.GTTGTCTGA.T.GCC.ATGTCC.	TC
1cMraze 1cMch3a	TACGCG.GTTGTCTGA.T.GCC.ATGCTCC.	G. A. TG. C. A. C. A. C. A. C. A. TACA, TITTT. AAAA. C. C. G-T. CCA. C
1cMch3b	TACGCTGG.GTTGTCTGA.T.GCC.ATGTGTC.	TCG.TA-TG.CTCCACAC.TACATTTTTAAAAC.CG-TCCACC
1cMch3c	TACGCTGG.GTTGTCTGA.T.GCC.ATGTGTCC.	
laHfa8	T	CA
laHfa17	TAATT.T	CA
laHch21	TAATT.T	TCA
laHch23	T AA AT . T	$\begin{array}{c} 1 \\ \hline \\$
laHch11a	TAATT.T	TCA
laHfaN4	TAATT.T	TCA
laHfaP4	T AA TT . T	
laHfaP8	TAAAA.T	
laHchP9	TAAAA.T	
laHrapiu	TAATT.T	CA
laHch3	TAATT.T	
laHch8	TAATT.T	
laHch21a	TAAAT.T	ТС
laHch22a_	TAATT.T	TCA
laHch4_	TAATT.T	TC
laHch12	TAATT.T	10
laHch9	TAATT.T	TCA

Box 1

laHch11	TAAAT.T	C		
laHch2	TAAAT.TTT-GGATTTAAATAATTAAC. <mark>T</mark> C	C		
laMfa6d	CAA		.A	
laMfald	CAA.A.TAATT.T		.A	
laMfa2d	CAA.A.TAATT.T		.A	_
laMfa3d	CAA.A.TAATT.T		.A	1
laMfa7d	CAA.A.TAATT.TT	• • • • • • • • • • • • • • • • • • • •	.A	
laMfa2d	-CAA.A.T.AA.T.T.T.T.T.T.T.T.T.T.G.A.GAT.AACAA.T.T.T.TA.G.T.T.T.G.T.T.G.T.T.G.T.T.G.T.T.G.T.T.T.T.G.T.T.T.G.T.T.T.G.T.T.T.T.G.T.T.T.T.G.T.T.T.T.G.T.T.T.T.G.T.T.T.T.G.T.T.T.T.G.T.T.T.T.G.T.T.T.T.G.T.T.T.T.T.G.T.T.T.T.T.G.T.T.T.T.T.G.T.T.T.T.T.G.T.T.T.T.T.T.G.T.T.T.T.T.G.T.T.T.T.T.T.T.G.T	• • • • • • • • • • • • • • • • • • • •	$A = \dots = (C - AA - TC, AC, TTGG, TTT, T = -AT - CGA, C = G, T = T, CC, CA - A, CC, TT, A$	
laMfa2c	-CAA.A.TAA.TT.T C.A.CAT. AA CAA. TT. TTAA CAA.A.T TT. TT TA. CAA.A.T AA. TT. T C.A.CAT. AA CAA.A.T TT. TT. CAA.A.T TT. CAA.A.T TT. CAA.A.T TT. TT. TT. TT. TT. TT. TT.	• • • • • • • • • • • • • • • • • • • •	$C = (C = \lambda + C) + C + C + C + C + C + C + C + C + $	
laMfafc	$-\alpha A_{2} A_{3} T_{2} A_{3} T_{3} A_{3} T_{3} T_{3} - \alpha A_{3} A_{$	• • • • • • • • • • • • • • • • • • • •	$a = a = \lambda + a = a = \lambda + a = a = a = a = a = -\lambda = -\lambda = -\lambda = -\lambda =$	
laMfa3c	-caa.a.t	••••••	C = C = A = A = C = A = A = C = A = C = A = C = A = C = A = C = A = C = C	
laMfa7c	CALATT - ALTT G-A GAT AL CAL TT TA G	••••••	C_{-} C_{-} A_{-} T_{-} A_{-} C_{-} A_{-} A_{-	
laMfalc			C	
laMfa6a	A.A.TAATT.TTTCA		.CCA.ATCAC.AT.GTTTTAT-CGA.CGT-TCCCATCCTTA	
laMfa7a	A.A.TAATT.T		.CCA.ATCAC.AT.GTTTTAT-CGA.CGT-TCCCATCCTTA	
laMfa2a	A.A.TAATT.T		.CCA.ATCAC.AT.GTTTTAT-CGA.CGT-TCCCATCCTTA	
1aMfa3a	A.A.TAATT.T		.CCA.ATCAC.AT.GTTTTAT-CGA.CGT-TCCCATCCTTA	
laMfa4a	A.A.TAATT.T		.CCA.ATCAC.AT.GTTTTAT-CGA.CGT-TCCCATCCTTA	
laMch13b	A.A.TAAAT.T		.CCA.ATCAC.TTGGTTTTAT-CGAGCGT-TCCCAACCTTA	
laMch3b	CAA.A.TAAAT.T		.CCA.ATCAC.TTGGTTTTAT-CGAGCGT-TCCCAACCTTA	
laMch5b	A.A.TAAT.T	• • • • • • • • • • • • • • • • • • • •	.CCA.ATCAC.TTGGTTTTAT-CGA.CGT-TCCCCCTTTA	
laMch4a	A.A.TAAAT.TT	• • • • • • • • • • • • • • • • • • • •	.C	
lamensa	A.A.TAA.AT.TT	• • • • • • • • • • • • • • • • • • • •		
laMfa6b	A, A-T, AA, II, II, II,, II, II, II, II, II, I	• • • • • • • • • • • • • • • • • • • •	$C = (C = \lambda + C) = C = \lambda + C = C = \lambda + C = C = C = C = \lambda + C = C = C = C = \lambda + C = C = C = C = C = C = C = C = C = C$	1aM
laMfa7b		••••••	C_{-} C_{-} A_{-} T_{-} A_{-} C_{-} A_{-} C_{-} C_{-} C_{-} C_{-} A_{-} A_{-	Tanti
laMfa1b	A. A. T		C	
laMfa2b			.C	
laMfa4b	A.A.TAATT.T		.CCA.ATCAC.ATGGTTTTAT-CGA.CGT-TCCG.CAACCTTA	1
laMfale	A.A.TAATT.T		.CCA.ATCAC.AT.GTTTTAT-CGA.CGT-TCCG.CA-ACCTCGA	
laMch8b	A.A.TAATT.T		.CCA.ATCAC.ATGGTTTTGT-CGA.CGT-TCCG.CAACCTTA	
laMch8c	A.A.TAATT.T.T		.CCA.ATCAC.ATGGTTTTAT-GGA.CGT-TCCG.CAACCTTA	
laMch8d	A.A.TAATT.T		.CCA.ATCAC.ATGGTTTTAT-GGA.CGT-TCCCAACCTTA	
laMch13d	A.A.TAATT.TA	A	.C	
laMch4b	A.A.TAATT.TA	A	.C	
1aMch3d		· · · · A. · · · · · · · · · · · ·	.CTA.ATCAC.ATGGTTTTAT-CGA.CGT-TCCG.CAACCTTA	
laMch13c		· · · · A. · · · · · · · · · · · · · · ·	.c	
laMch10h	AA.TAA.AA.T $$ $T-A.GAT. AA CA.T.TTA.CG.$	A	$C = T = \lambda \lambda = C = \lambda \Delta = C = \lambda \Delta = C = T = T =\lambda T = C = \lambda C = C = C = C = \lambda A = C = T = \lambda A = C = T = A = C = A = C = C = C = C = C = C = C$	
laMch10c	A A T AA TT T - A T A A T T T - A T A GAT AA - CA T T T A CG	Δ	C_{-} C_{-} A_{-} A_{-} A_{-	
laMch9c	A.A.T	A	C	
laMch9d	A.A.TAATT.TA	A	.CCA.ATCAC.AT.GTTTTAT-CGA.CGT-TCCG.CA-ACCTTA	
laMch10d	A.A.TAATT.TA	A	.CCA.ATCAC.AT.GTTTAT-CGA.CGT-TCCCAACTTTA	
laMch10a	A.A.TAA.TTT.T		.CCA.ATCAC.ATGGTTTTAT-GCA.CGT-TCCG.CAACCTTA	
laMch9a	A.A.TAA.TTT.T		.CCA.ATCAC.ATGGTTTTAT-GCA.CGT-TCCG.CAACCTTA	
laMch6b	A.A.TAA.TTT.TT		TCCA.ATCAC.ATGGTTTTAT-GCA.CGT-TCCG.CAACCTTA	
laMch6a	A.A.TAA.TTT.TT		.CCA.ATCAC.ATGGTTTTAT-GCA.CGT-TCCCAACCTTA	
laMch9b	A.A.TAATT.T	A	.CCA.ATCAC.ATGGTTTTAT-CCA.CGT-TCCG.CAACCTTA	
1aMch8a	A.A.TAATT.T	• • • • • • • • • • • • • • • • • • • •	.ccT.CA.ATCAC.TTGGTTTGT-CGA.CGT-TCCCAACCTTA	
laMch3a	-CAA.A.T.AA.T.T.T.T.T.T.T.T.T.G.A.GAT.AACAA.T.T.TA.G.T.T.TA.G.T.T.TA.G.T.T.T.T.G.T.T.T.G.T.T.T.T.G.T.T.T.T.G.T.T.T.T.G.T.T.T.T.G.T.T.T.T.T.G.T.T.T.T.T.G.T.T.T.T.T.G.T.T.T.T.T.G.T	• • • • • • • • • • • • • • • • • • • •	$C = \dots = C = A A = .TC = AC .TTG = .TTT = T = -AT = CGA C = .G = .T = .CCG .CA = .A .CC = .TT = .A .CC = .C$	
1b/Wah2		- 7 7		4
1b'Hch8		- A A	λ_{-} T λ_{-} C $-$ C - C	
1b'Hch4	CAATCA.A.CGCTC.T.TTGGG.C.ACA	A.A	.AT.ACG.AATG.TTCC.AGGTTTTAT-CGA.GTTCCCACC-	
1b'Hch12	CAATCA.A.CGCTC.T.TTGGG.C.ACA	A.A	.AT.ACG.AATG.TTCC.AGGTTTTAT-CGA.GTTCCCACCAC	
1b'Hch11	AAATCA.A.CGCTC.T.TTGGG.C.ACA	A.A	.AT.ACG.AATG.TTCC.AGGTTTTAT-CGA.GTTCCCACCAC	
1b'Hch3	CAATCA.A.CGCTC.T.TTGGG.C.ACA	A.A	.AT.ACG.AATG.TTCC.AGGTTCTAT-CGA.GTTCCCACCAC	
1b'Hch22	AAATCA.A.CG.GCTC.T.TTGGG.C.ACA	A.A	.AT.ACG.AATG.TTCC.AGGTTTAT-CGA.GTT.N.CCCACCAC	
1b'Hch21	CA	A.A	.AT.ACG.AATG.TTCC.AGGTTTTAT-CGA.GTTTCCCACCAC	
1b'Hch6	CA	A.A	.AT.ACG.AATG.TTCC.AGGTTTTAT-CGA.GTTCCCACCAC	46411
1b'Hch5	CA	····A.A	.AT.ACG.AATG.TTCC.AGGTTTTAT-CGA.GTTCTCACCAC	топ
ID'HEA2		· · · · - · A · A · · · · · ·	.AT.ACG.AATG.TTCC.AGGGTTTTAT-CGA.GTTCCCCCAC	
1D'HCN9	CA. ATCA.A.CGC. TC.TTT.G.TGG.C.ACA.	····-·A.A	.AT.ACG.AATGATTCAGGTTTTAT-CGA.GTTCCCCCAC	
1b/WfaN4b		- A A	$A \rightarrow T = C = A \rightarrow T = A = A = A = A = A = A = A = A = A =$	
1b'HfaP1b		- A A	\mathbf{A}_{-} T \mathbf{A}_{-} \mathbf{C}_{-} \mathbf{G}_{-} \mathbf{A}_{-} \mathbf{G}_{-} \mathbf{G}_{-	
1b'Hfa4b		A.A	AT.ACG.AATGATTCAGGTTTTAT-CGA.GTTCCCCCAC	
1b'Hfa8b	AAA.A.TT.AAATCA.A.C.TGCT.TGGG.C.ACA	A.A	.AT.ACG.AATG.TTCC.AGG.GTTTTAT-CGA.GTTCCCCCAC	
1b'HchP9b	AAA.A.TT.AAATCA.A.C.TGCT.TGGG.C.ACA	A.A	.AT.ACG.AATG.TTCC.AGGGTTTTAT-CGA.GTTCCCCCAC	1
1b'HfaP10b		A.A	.AT.ACG.AATGATTCAGGTTTTAT-CGA.GTTCCCCCAC	
1b'Hfa8a	AA.A.TT.AAATCA.A.C.TGCTTGGG.C.ACA	A.A	.AT.ACG.AATGATTCAGGTTTAT-CGA.GTTCCCCCAC	
1b'Hfa17b	AA.A.TT.AAATCA.A.C.TGCTTGGG.C.ACA	A.A	.AT.ACG.AATGATTCAGGTTTTAT-CGA.GTTCCCCCAC	
1b'Hfa2b	AA.A.TT.AAATCA.A.C.TGCTCGGGCACA	A.A	.AT.ACG.AATGATTCAGGTTTTAT-CGA.GTTCCCCCAC	1
1bHfaN4	TCAA. ATCA.A.CGCTC.T.TTGGG.C.ACA	A.AC	.AACG.AATGATTCAGCCTTTTTTTCAA.CGTCCCTCCT	
1bHfaP1		A.AC	.AACG.AATGATTCAGC.CTTTTTTTCAA.CGTCCCTCCT	1
1bufap9		····A.AC	.AACG.AATGATTCAGC.CTTTTTTTCAA.CGTCCCTCCT	1bH
1bWchp9		- A AC	AACG.AAIGATTC-AGC.CTTTTTTTCAA.CGTCC.CT.CCT	
1bHfap10		- A A	A	
1bHfa2a		A.A	AACG.AATGATTCAGCCTTTTTTTCAA.CGTCCCTCCT	
1bHfa8	TCAAATCA.A.CGCTC.T.TTGGG.C.ACA	A.AC	AACG.AATGATTC-AGC.CTTTTTTTCAA.CGTCCCTCCT	1
1bHfa17	TCAA.ATCA.A.CGC.TC.T.TTG.GG.C.ACA	A.AC	.AACG.AATGATTCAGCCTTTTTTTCAA.CGTCCCTCCT	J
2aHfa2_	CCAGCTA.ATTCTC.TC.AAA.AATACATCCAGCTA.ATTAAT.AA.T	2	TATGCATA.AGA.A.A.T.TGTC.ATTGTTAGC.GC-GGTTGAACC.CCCTTTTGGCG.C.GAAAT	TTTCGGAACAAG
2aHch8	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.T	C.A	TATGCATA.AGA.A.A.T.TGTC.ATTGTTAGC.GC-GGTTGAACC.CCCTTTTGGCG.C.GAAAI	TTTCGGAACAAG
2aHfa17b_	CCAGCTA.ATTCTC.TC.ATA.AATACATCCAGCTA.ATTAAT.AA.T	c	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGGC.GAAA	TTTCGGAACAAG
2aHch2	CAGCTA.ATTCAAT.AA <mark>TC</mark>	2	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGGCG.C.GAAAT	TTTCGGAACAAG

2aHch3	CCAGCTA.ATTCTC.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATTGTTAGC.GC-GGTTGAACC.CCCTTTTGGCG.AAATTTTCGGAACAAG	
2aHch4	CCAGCTA.ATTCTC.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATTGTTAGC.GC-GGTTGAACC.CCCTTTTGGCG.AAATTTTCGGAACAAG	
2aHch6	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGGC.G.C.GAAATTTTCGGAACAAG	221/14
2aHch12	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGGC.G.C.GAAATTTTCGGAACAAG	Zaivin
2aHch9	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCGTTTTGGC.G.C.GAAATTTTCGGAACAAG	
2aMfa7	C-AGCTA.AC.TA.TGTT.TC.TCAAA.AATCCATC-AGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGGCG.C.GAAATTTTCGGAACAG-	
2aMch6a	C-AGCTA.AC.TA.TGTT.TC.TCAAA.AATCCATC-AGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGGCG.C.GAAATTTTCGGAACAG-	
2aMch10b	CAGCTAAC.TA.TGTT.TC.TCAAA.AATCCATC-AGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAA.CACCCTTTTAGGCG.C.GAAATTTTCGGAACAAG	
2aMch8c	CCAGCTA.ATTGTT.TC.TCAAA.AATCCATCCAGCTA.ATTAAT.AA.	т	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAA.CACCCTTTTAGGCG.C.GAAATTTTCGGAACAAG	
2aMch8d	CCAGCTA.TA.TGTT.TC.TCAAA.AATCCATCCAGCTA.TAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGGCGGAAATTTTCGGAACAAG	
2aMfa3b	CCAGCTA.TC.TG.TT.TC.TCAAA.AATCCATCCAGCTATAAT.AA.	тс	TATGCATA.A.A.A.T.TGTC.ATT.TTTAGC.GC-GGTTGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	-
2aMfa4b	CCAGCTA.ATTGTT.TC.TCAAA.AATCCATCCAGCTA.ATTAAT.AA.	TC	TATGCATA.AGA.A.A.TATGTC.ATTGTTAGC.GC-AGGCGAACC.CCCTTTTAGCG.C.GAAATCTTCGGAACAAGG	
2aMfa5b	CCAGCTA.ATTGTT.TC.TCAAA.AATCCATCCAGCTA.ATTAAT.AA.	TC	TATGCATA.AGA.A.A.TATGTC.ATTGTTAGC.GC-AGGCGAACC.CCCTTTTAGCG.C.GAAATCTTCGGAACAAGG	
2aMch10a	C-AGCTA.ATTGTT.TC.TCAAA.AATCCATC-AGCTA.ATTAAT.AA.	т	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-AGGCGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aMfa4a	C-AGCTATTCTA.TGTT.TC.TCAAA.AATCCATC-AGCTATTAAT.AA.	тс	TATGCATA.AGA.A.A.TATGTC.ATTGTTAGC.GC-AGGCGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aMfa5a	C-AGCTATTCTA.TGTT.TC.TCAAA.AATCCATC-AGCTATTAAT.AA.	тс	TATGCATA.AGA.A.A.TATGTC.ATTGTTAGC.GC-AGGCGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aMch6b	CCAGCTA.C.TA.CGTT.TC.TCAAA.AATCCATCCAGCTATAAT.AA.	тс	TATGCATA.AGA.A.A.TATGTC.ATTGTTAGC.GC-AGGCGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aMch7	CCAGCTA.C.TA.CGTT.TC.TCAAA.AATCCATCCAGCTATAAT.AA.	тс	TATGCATA.AGA.A.A.TATGTC.ATTGTTAGC.GC-AGGCGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aMch8a	CCAGCTA	тс	TATGCATA.AGA.A.A.T.TGTC.ATTGTTAGC.GC-AGGCGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aMfa3c	CCAGCTA.TC.TG.TT.TC.TCAAA.AATCCATCCAGCTATAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GA-AGGCGAACC.CCCTTTTGCGGAAATTTTCGGAACAAGG	
2aMch8b	CCAGCTA.ATTAAT.AA.	.c	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-AGGCGAACC.CCCTTTTAGCG.C.GAAATTTTCGGAACAAGG	221/14
2aMfa3a	CTAGCTATTCTA.TGTT.TC.TCAAA.AATCGATCTAGCTATTAAT.AA.	тс	TATGCATT.A.A.A.A.T.TGTC.ATTTTTAGC.GC-GGTTGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	Zaivin
2aHfa8	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A-A.T.TGTC.ATTGTTAGC.GC-GGTTGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aHfaN4	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aHfaP1	CCAGCTA.AT.TGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAN.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aHfaP4	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aHfaP8	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aHchP9	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aHfaP10	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aHch21	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aHch22	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aHch23	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGCG.C.GAAATTTTCGGAACAAGG	
2aHch11	CCAGCTA.ATTGTT.TC.TCAAA.AATACATCCAGCTA.ATTAAT.AA.	тс	TATGCATA.AGA.A.A.T.TGTC.ATT.GTTAGC.GC-GGTTGAACC.CCCTTTTGG.CG.C.GAAATTTTCGGAACAAGG	
2bMch1	CTCT.AT.AC.CTCATGT.TT.TTCAAA.GAGAATCTCT.AT.ATATAAT.CA.		TATGCATAAAGA.AAT.TTTTTAACTTTTAGATCT-TTTTGAACCATTTTAATCTG.CC.ACAATTTCATAAGTA	
2bMch3	CTCT.AT.AC.CTCATGT.TT.TTCAAA.GAGAATCTCT.AT.ATTT.CA.		TATGCATAAAGA.AAT.TTTTTAACTTTTAGATCT-TTTTGAACCATTTTATCTG.CC.ACAATTTCATAAGTA	
2bMch5	CTCT.AT.AC.CTCATGTT.TTCAAA.GAGAATCTCT.ATATTT.CA.		TATGCATAAAGA.AAT.TTTTTAAGCTTTTAGATCTTTTGAACCATTTTATCTG.CACAATTTCATAAGTA	2bM
2bMch9	CAT.AC.CTCATGT.TT.TT.AAA.GAGA.TCTCT.AATTAAT.CA.		TATGCATAAAGA.AAT.TTTTTAACTTTTAGATCT-TTTTGAATCCATTTTTTAATCTG.CC.ACAATTTCATAAGTA	
2bMch2	CTCT.AAC.CTCATGTT.TTCAAA.GAGAATCTCT.AATTAAT.CA.		TATGCATAAAGA.AAA.TTTTTAACTTTTAGATCT-TTTTGAACCTATTTTATCTG.CC.ACAATTTCATAAGTA	
2bMch4	CAT.AC.CTCATGTT.TTCAAA.GAGAATCTCT.ATATTT.CA.		TATGCATAAAGA.AAT.TTTTTAACTTTTAGATCT-TTTTGAATCCATTTTATCTG.CC.ACAATTTCATAAGTA	
2bMch7	CAT.AC.CTCATGTT.TTCAAA.GAGA.TCTCT.ATATTT.CA.	<mark></mark>	TATGCATAAAGA.AAT.TTTTTAAGCTTTTAGATCT-TTTTGAACCATTTTATCTG.CC.ACAATTTCATAAGTA	

Supplementary Fig 4.1.7. Alignment of Box 1-containing sequences from unassembled reads of *M. incogita* sequenced genome. Sequences are compared with first sequence and positions identical to the first sequence are shown with dot. Box 1 is shaded with yellow.

	10 20	30	40 50	60 70	0 80	90	110	120	130	140 15	0 16	0 170	180	190 200
DN033B125VF10FM1			
RNOAAB3YE08AHM1													CCA	
RN0AAB140YN05FM1														
RN0AAB414YN09FM1														
RNUAAB5451MU4AHMI RNUAAA130VM16FM1														
RNOAAA519YK05RM1														
RN0AAB125YE10FM1														
RN0AAB3YE08AHM1														
RNOAAB140YN05FM1														
RN0AAB4141N09FM1 RN0AAB545YM04AHM1														
RN0AAA130YM16FM1														
RN0AAA519YK05RM1														
RNUAAB176YD12FM1														
RNOAAA179YC21RM1														
RN0AAA756YE07FM1														
RNOAAA591YF08RM1														
RNUAAA538YB16RM1														
RNOAAA669YI24RM1														
RN0AAA87YA19FM1														
RN0AAB380YP14FM1														
RNOAAB423YM10FM1														
RNOAAA64YH05FM1														
RN0AAB176YD12FM1													T.CACTTC	G-GTTTT.TT
RNOAAA286YA16FM1														
RNUAAA179YC21RM1													TTTGGTAAT	T-CTTCT
RNOAAA591YF08RM1														
RN0AAA538YB16RM1														
RN0AAB458YP20AHM1													TCT. CGGTAAT	A-GTTT.TAATTCG
RNUAAA669YI24RM1													TC.TTGGTAAT	A-GTTTAATTCG
RNOAAB380YP14FM1													AAATTGGTAAT	A-GTTTAATTCG
RN0AAB423YM10FM1													AAATTGGTAAT	A-GTTTAATTCG
RN0AAB147YJ10FM1													TTTGGTAAT	A-CTTTAA
RNUAAA64YHU5FM1													AATGGTAAT	A-GTTTAC.
RN0AAB3111B19AHM1 RN0AAB44YH23AHM1														
RN0AAA717YI15RM1													G-TTTGGTAAT	T-CCA
RN0AAB125YA16FM1													ACGGTAAT	NAGTTTAATTCG
RNUAAB437YE21AHM1													ACGGTAAT	A-GTTTAATTCG
RN0AAA131YF02RM1													ATGGTAAT	A-GTTTAATTCG
RN0AAA130YE05RM1													ATGGTAAT	A-GTTTAATTCG
RN0AAA579YK24RM1														
RNUAABIUUYPUSAHMI RNUAABISUYLOSEMI													AAT	A-GTTTAATTCG
RN0AAA175YL12RM1													A-TGGGGTAAT	A-GTTTAATTCG
RN0AAB484YE18FM1													TCGGTAAT	A-GTTTAATTCG
RNOAAA316YE18RM1													TTGGTAAT	A-GTTTAATTCG
RNOAAA691YK01RM1													GGTAAT	A-GTTTCTGA
RN0AAB526YI05AHM1													GGTAAT	A-GTTTCTGA
RN0AAB490YN21AHM1													TTTGGTAAT	T-CTTT
RNUAAA132YIU6RM1														T
RNOAAA727YI23RM1													TTGGGTAAT	A-CCACT.GT
RN0AAA90YK10FM1													TAGGGTAAT	T-CCAA.T
RN0AAB20YB17AHM1													ACGGTAAT	T-CCAA.T
KNUAAB577YG05AHM1 RNUAAB48YAU6AHM1													ATGGGTAAT	T-CCAA.T
RNOAAA133YD03FM1														
RN0AAA542YE07RM1													T.CGGTAAT	т-ссаа.т
RN0AAA601YB08RM1													AAGGGTAAT	T-CCAA.T
RNUAAA281YH13FM1													AAGGGTAAT	T-CCAA.T
RNOAAA437YA19RM1													AG.A.AAAGAC	TTTGG.ATTTGA
RN0AAA499YO02FM1													A.AAAGAC	TTTGG.ATTTGA
RNOAAA377YF05FM1													AG.A.AAAGAC	TTTGG.ATTTGA
RNOAAA222YD17RM1 RNOAAB173YC20AHM1						TTTGAT	CAGTTTTTTAACG	CTCTTCGAAATGA	TATATAGAACTTC	TATCTCAAATTT	AAATTCGCGA	ATTAT-AATTTAT	ACAAAA.TTTCAT	GTAATTAAAAATGT

RN0AAB161YD24FM1	
RN0AAB55YM18AHM1	
RN0AAA481YC13RM1	
RNOAAA81YKO4RM1	
RN0AAA229YJ17FM1	
RN0AAA222YD17FM1	TRCGTTANTCCTGGTGTACATTCAACTTGAAAATTAAATTGAAAAACAATTACCTGGCTTTTTGATACAGTTTTTAACGCTCTTTCGAATGATATATAGAACTTCTAACTCCGGAATTAT-AAATTATACAAAA.TTTGAAAAAACAATTACAAAAAATGT
RNOAAA303YG05RM1	ATTTCAAATTTAAATTCGCGAATTAT-AAATTATCAAAAA. TTTCATGTAATTAAAAAT. T
RNUAAA32YBU9FMI	
RNUAAA4/4112URMI	
PNOAAAA34VD23FM1	እጥ ጥጥጥን ከጥን እንደ እጥ ጥ
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RN0AAA474YG15FM1	
RN0AAA481YC13FM1	CGAGAATTAT-AAATTAAACTAAT. TTTCATGTAAAAAT. T
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RN0AAA76YA17RM1	
RN0AAA94YM05RM1	
RN0AAB55YM18FM1	ATACAGTTTTTAACGCTCTTTCGAATGATATATAGAACTTCTAACTGCTGGAATTAT-AAATTATACAAAT.TTTCATGTAATTAAAAAT.T
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RN0AAA513YA20RM1	
Box 1	
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RN0AAB3YE08AHM1	
RN0AAB140YN05FM1	····
RN0AAB414YN09FM1	СА
RN0AAB545YM04AHM1	СА
RN0AAA130YM16FM1	Сд
RN0AAA519YK05RM1	
RN0AAB125YE10FM1	
RNUAABSYEUSAHMI DNUAABSYEUSAHMI	
PNOAABI40IN05FMI	
RN0AAB545YM04AHM1	
RN0AAA130YM16FM1	
RNOAAA519YK05RM1	
RN0AAB176YD12FM1	A
RN0AAA286YA16FM1	TT
RN0AAA179YC21RM1	
RNUAAA/56IEU/FML	$ A_{1} = A_{1} = A_{1} = A_{1} = A_{1} = A_{1} = A_{1} =$
RNOAAA538YB16RM1	
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RN0AAA87YA19FM1	CCCCTT
RN0AAB380YP14FM1	CACCG.TA.AAA.A
RN0AAB423YM10FM1	
RNOAABI471010FM1 RNOAAA64VH05FM1	
RN0AAB176YD12FM1	ATAGTTCCCCCCC. CT
RN0AAA286YA16FM1	T
RN0AAA179YC21RM1	GCCTTA.G.TAAAG
RN0AAA756YE07FM1	GCCTTA.G.TAT.TA
RN0AAA591YF08RM1	CCTGC.ATC.TT.CATTGTAAA
RN0AAA538YB16RM1	
RN0AAB458YP20AHM1	CCTCACGTCA.T.TCA.CCA.T.TCA.T.TCA.T.TCA.T.TCA.
RNUAAA6691124RM1	$(CTT, \dots, A, CG, T, -, \dots, -, T-\dots, G, T, T, C,, \dots, -, TC, \dots, CT, C, \dots, T, T-G, C, \dots, -, C, \dots, T, C, \dots, CT, C, \dots,$
RNOAAR380VP14FM1	
RN0AAB423YM10FM1	
RN0AAB147YJ10FM1	ATCCTCCCCCCCC.ATTGTGC.TTT.T.AATCGT.T.AAACAAA.CAAAA.C
RN0AAA64YH05FM1	ATCCTCCCGTA
RN0AAB311YB19AHM1	
RN0AAB44YH23AHM1	ACATAG.TAG.GCAT.T.T.ATCCCA.C
RN0AAA717YI15RM1	CCCCCT.TATTCGATT.AAACATTTTGG-CACCCCGATACGA.ACCC.TAA.TA.ACATAG.TAG.GCAT.T.T.TT.A-CCCCA.C
RN0AAB125YA16FM1	CCTCCT.TATTTC.TTTC.T.CACT.AC-ACT.ACCACT.ACC
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RNOAAA579YK24RM1	GTTTTTCCCC.TTAATT.CATCA.G.TCTT.T.TGT-C.AA.A.CCA.A.CCA.A.A.GA.A.CTC.TAA.TACATAGGTTA.G.TCTT.TTT.ATA-ACGCA.C
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RN0AAA175YL12RM1	CCTCC.CT.TATTTC.TTTTCATTTTGG-C.ACCCC
RNUAAB484YE18FM1	CTTC.TT.TCT.TCT.TC-AC.ACT.TT.T.TCA-C.A.AC.A.AC.A.A.A.A.A.CA.C.A.CTT.A.A.A.AGA.CTG.G.CCGT.TAT.TT.TCC-AC.ACAT.
RNUAAA316YE18RM1	
RNOAAA141A24KMI RNOAAA691VKO1PM1	1 0 -1 -1 -1 -1 -1 -1 -1 -1
RNOAAB526YI05AHM1	AT. CCC. C CC T. T. T T
RN0AAB490YN21AHM1	GTCTTATG.T.TATTTCAT.CC.AAAATTTC.TGG-ATTC.C.C.A.C.AC
RNOAAA132YI06RM1	GCCTTATG.T.TATTCCATCC.AAAATTTCTGA-ATTCAA.CCCCAA.T.GCGAACGA.ACTC.TAA.TACATAG.TAG.GCAT.T.T.TT.ATC-ACCAAC
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RN0AAA727YI23RM1	CTCCCT.TATTCGT.AAGTTTTTGG-C.ACAAC
KNUAAA9UYK10FM1	
MINUMADZUIBL/AHMI	GATACGA.ACCC.TAA.TA.ACATAG.TAG.GCAT.T.T.TT.ATCCCA.C

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RN0AAA281YH13FM1	CCCCT.TATT.A.CGATT.AAACATTTTGG-C.A
RN0AAA699YB04FM1	GCCCTATG.T.TATTTCATCC.AAAATTTCTGGA.TTCCCC
RN0AAA437YA19RM1	AAGTAGCC.CC.TTTTTCT.CACTCTCGC.GCT.T.T.C.A.CC.A
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RN0AAA222YD17RM1	
RN0AAB173YC20AHM1	AA. TTACG AA. T GG GTA. A. T A. C GA. AAA AAAA GAAAAACA T CCT GGCG T TTTTG CAG TTT C. CT T AT . TATA GAAC C
RN0AAB161YD24FM1	
RN0AAB55YM18AHM1	TGG.GTA.A.TA.CGAAAAAAT.GAAAAACATCCTGGCT-TTTTGCAGTTC.CTTATTATAGAACCATC.CA.AT.TAA.TT-CGTGAA.TATATTATACAAAAT.CA
RN0AAA481YC13RM1	AA. TTACG AA. T. G. TG. GTA. A. T A. C GA-AAA AAAT. GAAAAACA T CCT GGC T-CTTTG CAG TTT C. CT AT. TATAGAAC GT. TAA. TA-CGCGAA. TATATTATACAAA CA
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RN0AAA303YG05RM1	AA. TTACG AA. T GG GTA. A. T A. C GA. AAA AAAA GAAAAACA T CCT GGCG T TTTTG CAG TTT C. CT T AT . TATA GAAC TAA. TT-CGCGAA. TAT ATTATACAA A CA
RN0AAA32YB09FM1	
RN0AAA474YI20RM1	AA. TTACG AA. T GG GTA. A. T A. C GA. AAA AAAA GAAAAACA T CCT GGC T - TTTTG CAG TT C. T
RN0AAA373YI20FM1	
RN0AAA434YP23FM1	AA. TTACG AA. T GG. GTA. A. T A. C GA. AAA AAAAT. GAAAAACA T CCT GGC T - TTTTG CAG TTT C. CT
RN0AAA462YN08FM1	AA. TTACA AA. T GGCG.A. A. T. A. C GAGAAAA AAAT. GAAAAACAT CCTGGCG.T. TTTTGCAG TTTC. CTT AT. TATAGAACAC AT. TATAGAAC ATA. T. TCGCGAA. TAT ATTATACA AATACA
RN0AAA474YG15FM1	AA.TTACGAA.TTG.GTA.A.TA.GGA-AAAAAAT.GAAAAACATCCTGGCT-TTTTGCAGTTTC.CTTAT.TATAGAACAC.CA.AATC.CA.AATC.CA.AATC.CA.AATC.CA.AATC.CA.AATC.CA.AATC.CA.AATC.CA.AATC.CA.AATC.CA.AATC.CA.A
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RN0AAA556YI14FM1	A.TT.GTAC.A.AA.G.G.CG.GTA.A.T-TT.CG.CCG.C.TT.AAAAAACATCCTGGCT-TTTTGCAGTTC.CTTAT.TATAGAACAC.CAATTAA.TT-CGCGAA.TATATACAAAAAACA
RN0AAA76YA17RM1	CATC.CA.AGAA.TT-CGCGATATATTATACAAA.ACA
RN0AAA94YM05RM1	A. TTACG A. T GG. GTA. A. T A. C GA-TAA AAAT. GAAAAACA T CCT - GGC T TTTTG CAG TT C. CT T A AT. TATA GAAC ATC. CA A TT-CGTGAA. TAT ATTATACA AATA CA
RN0AAB55YM18FM1	A. TTACG A. T GG. GTA. A. T. A. C GA-AAA AAAT. GAAAAACAT CCT GGC T TTTTG CAG TT C. CT T A AT. TATA GAAC AT A. TCGCGAA. TAT ATTATACA AATA CA
RN0AAB56YP24FM1	
RN0AAA513YA20RM1	
Box 1	

	410	420	430	440	450	460	470	480	490	500	510	520 5	30 540	55	50 560	570	580	590	600
							.	.					. <mark> </mark>	· · ·		.			
RN0AAB125YE10FM1	GATGCTGAAAGGO	JATTAAAACA-	-AATGCTC-A	ATAACTA	-TGTTTATTT-	AAGT	-CGGATTTC-	-GATGAAT	CTAG	TACCGTT	CGACTCAG	GCTCGA	AG <mark>AGCTCTTTCGAA1</mark>	<mark>GATA</mark> T?	ATAATTTGCCAT/	AGAATGTTTTZ	AAAA'	ТСБАААААА-А1	'AGA
RN0AAB3YE08AHM1									••••	•••••			· · · <mark>· · · · · · · · · · · · · · · · </mark>	• • • • • •		.AA.			
RN0AAB140YN05FM1									••••	•••••			· · · <mark>· · · · · · · · · · · · · · · · </mark>	• • • • • •		.A.TA.			
RN0AAB414YN09FM1									••••	•••••			· · · <mark>· · · · · · · · · · · · · · · · </mark>	T.		.AA.			
RN0AAB545YM04AHM1									••••	•••••			· · · <mark>· · · · · · · · · · · · · · · · </mark>	T.		.AA.			
RN0AAA130YM16FM1									••••	•••••			· · · <mark>· · · · · · · · · · · · · · · · </mark>	T.		.AA.			
RN0AAA519YK05RM1									••••	•••••			· · · <mark>· · · · · · · · · · · · · · · · </mark>	T.		.AA.			
RN0AAB125YE10FM1									••••	•••••			· · · <mark>· · · · · · · · · · · · · · · · </mark>	• • • • • •					
RN0AAB3YE08AHM1									••••	•••••			· · · <mark>· · · · · · · · · · · · · · · · </mark>	• • • • • •		.AA.			
RN0AAB140YN05FM1									••••	· · · · · · · ·			<mark></mark>			A.TA.			
RN0AAB414YN09FM1									••••	· · · · · · · ·			<mark></mark>	T.		.AA.			
RN0AAB545YM04AHM1									••••	· · · · · · · ·			<mark></mark>	T.		.AA.			
RN0AAA130YM16FM1									••••	· · · · · · · ·			<mark></mark>	T.		.AA.			
RN0AAA519YK05RM1									••••	· · · · · · · ·			<mark></mark>	T.		.AA.			
RN0AAB176YD12FM1	T	c							т	A			<mark></mark>			AAA.			
RN0AAA286YA16FM1	AT		G				т-		т	G	тт.	т	<mark></mark>	<mark></mark>		AA.AA.		c	.G
RN0AAA179YC21RM1	T						т-		т	· · · · · · A ·			<mark></mark>	.TA	.AA	ATCAT	.GG	.GAT	
RN0AAA756YE07FM1	T						т-		т	· · · · · · A ·			<mark></mark>	.TA	.AA	AT CA1	.GG	.GAA	
RN0AAA591YF08RM1	.CCAAGGT.	AA	-GGGG	Ст-т	c.c	T	AA	-ATT	TA	.CT.A			<mark></mark>			ААААА.		CTA.GA	
RN0AAA538YB16RM1	.CCAACGT.	.GAT	-GGG	Ст-т	c		AC	тт	та	.GT.A			<mark></mark>			AAGAA.	T-	CTA.GA	
RN0AAB458YP20AHM1	.CCAACGT.	.GAT	-GGG	Ст-т	c.c		AC	тт	TA	.GT.A			<mark></mark>			AGAA.		CTA.GA	
RN0AAA669YI24RM1	.CCAACGT.	.GATG-	C.G	Ст-т	c.c		A	тт	TA	.GT.A		т	<mark></mark>			.AAGAAG	T	CTAGGA	
RN0AAA87YA19FM1	.CCAACG	AT	C.G	C.GT-TT	TCGC	т	AAT	тт	TA	.GT.A	A	Ac				AGAA.	T	СТАА	
RN0AAB380YP14FM1	.CA.A.TCGT.	.GA	C.GG	Ст-т	C.A	A	A	тт	т			т	<mark></mark>			AC.AGAA.		CTAGGA	
RN0AAB423YM10FM1	.CA.A.TCGT.	.GA	C.G	Ст-т	C.A	A	A	тт	т	т.т		т	<mark></mark>			AC.AGAA.		CTAGGA	
RN0AAB147YJ10FM1	CCCACAG		C.G	T-T-	TG	A	AT-	-AT.C.T	т		тт		<mark>.</mark> ATA	т.	ATT	AAGAA.	.AAAT	C.AAGG	G.G
RN0AAA64YH05FM1	ACCGGT.		CG	Ст-А-			A	-ATC	т	AAC	AT	т	<mark></mark>		G		A.TT	GAAA	
RN0AAB176YD12FM1	T	c							т	A			<mark></mark>						
RN0AAA286YA16FM1	AT		G				т-		т	G	T					A A. A A.		c	.g
RN0AAA179YC21RM1	T						т-		т	A			<mark></mark>	.TA	.AA	AT CAT	.GG	.GAT	
RN0AAA756YE07FM1	T						т-		т	A			<mark></mark>	.TA	.AA	AT CAT	.GG	.GAA	
RN0AAA591YF08RM1	.CCAAGGT.	AA	-GGGG	Ст-т	c.c	т	AA	-ATT	та	.CT.A			<mark></mark>			A AAAA.		CTA.GA	
RN0AAA538YB16RM1	.CCAACGT.	.GAT	-GGG	Ст-т	c		AC	тт	та	.GT.A			<mark></mark>			AAGAA.	T-	CTA.GA	
RN0AAB458YP20AHM1	.CCAACGT.	.GAT	-GGG	Ст-т	c.c		AC	тт	та	.GT.A			<mark></mark>			AAGAA.		CTA.GA	
RN0AAA669YI24RM1	.CCAACGT.	.GATG-	C.G	Ст-т	c.c		A	тт	та	.GT.A		т	<mark></mark>			AAGAAG	T	CTAGGA	
RN0AAA87YA19FM1	.CCAACG	AT	C.G	C.GT-TT	TCGC	т	AAT	тт	та	.GT.A	A	Ac				AAGAA.	т	стаа	
RN0AAB380YP14FM1	.CA.A.TCGT.	.GA	C.GG	Ст-т	C.A	A	A	тт	т	т.т		т	<mark></mark>			AC.AGAA.		CTAGGA	
RN0AAB423YM10FM1	.CA.A.TCGT.	.GA	C.G	Ст-т	C.A	A	A	тт	т	т.т		т	<mark></mark>			AC.AGAA.		CTAGGA	
RN0AAB147YJ10FM1	CCCACAG		C.G	T-T-	TG	A	AT-	-AT.C.T	т		тт		<mark>.</mark> ATA	т.	ATT	AAGAA.	.AAAT	C.AAGG	G.G
RN0AAA64YH05FM1	ACCGGT.		CG	Ст-А-			A	-ATC	т	AAC	AT	т	<mark></mark>		G		A.TT	GAAA	
RN0AAB311YB19AHM1	.GCA.AATCTT	GCCT	G.A		TAATGGC-		AG	-ATCAG	GCC	ATT.A.GG.	ATC.T	-ATCAAGC			AT-1	TATG.A.CAA.	CAA	AA.CTCAT-	G
RN0AAB44YH23AHM1	ATCA.AACAC	-G.CC.TC	-G.G.A		TAAA.CTG	c	AT.C	CCA	ACC	G.A.A.AG.	ATC.TT-	ACTCAGC	.c <mark></mark>		TGA.AT-1	TATCAAG	CA	AA.CTCAT-	G
RN0AAA717YI15RM1	ATCA.AACAC	-G.CC.TC	-G.G.A		TAAA.CTG	c	AT.C	CCA	ACC	G.T.A.AG.	ATC.TT-	ACTCAGC	.c <mark></mark>			TATCAGO	CA	AA.CTCA	G
RN0AAB125YA16FM1	.GCA.AATTT	ccc	-T.G.A		CAATGG	A	AG	-ATCAG	GCC	A.T.AGGG.	ATC.TG-	ACCGAGC I	AG		GAA.AT-1	A.G.A.CAA	CAA	ACTCA	G
RN0AAB437YE21AHM1	.GCA.AATTT	ccc	-T.G.A		CAATGG	A	AG	-ATCAG	GCC	A.T.AGGG.	ATC.TG-	ACCGAGC I	AG		GAA.AT-1	A.G.A.CAA	CAA	ACTCA	G
RN0AAB266YH16AHM1	.GCA.AATTG		-T.G.A'		TAATGG		AG	-ATCAG	GCC	A.T.A.GG.	ATT.T	CGAGC T	AG		GA.AT-1	C.G.A.CAA	CAA	ACTA	G
RN0AAA131YF02RM1	.GCA.AATTT	ccc	-T.G.A		TAATGG		AG	-ATCAG	GCC	A.T.A.GG.	ATC.TG-	-ACCGAGC T	AG		GAA.AT-1	TATG.T.CAA.	CAA	ACTCA	G
RN0AAA130YE05RM1	.GCA.AATTT		-T.G.A		TAATGG		AG	-ATCAG	GCC	A.T.A.GG.	ATC.TG-	-ACCGAGC T	AG		GAA.AT-1	TATG.T.CAA.	CAA	ACTCA	G
RN0AAA579YK24RM1	CAT	-TC.GC	-G.G.A	C.G. TC-A	TAA.ATG	G	AC	-CTCA	GCC	G.A	G-	-ACCCAGC	G.			ACCGAC	CAA	CTC A	
RN0AAB100YP08AHM1	TGCA.AAAATT	ccc	-G.G.A	GT.TT-A	TAAT.G		A.GC	-ATCAG.G	GCC	A.TTT.GG.	ATC.TG-	ACAAAGC	TC		GA.AT-1	TATA.CAA.	CAA	ACTCA	G
RN0AAB180YL08FM1	TGCA.AAAATT	ccc	-G.G.A	GT.TT-A	TAAT.G		A.GC	-ATCAG.G	GCC	A.TTT.GG.	ATC.TG-	ACAAAGC	тс.		GA.AT-1	TAT A. CAA.	CAA	ACTCA	G

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DN0333331 CVE1 0DW1		
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PNOAAB289VD03FM1		TG-DD DT-TDT CCDDCCDD DD CTC DG
KNORAD2091D05FMI		
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RN0AAA90YK10FM1	ATCA.AACACG.CC.TCG.G.AT.GG.TC-ATAAA.CTGCAT.CAT.CCCAACCG.T.A.AGATC.T.T-ACTCAGCC	
DNO 3 3 DOOVD1 73 UN1		
RNUAABZUIBI/AHMI	ATCA.AACACG.CC.TCG.G.ATG.TC-ATAAA.CTGCTAT.CCCAACCG.T.A.AGATC.T.T-ACTCAGCC	······································
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DN0333400W0007W1		
RNUAAA4991002FM1	.GCA.AA======CTTC====GAA.==TCTGTC=ATAACTG====C======AG====ATC==ATC==ACTCAGCA	I
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RNOAAA481 VOI 3DM1	a. Tab	
Descent of the second second		
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KNOARD501F24FML	ATAATTTCC-C.C.T.CGTTATCTGGTGCAT.CA.CG.AAATTAAGAAAA.CA.T.ACGGCTTTTTTTATT.TTA	
RNOAAA513YA20RM1	A. TAATITUU-C. C. T. UGTTAT CTUGTU CA-T. CA.CGAAATAA GAAAA.CA.T. ACUGCTTTTTT. T. A	
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RNOAAA513YA20RM1 Box 1	A. TAA THICC-CLCT. CUT	2GAACTTTC.CAA.TTTATC-GATCT
RNOAA513YA20RM1 Box 1	A. TAATTTCU-C.C.T. CGTTAT. CTCGTGCA-T. CA.CGAAATTAAGAAAA.CA.T.ACGGCTTTTTT.TT.ATT.TTA 	ZGAACTT. TCAA.TTT ATC-GATCT 740 750 760 770 780 790 800
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RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB3YE08AHM1	A. TAA TTUC-C.C.T. CBTT. AT. CTOGTGCA-T. CA.CGAAATTAA GAAAA.CA.T. ACGGCTTTTTT.T. ATT.TT- A AA. CA.T. ACGGCTTTTTT. TATT.TT- A 610 620 630 640 650 660 670 680 690 700 710 720 730 	ZGAACTT. TCAA.TTT ATC-GATCT 740 750 760 770 780 790 800
RNOAA513YA20RM1 Box 1 RNOAAB125YE10FM1 RNOAAB125YE08AHM1 RNOAAB140YNO5FM1	A. TAA TTUC-CLCTTOST-T.AT. CROTOCA-T.CA.CGAAATAAGAAAA.CA.T.ACGGCTTTTT.T.ATT.TT.A	2
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RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB12VN05FM1 RNOAAB414YN09FM1 DNOAB545VN045VM1	A. TAA THE COLOR CONTENT - AT CROUTE - CA T. CA. C	2
RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB140YN05FM1 RNOAAB14VN05FM1 RNOAAB545YM04AHM1	A. TAA	2BAACTTTC.CAA.TTTATC-GATCT 740 750 760 770 780 790 800
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RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB3YE00AHM1 RNOAAB3YE00AHM1 RNOAAB410YN05FM1 RNOAAB414YN09FM1 RNOAAB415YN06AHM1 RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB3YE00AHM1 RNOAAB3YE00AHM1	A. TAA TTCC-C.C.T. COTTA.T. CROTOCAT.CA.CGALATTAAGAAAA.CA.T.ACGGCTTTTT.T.T.ATT.TT.A.	2
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RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB140YN05FM1 RNOAAB14YN05FM1 RNOAAB545YM04AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1	A. TAATTCC-C.C.T. C0TTAT. C.C.GTCCAT. CA.CG.GAAATAA. CA. T. ACG.GCTTTTT. T. A TT. TT. A A	2BAACTTTC.CAA.TTTATC-GATCT 740 750 760 770 780 790 800
RNOAAS13YA2ORMI Box 1 RNOAAS12SYE10FM1 RNOAAS3YE08AHM1 RNOAAS140YN05FM1 RNOAAS140YN05FM1 RNOAAS15YN04AHM1 RNOAAS19YK05RM1 RNOAAS12SYE10FM1 RNOAAS12SYE10FM1 RNOAAS140YN05FM1 RNOAAS140YN05FM1 RNOAAS13YN05FM1 RNOAAS13YN05FM1 RNOAAS13YN05FM1	A. TAATTCC-C.C.T. CUT-T AT. C.C.T T. CA.CC.AAATTAA GAAAA.CA.T. ACCGCTTTTTTATTT. TA	2
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RNOAABJ25YE10FM1 RNOAABJ25YE10FM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE05FM1 RNOAAB3YE05FM1 RNOAAB3YE05FM1 RNOAAB3YE08AHM1 RNOAB3YE08AHM1	A. TAA	2
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RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB140YN05FM1 RNOAAB14YN05FM1 RNOAAB545YM04AHM1 RNOAAB14YN05FM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04FM1 RNOAAB545YM04FM1 RNOAAB545YM04FM1 RNOAAB545YM04FM1 RNOAAB545YM16FM1 RNOAAB326YA16FM1	A. TAA	2BAACTTTC.CAA.TTTATC-GATCT 740 750 760 770 780 790 800
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RNOAA513YA20RM1 RNOAA512SYE10FM1 RNOAA512SYE10FM1 RNOAA5140YN05FM1 RNOAA5140YN05FM1 RNOAA515YN06AHM1 RNOAA51YN06AFM1 RNOAA51YN05FM1 RNOAA51YSYE30FM1 RNOAA5140YN05FM1 RNOAA5140YN05FM1 RNOAA51YN05FM1 RNOAA51YSYE30FM1 RNOAA5176YD12FM1 RNOAA5176YD12FM1 RNOAA5176YD22RM1 RNOAA756YE07FM1 RNOAA756YE07FM1	A. TAA	2
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RNOAA5133720RM1 RNOAA5135720RM1 Box 1 RNOAAB37E08AHM1 RNOAAB37E08AHM1 RNOAAB1407N05FM1 RNOAAB4147N09FM1 RNOAAB37E08AHM1 RNOAAB37E08AHM1 RNOAAB37E08AHM1 RNOAAB37E08AHM1 RNOAAB37E08AHM1 RNOAAB37EN06AHM1 RNOAAB37EN06AHM1 RNOAAB37EN06AHM1 RNOAAB37EN06AHM1 RNOAAB37E072C1RM1 RNOAAB37F072C1RM1 RNOAAB37F072C1RM1 RNOAAA5387B16RM1 RNOAAA5387B16RM1	A. TAA TTTC-C.C.T. CIT-T AT CTGGTGCA-T. CA.CG.GAAATA.C.A.T. ACG.GCTTTTT.T. T. A AAA.C.A.T. ACG.GCTTTTT. T.T. A AAA.C.A.T. ACG.GCTTTTT. T.T. A AAA.C.A.T. AC	2
RNOAA51337A20RM1 RNOAA51357E06AHM1 RNOAAB3YE06AHM1 RNOAAB3YE06AHM1 RNOAAB44YN05FM1 RNOAAB545YN06AHM1 RNOAAB545YN06AHM1 RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB124YN05FM1 RNOAAB545YN06AHM1 RNOAAB545YN06AHM1 RNOAAB545YN06AHM1 RNOAAB176YD12FM1 RNOAAB176YD12FM1 RNOAAB176YD12FM1 RNOAAA571YF05RM1 RNOAAA574YF05RM1 RNOAAA591YF06RM1 RNOAAA531YF06RM1 RNOAAA591YF06RM1 RNOAAA591YE06RM1	A. TAA	2BAACTTTC.CAA.TTTATC-GATCT 740 750 760 770 780 790 800
RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB140YN05FM1 RNOAAB14YN05FM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB125YE10FM1 RNOAAB140YN05FM1 RNOAAB141N05FM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04FM1 RNOAAB545YM04FM1 RNOAAB545YM04FM1 RNOAAB545YM07FM1 RNOAAB545YF16FM1 RNOAAB545YF16FM1 RNOAAB458YF16FM1 RNOAAB458YF16FM1 RNOAAB458YF16FM1	A . TAA TTTCCCC.C.T. CUT - T AT CUGUU - CAA T. CA.C GOCTTTT	2
RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB1YE0GAHM1 RNOAAB140YN05FM1 RNOAAB140YN05FM1 RNOAAB125YE07M1 RNOAAB125YE07M1 RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB140YN05FM1 RNOAAB140YN05FM1 RNOAAB140YN05FM1 RNOAAB140YN05FM1 RNOAAB145YN05AM1 RNOAAB176YD12FM1 RNOAAB176YD12FM1 RNOAAA35YE05RM1 RNOAAA35YE16FM1 RNOAAA35YE16FM1 RNOAAA5YE1708RM1 RNOAAA5YE120HM1 RNOAAA5YE120HM1 RNOAAA5YE120HM1 RNOAAA5YE120HM1 RNOAAA65Y124KM1	A. TAA	2BAACTTTC.CAA.TTTATC-GATCT 740 750 760 770 780 790 800
RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB140YN05FM1 RNOAAB14VN05FM1 RNOAAB14VN05FM1 RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB14VN05FM1 RNOAAB14VN05FM1 RNOAAB545YM04HM1 RNOAAB545YM04HM1 RNOAAB545YM04HM1 RNOAAB545YM04HM1 RNOAAB545YM04HM1 RNOAAB545YE07FM1 RNOAAA5YE16RM1 RNOAAA5YE16RM1 RNOAAB545YE10AHM1 RNOAAB545YE10AHM1 RNOAAB5YE10AHM1 RNOAAA5Y124BM1	A . TAA TTCC-C.C.T. CUT - T AT CTGGTG CA-T. CA.C	2
RNOAA5133720RM1 RNOAA5133720RM1 Box 1 RNOAA5125YE10FM1 RNOAA5140YN05FM1 RNOAA5140YN05FM1 RNOAA515YN06AHM1 RNOAA515YN06AHM1 RNOAA519YN05FM1 RNOAA519YN05FM1 RNOAA519YN05FM1 RNOAA519YN05FM1 RNOAA519YN05FM1 RNOAA519YN05FM1 RNOAA519YN57FM1 RNOAA519YN57FM1 RNOAA539YN57FM1 RNOAA539YN57FM1 RNOAA539YN57FM1 RNOAA539YN57FM1 RNOAA539YN57FM1 RNOAA539YN57FM1 RNOAA539YN57FM1 RNOAA539YN57FM1 RNOAA539YN57FM1 RNOAA539YN57FM1 RNOAA539YN57FM1 RNOAA539YN57FM1 RNOAA539YN57F0 RN1 RNOAA539YN57F0 RN1 RNOAA539YN57F0 RN1 RNOAA539YN57F0 RN1 RNOAA539YN57F0 RN1 RNOAA539YN57F0 RN1 RNOAA659YN24FM1 RNOAA659YN24FM1	A. TAA	2
RNOAASI3 3YA20RMI RNOAASI3 3YA20RMI BOX 1 BOX 1 RNOAABI45YE08AHMI RNOAAB3YE08AHMI RNOAAB3YE08AHMI RNOAAB3YE08AHMI RNOAAB3YE08AHMI RNOAAB14YN05PMI RNOAAB17YN05PMI RNOAAB125YE10PMI RNOAAB12YK05PMI RNOAAB14YN05PMI RNOAAB14YN05PMI RNOAAB14YN05PMI RNOAAB545YM04AHMI RNOAAB545YN05PMI RNOAAB545YN05PMI RNOAAB545YN05PMI RNOAAB545YN05PMI RNOAAB545YN05PMI RNOAAB545YN05PMI RNOAAB545YN05PMI RNOAAB545YN05PMI RNOAAB545YN05PMI RNOAAB515YN05PMI RNOAAB517YD12PMI RNOAAB517YD212PMI RNOAAB59YN05PMI RNOAAB59YN05PMI RNOAAB59YN02PMI RNOAAA591YF08RMI RNOAAB458YP20AHMI RNOAAB380YP14PMI RNOAAB380YP14PMI	A. TAA	2
RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB140YN05FM1 RNOAAB14YN05FM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB3YE08AHM1 RNOAAB140YN05FM1 RNOAAB140YN05FM1 RNOAAB144YN05FM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04FM1 RNOAAA519YE05RM1 RNOAAA559YE07FM1 RNOAAA55YF207FM1 RNOAAA55YF20AHM1 RNOAAB455YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAAB545YF20AHM1 RNOAB453YF10FM1	A. TAA	2
RNOAA5133720RM1 RNOAA513720RM1 Box 1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB34537N04AHM1 RNOAAB3537N05RM1 RNOAAB37N7 RNOAAB37N7 RNOAAB37N16FM1 RNOAAB37N16FM1 RNOAAB37N16FM1 RNOAAB37N16FM1 RNOAAB37N16FM1 RNOAAB37N16FM1 RNOAAB37N16FM1 RNOAAB37N16FM1 RNOAAB37N16FM1 RNOAAB37N16FM1 RNOAAB387N16FM1 RNOAAB387N16FM1 RNOAAB387N16FM1 RNOAAB3807P14FM1 RNOAAB3807P14FM1 RNOAAB38177J19FM1 RNOAAB347N19FM1	A. TAA	2
RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB140YN05FM1 RNOAAB14YN05FM1 RNOAAB14YN05FM1 RNOAAB545YM04AHM1 RNOAAB14YN05FM1 RNOAAB14YN05FM1 RNOAAB14YN05FM1 RNOAAB14YN05FM1 RNOAAB14YN05FM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04FM1 RNOAAB545YF07FM1 RNOAAB545YF07FM1 RNOAAB45YF124FM1 RNOAAB45YF124FM1 RNOAAB45YF124FM1 RNOAAB45YF124FM1 RNOAAB45YF124FM1 RNOAAB45YF124FM1 RNOAAB45YF124FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1	A. TAC	2
RNOAA51337A20RM1 RNOAA51337A20RM1 Box 1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE05RM1 RNOAAB14YN05FM1 RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB14YN05FM1 RNOAAB378YE05RM1 RNOAAB378YE05RM1 RNOAAB378YE05RM1 RNOAAB378YE05RM1 RNOAAB379YC21RM1 RNOAA531YF06RM1 RNOAA531YF06RM1 RNOAA531YF08RM1 RNOAA531YF08RM1 RNOAA531YF08RM1 RNOAAA53Y124RM1 RNOAAA53Y120FM1 RNOAAA53Y10FM1 RNOAAB380YF14FM1 RNOAAB380YF14FM1 RNOAAB380YF14FM1 RNOAAB3817FYD12FM1 RNOAAB317FYD12FM1 RNOAAB17FYD12FM1	A. TAA	2
RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB545YM04HM1 RNOAAB545YM04HM1 RNOAAB125YE10FM1 RNOAAB140YN05FM1 RNOAAB141N09FM1 RNOAAB545YM04HM1 RNOAAB545YM04HM1 RNOAAB545YM04HM1 RNOAAB545YE10FM1 RNOAAB545YE10FM1 RNOAAB59YE12FM1 RNOAAB59SYE16FM1 RNOAAB59SYE16FM1 RNOAAB59SYE16FM1 RNOAAB59SYE12HM1 RNOAAB545YE12HM1 RNOAB545YE12HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14HM1 RNOAB545YE14	A. TAC	2
RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB140YN05FM1 RNOAAB140YN05FM1 RNOAAB125YE07M1 RNOAAB125YE07M1 RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB140YN05FM1 RNOAAB140YN05FM1 RNOAAB140YN05FM1 RNOAAB140YN05FM1 RNOAAB175YE07FM1 RNOAAB175YE07FM1 RNOAAB175YE07FM1 RNOAAA53YF06RM1 RNOAAA53YF06RM1 RNOAAA53YF20AHM1 RNOAAA53YF20AHM1 RNOAAB30YF14FM1 RNOAAB30YF14FM1 RNOAAB30YF14FM1 RNOAAB347Y10FM1 RNOAAB347Y10FM1 RNOAAB347Y10FM1 RNOAAB347Y10FM1 RNOAAB147Y10FM1 RNOAAB147Y10FM1 RNOAAB247Y12FM1 RNOAAB147Y10FM1 RNOAAB247Y12FM1 RNOAAB147Y10FM1 RNOAAB247Y12FM1 RNOAAB247Y12FM1 RNOAAB247Y12FM1 RNOAAB247Y12FM1 RNOAAB247Y12FM1 RNOAAB247Y12FM1 RNOAAB247Y12FM1 RNOAAB247Y12FM1 RNOAAB247Y12FM1 RNOAAB247Y12FM1 RNOAAB247Y12FM1 RNOAAB247Y12FM1 RNOAAB247Y12FM1 RNOAAB247Y12FM1 RNOAAB247Y221RM1	A. TACGAAA CA. T. &CGACTTTT. TATT. TATTT. TATT. TATT. TATT. TATT. TATTT. TATTT. TATTT. TATTT	2
RNOAASJ 3YA20RMI RNOAASJ 3YA20RMI BOX 1 BOX 1 BOX 1 RNOAABJ2SYE08AHMI RNOAABJ40YN05FMI RNOAABJ4VN05FMI RNOAABJ2YR05RMI RNOAABJ2SYR05RMI RNOAABJ2SYR05RMI RNOAABJ2SYR05RMI RNOAABJ2SYR05RMI RNOAABJ4VN05FMI RNOAABJ2SYR05RMI RNOAABJ4VN05FMI RNOAABJ4VN05FMI RNOAABJ4VN05FMI RNOAABJ4VN05FMI RNOAABJ4VN05FMI RNOAABJ4VN05FMI RNOAABJ4VN05FMI RNOAABJ4VN16FMI RNOAABJ76V12FMI RNOAABJ76V212FMI RNOAABSVENSTB16RMI RNOAABSVENSTB18 RNOAABSVENSTEMI RNOAABSVENS	A. TRO-C. C. T. COT-TA. C. CAC. C CO. CALTIAL	2
RIVOAAB125YE10FM1 RIVOAAB125YE10FM1 RIVOAAB140YN05FM1 RIVOAAB140YN05FM1 RIVOAAB140YN05FM1 RIVOAAB140YN05FM1 RIVOAAB141N05FM1 RIVOAAB140YN05FM1 RIVOAAB140YN05FM1 RIVOAAB140YN05FM1 RIVOAAB140YN05FM1 RIVOAAB140YN05FM1 RIVOAAB141N05FM1 RIVOAAB545YN04AHM1 RIVOAAB545YN04AHM1 RIVOAAB545YN04AHM1 RIVOAAB545YN04AHM1 RIVOAAB545YN04AHM1 RIVOAAB545YN04AHM1 RIVOAAB545YN04HM1 RIVOAAB545YP20AHM1 RIVOAAB545YP20AHM1 RIVOAAB4751Y216FM1 RIVOAAB4751Y210FM1 RIVOAAB423YM10FM1 RIVOAAB4751Y10FM1 RIVOAAB4751Y10FM1 RIVOAAB4751Y10FM1 RIVOAAB4751Y10FM1 RIVOAAB475Y10FM1 RIVOAAB647012FM1 RIVOAAB647012FM1 RIVOAAB647012FM1 RIVOAAB647012FM1 RIVOAAB647012FM1 RIVOAAB647012FM1 RIVOAAB74721RFM1	A. TAC	2
RNOAASJ 3YA20RMI RNOAASJ 3YA20RMI BOX 1 BOX 1 RNOAABJ2SYE08AHMI RNOAABJ40YN05FMI RNOAABJ40YN05FMI RNOAABJ4VN05FMI RNOAABJ4VN05FMI RNOAABJ2SYK05RMI RNOAABJ2SYK05RMI RNOAABJ2SYK05RMI RNOAABJ2SYK05RMI RNOAABJ4VN05FMI RNOAABJ4VN05FMI RNOAABJ4VN05FMI RNOAABJ4VN05FMI RNOAABJ76YD12FMI RNOAABJ9YK05RMI RNOAABJ9YK05RMI RNOAABSYNES RNOAABSYNES <	A. TRO-C. C. T. CUT-TA. C. CAC. C CA. C CAAATAA. CA. T. A	2
RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB140YN05FM1 RNOAAB14VN05FM1 RNOAAB14VN05FM1 RNOAAB545YM04AHM1 RNOAAB14YN05FM1 RNOAAB14VN05FM1 RNOAAB14VN05FM1 RNOAAB14VN05FM1 RNOAAB14VN05FM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04FM1 RNOAAB545YF04FM1 RNOAAB545YF124FM1 RNOAAB453YF124FM1 RNOAAB453YF124FM1 RNOAAB45Y124FM1 RNOAAB45Y124FM1 RNOAAB45Y124FM1 RNOAAB45Y124FM1 RNOAAB45Y124FM1 RNOAAB45Y124FM1 RNOAAB45Y124FM1 RNOAAB45Y124FM1 RNOAAB45Y124FM1 RNOAAB45Y124FM1 RNOAAB45Y124FM1 RNOAAB45Y124FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB45Y126FM1 RNOAAB45Y126FM1 RNOAAB45Y126FM1 RNOAAB45Y127012FM1 RNOAAB45Y126FM1 RNOAAB45Y126FM1 RNOAAB45Y126FM1 RNOAAB45Y126FM1 RNOAAB45Y167FM1 RNOAAB45Y167FM1 RNOAAB45Y167FM1 RNOAAB5Y1767FM1 RNOAAB5Y1767FM1 RNOAAB5Y1767FM1 RNOAAB5Y1767FM1 RNOAAB5Y1767FM1 RNOAAB5Y1767FM1 RNOAAB5Y1767FM1 RNOAAB5Y1767FM1 RNOAAB5Y1767FM1 RNOAAB5Y17757FM1 RNOAAB5Y17757FM1 RNOAAB5Y17757FM1 RNOAAB5Y1775777777777777777777777777777777777	A. TAC	2
RNOAA51337A20RM1 RNOAA5137A20RM1 Box 1 ENOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE05RM1 RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB14YN05FM1 RNOAAB174YN05FM1 RNOAAB174YN05FM1 RNOAAB174YN05FM1 RNOAAB174YN05H1 RNOAAB174YN15FM1 RNOAAB174YN15FM1 RNOAAA59YE16RM1 RNOAAA59YE16RM1 RNOAAA53YN16FM1 RNOAAA53YN16FM1 RNOAAB380YF14FM1 RNOAAB380YF14FM1 RNOAAB380YF14FM1 RNOAAB380YF14FM1 RNOAAB38147YJ10FM1 RNOAAB175YD12FM1 RNOAAB179YC21RM1 RNOAAB179YC21RM1 RNOAAB179YC21RM1 RNOAAB179YC21RM1 RNOAAB179YC21RM1 RNOAAB179YC21RM1 RNOAAB179YC21RM1 RNOAAB179YC21RM1 RNOAAB380YF14FM1 RNOAAB179YC21RM1 RNOAAB380YF14FM1 RNOAAB179YC21RM1 RNOAAB179YC21RM1 RNOAAB179YC21RM1 RNOAAA750YF08RM1	A. TAA THEC-C. C. T. GT - AT CROTO CA CA C CA C GCTTT T. T. A T T. T. T	2
RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB545YM04HM1 RNOAAB545YM04HM1 RNOAAB545YM04HM1 RNOAAB125YE10FM1 RNOAAB140YN05FM1 RNOAAB545YM04HM1 RNOAAB545YM04HM1 RNOAAB545YM04HM1 RNOAAB545YM04HM1 RNOAAB545YE10FM1 RNOAAB545YE10FM1 RNOAAB545YE10FM1 RNOAAB55YE10FM1 RNOAAB55YE10FM1 RNOAAB55YE10FM1 RNOAAB55YE10FM1 RNOAAB57Y12FM1 RNOAAB57Y170FM1 RNOAAB57Y170FM1 RNOAAB57Y170FM1 RNOAAB57Y170FM1 RNOAAB57Y170FM1 RNOAAB57Y170FM1 RNOAAB57Y170FM1 RNOAAB57Y10FM1 RNOAAB57Y170FM1 RNOAB57Y170FM1 RNOAB57Y170FM1 RNOAB57Y70FM1 RNOAF777777777777777777777777777777777777	A. TAC	2
RNOAA51337A20RM1 RNOAA51337A20RM1 Box 1 Box 1 RNOAAB1455YE10FM1 RNOAAB3YE08AHM1 RNOAAB140YN05FM1 RNOAAB1455YN04AHM1 RNOAAB145YN05FM1 RNOAAB175YE05FM1 RNOAAB125YE10FM1 RNOAAB14YN05FM1 RNOAAB14YN05FM1 RNOAAB14YN05FM1 RNOAAB545YE08AHM1 RNOAAB14YN05FM1 RNOAAB176YD12FM1 RNOAAB176YD12FM1 RNOAAA517FV012FM1 RNOAAA57HFM1 RNOAAA59Y20AHM1 RNOAAA59Y20AHM1 RNOAAA59Y120FM1 RNOAAA59Y120FM1 RNOAAA59Y120FM1 RNOAAA59Y121FM1 RNOAAB176YD12FM1 RNOAAB177YJ0FM1 RNOAAA59Y121FM1 RNOAAB176YD12FM1 RNOAAB176YD12FM1 RNOAAB307Y14FM1 RNOAAB176YD12FM1 RNOAAB177Y10FM1 RNOAAB177Y201FM1 RNOAAB375YE07FM1 RNOAAA59Y20AHM1 RNOAAA59Y201FM1 RNOAAA59Y201F0 RNOAAB39Y1678K1 RNOAAA59Y201F0 RNOAAB39Y1778RM1 RNOAAA59Y201F0	A. TAK - THECCE TEGT - TAK - COMMENTAL - CANA TAK - CA TAK GOTTT TT - A AA. CA TAK	2
RNOAA513YA20RM1 RNOAA513YA20RM1 Box 1 RNOAA51YE08AHM1 RNOAA51YE08AHM1 RNOAA51YE08AHM1 RNOAA51YE08AHM1 RNOAA51YE08AHM1 RNOAA519YK05RM1 RNOAA519YK05RM1 RNOAA519YK05RM1 RNOAA51YK08AHM1 RNOAA51YK07M1 RNOAA51YK07M1 RNOAA51YK07M1 RNOAA51YK07KM1 RNOAA51YF02IRM1 RNOAA51YF02IRM1 RNOAA51YF02RM1 RNOAA51YF02RM1 RNOAA51YF02RM1 RNOAA51YF08M1 RNOAA51YF08M1 RNOAA51YF07M1 RNOAA61Y12YM1 RNOAA61Y12YM1 RNOAA61Y12YM1 RNOAA61Y12YM1 RNOAA61Y12YM1 RNOAA51YF02RM1 RNOAA61Y12YM1 RNOAA61Y12YM1 RNOAA61Y12YM1 RNOAA51YF02RM1 RNOAA51YF02RM1 RNOAA61Y12YM1 RNOAA61Y12YM1 RNOAA61Y12YM1 RNOAA61Y12YM1 RNOAA61Y12YM1 RNOAA61Y12YM1 RNOAA61Y12YM1 RNOAA65Y124RM1 RNOAA65Y124RM1 RNOAA65Y124RM1 RNOAA65Y124RM1 RNOAA65Y124RM1 RNOAA65Y124RM1 RNOAA65Y124RM1 RNOAA65Y124RM1 RNOAA65Y124RM1 RNOAA65Y124RM1	A. TAK-: THECCORT CONTENT - AT . COGNE CAF - CAC	2
RINOAAB125YE08AH1 RNOAAB125YE10FM1 RNOAAB140YN05FM1 RNOAAB140YN05FM1 RNOAAB140YN05FM1 RNOAAB141N09FM1 RNOAAB141N09FM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB140YN05FM1 RNOAAB140YN05FM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04HM1 RNOAAA5YM7012FM1 RNOAAA5YM12F08H1 RNOAAA5YM12F08H1 RNOAAA5YM12FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB423YM10FM1 RNOAAB453W702C1RM1 RNOAAB453W702C1RM1 RNOAAB453W702C1RM1 RNOAAB453W702C1RM1 RNOAAB453W705W14FM1 RNOAAB453W705W14FM1 RNOAAB453W714FM1 RNOAAB453W714FM1 RNOAAB453W714FM1 RNOAAB453W714FM1 RNOAAB453W714FM1 RNOAAB453W714FM1 RNOAAB7741FFM1 RNOAAB774771FFM1 RNOAAB774771FFM1 RNOAAB774771FFM1 RNOAAB774771FFM1 RNOAAB774771FFM1 RNOAAB774771FFM1 RNOAAB774771FFM1 RNOAAB774771FFM1 RNOAAB774771FFM1 RNOAAB774771FFM1 RNOAAB7774771FFM1 RNOAAB77774771FFM1 RNOAAB777477777777777777777777777777777777	A. TAK A. TAK COGNUCA. T. CA. T. C	2
RNOAAB125YE08M1 RNOAAB125YE10FM1 RNOAAB145YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YE08AHM1 RNOAAB3YR05FM1 RNOAAB14YN05FM1 RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB147N05FM1 RNOAAB147N05FM1 RNOAAB147N05FM1 RNOAAB3YM16FM1 RNOAAB3YM16FM1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF127M1 RNOAAB3YF20HM1 RNOAB3YF14FM1 RNOAB3YF14FM1 RNOAB3YF14FM1 RNOAB3YF14FM1 RNOAB3YF14FM1 RNOAB3YF14FM1 RNOAB3YM10FM1	A A	2
RNOAAB125YE10FM1 RNOAAB125YE10FM1 RNOAAB145YE08AHM1 RNOAAB140YN05FM1 RNOAAB140YN05FM1 RNOAAB14VN05FM1 RNOAAB14VN05FM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB145YE10FM1 RNOAAB144YN05FM1 RNOAAB144YN05FM1 RNOAAB144YN05FM1 RNOAAB144YN05FM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB545YM04AHM1 RNOAAB54FVD12FM1 RNOAAB54FVD12FM1 RNOAAB54FV2124FM1 RNOAAB35YF05FM1 RNOAAB455YF124FM1 RNOAAB455YF124FM1 RNOAAB455YF124FM1 RNOAAB455YF124FM1 RNOAAB455YF124FM1 RNOAAB455YF124FM1 RNOAAB455YF124FM1 RNOAAB455YF124FM1 RNOAAB455YF124FM1 RNOAAB4575YF12FM1 RNOAAB4575YF12FM1 RNOAAB4575YF12FM1 RNOAAB4575YF12FM1 RNOAAB4575YF12FM1 RNOAAB4575YF12FM1 RNOAAB4575YF12FM1 RNOAAB4575YF170FM1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB45715FF1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB45712FM1 RNOAAB477171FM1	A A	2

RN0AAA64YH05FM1	
RN0AAB311YB19AHM1	GT-CGC.AT
RN0AAB44YH23AHM1	GT-CGGTAGG
RN0AAA717YI15RM1	GT-CGGTAG
RN0AAB125YA16FM1	GT-CGC.G
RN0AAB437YE21AHM1	GT-CGC.G
RN0AAB266YH16AHM1	
RN0AAA131YF02RM1	
RN0AAA130YE05RM1	
RN0AAA579YK24RM1	
PNOAAB100YP08AHM1	
PNOAAB180VL08EM1	
PNOAAA175VL12PM1	01 °
PNOAAB484VE18EM1	
PNOAAA316VE18PM1	
PNOAAA14VA24PM1	GT_C_ G_ C_
PNOAAA691VK01PM1	
PNOAAB526VTO5AUM1	01 ° 0
DNOAADJ20110JAIMI	ст. с.
DNOAAD4901N2IAAAAI	
DNOAAD290VD02EM1	
DNOAAA2091D03FML	
DNOAAA7271125RM1	
RNUAAA9UIKIUFMI	
RNUAAB201B17AHM1	
RNUAAB5771GUSAHM1	
RNUAAB481AU6AHM1	
RNUAAA1331D03FM1	
RNUAAA5421E07RM1	
RNUAAA601YBU8RMI	GT-CGGTAG-
RNUAAA281YH13FM1	
RNUAAA699YBU4FMI	-TIC-TCTUG. CT
RNUAAA437YA19RM1	.1-CGC-
RN0AAA499YO02FM1	.1C
RNUAAA377YF05FM1	.T-CC
RNUAAA2222YD17RM1	.ATT- TCC TATTTCATGTAATTAAAAATTCCAACTTAGTTACATCGG-GAAAAATAAAATAACCAATTACTAGCTGGCTTTTTTTGATACAAGACTACTAGAACAACTACTAGTAGTAGAACAACTACTAGTAGTAGAAGAACAACTACTAGTAGTAGAAGAACAACTAGTAGTAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA
RN0AAB173YC20AHM1	.ATTTACATTTCATGTAATTACGTCTTTTGATAATTACGAACTTCTACGTTAATTCCTTGG-TACATTCAAGTTGAAAAACAATTACCTGGCTTTTTTTGATACAGTTTTTAACGTCTTTCGAAATAATAGAACTTCTACGTTAATTCGC-GAATTAC
RN0AAB161YD24FM1	.ATTTACATTTCATGTAATTAGATATTACGATATATAGAACTTCTACGTTAATTCCAGGGT_TACATTCAAATTCCT_GGATGAAAAACAATTACCTGGCTTTTTTTGATACAGTTTTTAAGGCTCTTTCGAAATAATAGAACTTCTACGTGGTGATATAATTCGAAATAACAATTACCTGGCTGG
RN0AAB55YM18AHM1	.TTTTACTATTTCATGTAATTAGATATTACGATATATAGAACTTCTACGTTAATTCCAGGGT_TACATTCAAATTCCTGGGT_TACATTCAAATTCGAAATAACAATTACGACTTTTTTGATACAGTTTTTTCATGTAATTCGAAATAATAGAACTTCTACGTTAATTCCAAATTACGACTCAACTTGAAAAT
RN0AAA481YC13RM1	.ATTTACATTTCATGTAATTAAAAATGTCCAACTTACGTTAATTCCTTGTG-TACATTCAAGTTGAAAAACAATTACCTGGCTTTTTTTGATACAGTTTTTAACGCTCTTTCGAAATAATAGAACTTCTACGTTATTCGAAATAACAATTACCTGGCTTTTTTGATACAGTTTTTAACGCTCTTTCGAAATAATAGAACTTCTACGTTGTG-TACATTCAAGTTGAAAATGAAAAACAATTACCTGGCTTTTTTTGATACAGTTTTTAACGCTCTTTCGAAATAATAGAACTTCTACGTTACGT
RN0AAA81YK04RM1	.ATTCACATTTCATGTAATTAAAAATTTCCAACTTACGTTAATTCCTGGGTG-TACATTCAAACAACTTGAAAAAACAATTACCTGGCTTTTTTTGATACAGTTTTTAACGCTCTTTCGAAAAAATTACCTGGCTGCTTTTT
RN0AAA229YJ17FM1	TATTACTATTTCATGTAATTACTTACGTTAATTCCTGGGTG-TACATTCAACTTGAAAATTAAATTGAAAAACAATTACCTGGCTTTTTTTGATACAGTTTTTAAACGTCTTTCGAAACCATCGGTCGCCGTTTTAAATACGCTACCATCGGTG
RN0AAA222YD17FM1	.ATTTACATTTCATGTAATTAAAAATTTCCAACTTACGTTAATTCCTGGGTG-TACATTCAACTTGAAAATTAAATTGAAAAAACAATTACCTGGCTTTTTTTGATACAGGTTTTAACGCTCTTTCTAATGAAAAAATTACCTGGCT
RN0AAA303YG05RM1	.TTTTACTATTTCATGTAATTAGATATTACGATATATAGAACTTCTACGTTAATTCCAGGGT_TACATTCAAATTCCTGGGT_TACATTCAAATTCGAAATAACAATTACGACTTTTTTGATACAGTTTTTTCATGTAATTCGAAATAATAGAACTTCTACGTTAATTCCAAATTACGACTCAACTTGAAAAT
RN0AAA32YB09FM1	.ATTCCCGCTA
RN0AAA474YI20RM1	.ATTTACTATTTCATGTAATTAAAAATTTCCAACTTACGTTAATTCCTGGGTG-TACATTCAACTTGAAAATTAAATTGAAAAAACAATTACCTGGCTTTTTTTGATACAGTTTTTAACGCTCTTTCGAAAAAATTACCTGGCTG-TACATTCAA
RN0AAA373YI20FM1	.ATTTACATTTCATGTAATTAAAAATGTCCAACTTACCTTTCCTGCAGGCG-GGCGGTCGATATGAATGTATAATAGATCAGCAATTAC
RN0AAA434YP23FM1	. ATTTAC-C ATTTCATGTAATTAGGTCTTTTCGAAAAAGATTCCCTGGTG-TACATTCAGGTCACACGGCTATTTTGATACAGTTTTTTGATACAGTTTTTTCGAAAGAAGATATTAGAACATCCCTGGGTG-TACATTCCCAGGTGCTATTCGAAAAAACAATTCGCCGAGGTTTTTTGATACAGTTTTTGATACAGTATTAGAACAAGTTCCCAGGTGCTATTCGAAAAAAACAATTCGCGGAGAAAAAACAATTCGCGAGATATAA
RN0AAA462YN08FM1	.ATTTACTATTTCATGTAATTAAAAATGTCCAACTTACGTTAATTCCTTGTG-TACATTCAACTTGAAGATTATA
RN0AAA474YG15FM1	.ATTTACTATTTCATGTAATTAAAAATTTCCAACTTACGTTAATTCCTAGGTG-TACATTCAACTTGAAAATTAAATTGAAAAACAATTACCTGGCTTTTTTTGATACAGTTTTTAAAGCTCTTTTCGAAATAATAATCCCTGGTG-TACATTCAAATTCCAAATTACACTCTACCTCAACTACTAATTCCAAAATTCCAAAAAA
RN0AAA481YC13FM1	.TTTACANTTTCATGTAATTANAATTATCCAACTTACGTTAATTCCGAGGT-AACATTCAACTTGAA-AATTCAATTCGAAAAACCATTTTTGATACGAGTTTTTTGATACGAGTTTTTTGATACGAGTATATAGAATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGATTCGAAAAATTAGAATTGAAATTGAAATTGAAATTAGAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAAATTAGAATTGAAAAATTAGAATTGAAAATTGAAAATTGAAAATTGAAATTGAAAATTGAAAATTGAAAAATTGAAAAATTGAAAAATTAGAATTGAAAAATTAGAATTGAAAATTAGAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAAATTGAAAAATTGAAAAATTGAAAAATTGAAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAA
RN0AAA556YI14FM1	.ATTTACAATTTCATGTAAGTAAAAATTTTCCAAC
RN0AAA76YA17RM1	.ATTTACATTTCATGTAATTAAAAATTTCCAACTTACGTTAATTCCTTGTG-TACATTCAACTTGAAAATTGAAAATCAAAAACAATTACCTGGCTTTTTTGATACAGTTTTTAACGCTCTTTTCGAAAAATTAAGTGAAAATTGAAAAT
RN0AAA94YM05RM1	.ATTTA
RN0AAB55YM18FM1	.ATTTACATTTCATGATACAGTTTTTGATACAGTTTTTCGATACAGATTACGATAAGAGTTTTTCCAACAGTTTTTCGATACAGATTACAGALTACAGALTAGALACAGALTACAGALTAGALACAGALTACAGALTAGALACAGALTAGALACAGALTAGALACAGALTAGALACAGALTAGALACAGALTAGALACAGALTAGALACAGALTAGALACAGALTAGALACAGALTAGALACAGALTAGALACAGALTAGALACAGALTAGALACAG
RN0AAB56YP24FM1	. ATT TAC TATT TCATGTAATTAAAAATTTCCCAACTTACGTTAATTCCCGGGGGGCACAATCCACTCGAAAATA TAAATTGAAAAACAATTACCGGCTTTTTTTGATACCGGT
RN0AAA513YA20RM1	TATTTACTATTTCATGTAACTGCCAATTTGCCAATTT
Box 1	

Supplementary Figure 4.2.1. LOCAL BLAST search of newly TRF satDNA families with RepeatScout library repeat families published in Wang et al 2008. **a)** results for search with Cl4 monomer **b**) results for search with Cl5 monomer

a) results for search with Cl4 monomer

151	7e-038
151	7e-038
151	7e-038
143	2e-035
127	1e-030
127	1e-030
125	4e-030
	151 151 143 127 127 125

	Dotplot						
	Percentage: 60); Window: 30;	Min Quality: 1				
	Filter Top: 2 ->	151, Bott om:	0 -> 15				
	Seq1(1>627)		Seq2(1>181)		Total		
	R=482.seq		CI4 monom.se	eq D	iagonals		
	(1>627)		(1>181)		56		
	-						
	10	20 20	00 30	00 4	00 5	00 6	00
100							
	\searrow						

Percentage: 6 Filter Top: 1 -:	0; Window	∴ 30; Min C 0m: 1 -> 75	Quality : 1					
Seq1(1>992) R=135.seq	- 20, 20110	Seq2 Cl4 r	?(1>181) monom.s	eq	Diag	Total jonals		
(1>992)		(1>18	81)			89		
100	200	300	400	500	600	700	800	900
			1					



Dotplot Percentage: 70; Win Filter Top: 1 -> 73, E	ndow: 30; Min Quality: 1 3ottom: 1 -> 14																		
Seq1(1>11954) R=0.seq	Seq2(1>181) Cl4 monom.seq	Total Diagonals																	
(1>11954)	(1>181)	95																	
500	1000 1500	2000 2500	3000	3500 4000	4500	5000	5500	6000	6500	7000	7500	8000	8500	9000	9500	10000	10500	11000	11500
									\backslash		$\langle \rangle$,				







b) results for search with CI5 monomer

R=1877 TRF=0.000 NSEG=0.261 Mid	172	4e-044
R=66 TRF=0.034 NSEG=0.471 HighA	131	1e-031
R=140 TRF=0.000 NSEG=0.215 Mid	92	1e-019





	Dotplot										
	Percentag	e: 70; \	Nindov	v: 30; N	lin Quality	v: 1					
	Filter Top:	1 -> 11	IO, Bot	tom: 1	-> 6						
	Seq1(1>10	025)		S	Seq2(1>27	75)		Total			
	R66.seq			C	C5.seq		C	iagonals			
-	(1>1025)			(1>275)			50			
	100) 2	00	300	400	500	600	700	800	900	1000
100											
200											
200						`					

Supplementary Figure 4.2.2. Alignments of 9 clusters obtained by TRF. a) alignment of cluster 1; b) alignment of cluster 2; c) alignment of cluster 3; d) alignment of cluster 4; e) alignment of cluster 5; f) alignment of cluster 7; g) alignment of cluster 8; h) alignment of cluster 9; i) alignment of cluster 10

a) alignment of cluster 1

0	1 10	ນ 20	зр	40	50	60	70	ap	ခုဝ	100	110	120	130	140	150	160	170	160	190	200
	ARTTARTIGA	G TG TT T CTAR	G TAG AATGAC		AA-ATTIGCAA	GAA	TUAKS TUS CTAC		GALTARCOS TTUE	G AAAA TA TCG	GCAAAAA-	TT TAGECTTG TCAI		ATTIG -	RETAAACCAAACTTT	-CTTCATTA	TTTCCARCTT	TTC	GG AGT TATT TOCTTAG	GG
1. ChLG4_R180280874RC_C13 2. ChLG4_R180280874RC_C17	AATTAA	g tg tt t ct t ak g tg tt t ct t ak	GTANAATGAC		AA-ATCIACAA	GAA	TCACATCG CTAC		GETTAACCE TFC	g am <mark>g</mark> ata tog g am <mark>g</mark> a ta tog	TCAAAAA-	TATAGTC TCG TAAL	A	AAATA T	PTCAACTAAACTTA PTCAACTAAACTTA	-CGTCATTA	TCIG TTG AT TG	TTT	GG AGCTATTTCCTTA GG AGCTATTTCCTTA	
3. ChLG4_R180280874RC_C7	AATTAA	g tg tt t ct t m	G TANAA TGAC	-CGGCGGAATC	AA AT CTACAR	GAA	TCAGATCG CTAC-		GGTTAACOS TTO	GARGATATOS	CAAAAA	TATAGTCTCGTAA	A	AAATA	TCARCTARACTT	CGTCATTA	TCTGTTGATTG	TTT	GG AGCTATTTCCTTA	á –
4. ChLG4 R180280874RC C2	AATTAA	GRGTCTAA	GTAAATGAC	- CG CAGG AAT C	TAA AT CTG CAA	GAA	TCAGATCG CTAC		GGCTAACOG CTCG	GAAGATATOG	TCAAAAA	TATAGTCTCGTAA	AA	AAATA 1	TTCARCTARACTTA	CGTCATTA	TCTGTTGATTG	TTT	GAGCTATTTCCTTA	4
5. ChLG4_R180280874RC_C4 6. ChLG4_R180280874RC_C9	AATCAM	g 19 TTTCFAM G 19 TTTCFAM	GTAAATGAC		AA - AT CIG CAA	GAA	TCACATCG CFAC		GECTAACCE TTCC	E AAGATATOG	TCAAAAA-	TADAGTCTCGTAA		AAATA-1	TTCAACTAAACTTA	-CGTCATTA	TCTGTTGATTG	TTT	GG AGCTATTTCCTTA GG AGCTATTTCCTTA	4
7. ChLG4_R180280874RC_C5	ARTIGA	GIGTTTCTAM	GTANAATGAC	CGGCGGAATC	AA AT CTG CAR	GAA	TCAGATCG CTAC		GGCTAACOS TTO	GAAGATATOG	CRAAAA	TATAGTCTCGTAA	AA	AAATA	TTCARCTARACTT	CGTCATTA	TCTGTTGATTG	ттт	GG AGCTATT TC CTTA	á –
8. ChLG4_R180280874RC_C19	AATTAA	GIGICTAM	G TAG AA TGAC		CAA AT CIG CAA	GAA	TCAGATCG CAAC		GCTAACOG TTO	GARGATATOG	TTAAAAA	-AIGGTCTCGTTA	hA	AAADG - 1	TTCAACTBAACTTA	-CGTCATTA	TCTGTCAACTG	TTT	GGAGCTATTTCCATA	4
10. Chi G4. R180280874RC C10	ARTIGA	g 15 TTTCTAM	GTARAATGAC		AA AT CTG CAA	GAG	GCAGATCG CTAC		GCTAAC STTC	GAAGTTATCG	TCAAAAA	AAIGGTCTTGTTA	A	AAATG - 1	GTCAACTAAACTTA	-CGTCATTA	TCTGTCTATTT	TTT	GASCTATTTCTTA	.
11 ChLG4_R180280874RC_C15	AATTAA	g tg tt t c <mark>c</mark> am	G TAAATGAC	CGGCGGAATC	AA AT CTG CAA	ga <mark>g</mark>	GCAGATCG CTAC		G <mark>G</mark> CTAAC <mark>I</mark> G TFCG	g ar <mark>g t</mark> tatog	TCAAAAA	AAIGGTCTTGTTA	A .	AAA DG - 1	GTCARCTAAACTTA	-C <mark>G</mark> TCATTA	t <mark>c t_{g t}c t</mark> at t	TT	R S AGCTATT T TT TTAT	4
12. ChLG4_R180280874RC_C12	ATTTAM	g ig it i c <mark>e</mark> am	G TAAAATGAC		RA-AT CIG CAA	GAG	GCAGATCG CTAC		GCTAAC GTTCG	GAAGTTATCG	TCAAAAA	TATAGTC TCG TTAL	AA	AAA IG - 1	ETTCAACTAATCTTA	-CCTCATTA	TCTCTCTATTT:	TT	GG AGT TATT TC CCT A	4
14. ChLG4_R180280874RC_C10	AATTGA	GIGTTTCTAM	GTANAATGAC		AA AT CTACAA	GAA	TCAGATCG CTAC		GGTTAACOS TTOS	GARGETATOS	TCRARRA-	GATAGECTCGTEA	A	AAATG - 1	TCARCTARACTI	CGTCATTA	TCTGTCTATTT	TT	GGAGTTATTTCCCTA	é .
15. ChLG4_R180280874RC_C11	AATTAA	g to tt t c <mark>c</mark> am	CTANANTGAC	CGGC	AA-AT CI <mark>A</mark> CAA	GAA	TCAGATCG CTAC		G <mark>C</mark> TAACCS TTC	SAN <mark>G</mark> ATATOS	TCAAAAA-	AAIGGTCTCCTTA	A	A AA BG - 1	PCTCARC <mark>T</mark> ARACTT	-C <mark>C</mark> TCATTA	t <mark>cict</mark> ctatt:	TT <mark>T</mark>	GRAGTTATTTCCTTA	4
16. ChLG4_R180280874RC_C18 17. ChLG4_R180280874RC_C8	AATTGA	g tig tit t ceam g tig tit t ceam	GTANAATGAC	CGGCGGAATC	BABATAT CPACAA	GAA	TCAGATCACTAC		GCTAACCE TTCE GACTAACCE TTCE	gargatatcg gargatat	TCAAAAA	AAIG CPC TCG TPAC AATG GPC TCG TPAC		AAANG - 1 AAANG - 1	PCTCAACTAAACTTA PCTCAACTAAACTTA	-CGTCATTA	TCTGTCTATTT TCTGTCTATTT	TT T	GAGTTATG TCATTA CAGTTATG TCATTA	4
18. ChLG3 1 R180292662 C4	AATTAA	GTGTTTCCAA	GTAAAATAAC	CAGCEGAATC	CAA AT TTG CAA	GAA	TCAGATCG CTAC	· i	GACTAACCATTCO	GARGATATOS	TCAAAAA	TATCGTCTAGTTC	AA	AAA DG - 1	CTCARCTARACTTA	TGTCATTG	TCAGTCAATTT	TTT	GGAGTTATATCCTTA	á –
19. ChLG3_1_R180292662_C7	AATTAA	g te tt t c <mark>e</mark> aa	G TAAAATAAC		CAR AT TTO CAR	GAA	TCACA TCG CTAC		GACTAACCATTC	GAR <mark>G</mark> ATATCE	TCAAAA	TAICCTCTACTCC	AA	A <mark>AA</mark> IIG - 1	PCTCAACTAAACTTA	TGTCATTG	T CRGT CAA T TT	TTT.	gg agt tat <mark>a</mark> tc ctt a	4
20. ChLG3_1_R180292662_C6 21. ChLG3_1_R180292662_C3	AATT AA	g tg tt t ccaa g tg tt t ccaa	GTAAAATAAC		CAA - AT TTG CAA CAA - AT TTG CAB	GAA	TCAGATCGCTAC		GACTAACTATTCG	g a a <mark>g</mark> a ta tog g a ag <mark>a</mark> a ta tog	TCAAAAA-	TAIGGTCTAGTTG TAIGGTCTAGTTG	AA	A AA TG - 1 A AA TG - 1	PCTCAACTAAACTT	TGTCATTG TGTCATTG	TCAGTCAATTT TCAGTCAATTT	TT T	GG AGT TATATC CTTAT GG AGT TATATC CTTAT	4
22. ChLG3 1 R180292662 C8	AATTAA	GIGTTTCCAA	GTAAAATAAC	-CAGCGG AATC	CAA GTTTG CAA	GAA	TCAGATCG CTAC	· i	GACTAACCATTC	GARGATATOG	TCAAAAA	TAIGGTCTAGTTA	A	AAATG -C	CTCARCTBAACTTA	TGTCATTG	TCAGTCAATTT	TTT	GGAGTTATATCCTTA	i -
23. ChLG3_1_R180292662_C5	AATTAA	GTGTTTCCAA	GTAAAATAAC		CAA AT TTG CAA	GAA	TCAGATCG CTAC		GACTAACCATTC	BAAGATATCG	TCAAAAA	TAIGGTCTAGTA	AA	AAA TG - 1	PCTCAACTAAACTTA	TGTCATTG	T CAG TT AA T T T	TTT	GG AGT TAT <mark>A</mark> TC CTT A	4
24 Chi G3 1 R180292002 C2	GATTGA	g tg tt t ctam	G TAAAATGAC		CAA AT CITCAR	GAA	TCAGATOGOTAC		GACTAN COTTO	GAAGATATOS GAAGATATOS	CAAAAA	TATESTCTASTTA	A	AAADG - 1 AAADG - 1	CTCARCTARACTTA	TGTCATTA	TCIGTCAATTT	TTT	GG AGT TACTOTAL GG AGT TAG TGT CTT A	4
26. ChLG3_1_R180293313_C3_	GATTGA	g ig ti t ci <mark>t</mark> a	g ta a aa tgac	CAGCGGAATC	AA -AT TTG CAA	GAA	TCAGATCG CTAC		GACTAAAOGTTCG	AAAGATATOG	TTAAAAA	TAIGGTCTTGATA	A	A <mark>AA</mark> IIG - 1	ICT <mark>CAAT</mark> CAAACATA	- TGTCATTA	t <mark>ctgt</mark> caa <mark>t</mark> tt:	TT	GGAGTTA <mark>G</mark> TT <mark>T</mark> CTTA <mark>I</mark>	4
27. ChLG3_1_R180293313_C12	GATTAA	g tig tit t ctaat	GTAAAATGAC		CAA AT TTG CAA	GAA	TTAGATCG CTAC		GACTAACCE TTC	SAAGATATOS	TCRAAAA	TATEGTCTCCATA	A		PCTCARGCAAACTTA	TGTCATTA	TCTGTCAATTT TCTGTCAATTT	TTT	GG AGT TAGT TTCTT AT	4
29. ChLG3 1 R180293313 C7	TATTAM	g të tt t ctaa	GTAAATGAC		CAA -AT TTG CAA	GAA	TCACATCG CTAC		G ACCAACOG TTO	GARGATATOS	CAAAAA-	TAICGTCTCCATA	A	AAADG - 1	CTCARCTARACTTA	-CGTCATTC	TCTATAAATTT	TTT	GG AGATAGT TTTCAT	á –
30. ChLG3_2_R180296434RC_C2	GATTGA	GIGTTTCTAA	g ta a aa tga a		AA - AT TTG CAA	GAA	TCAGATCG TRAC		GACTAACCE TTO	GARGATATCG	TCAAAAA	TAIGGTCTCGTTA	AA	AACTIG - C	CTCAACTAAACTTA	-CGTCATTA	T <mark>CIGT</mark> CAA <mark>T</mark> TT.	T <mark>C T</mark>	GG AG <mark>A</mark> TA <mark>G</mark> T T <mark>T</mark> CTT AI	4
31. ChLG3_1_R180293313_C8 32. ChLG3_2_R180296434RC_C9	GATTGA	STGTTTCTAM	G TARAA TGAC		CAA AT TTGCAA	GAA A	TCAGATCGCTAC		GACTARCOS TTOS GACTARCOS TTOS	GARGATATCG GARGATAT	CAAAAA	TATAGECTEGTEA TATAGECTEGTEA	A	AAATIG - 1 AAATIG - 1	PCTCAACTAAACTTA PCTCAACTTGAACTTA	-CGTCATTA	TCTGTCACTTT TCTGTCAATTT	TTT	GG AGT TAG T T T T TT AT GG AGT T TG T T T C TT AT	
33. ChLG3 1 R180293313 C5	GATTAM	g to t <mark>s</mark> t c e am	G TAAATGAC		CAA AT TTO CAA	GAA	TCACA TCG CTAC		GACTARCOS TTO	GARGATATOS	TCAAAAA	TATAGTC TOG TTA	A	AA DG - 1	CTCAACTAAACTTC	CGTCATTA	TCT <mark>GT</mark> CAATTT	TTT	GG AGT TAG T TTCTT A	á –
34. ChLG3_1_R180293313_C4	GATTGA	g ts tt t ctak	GTAAATGAC		CAA - AT CTG CAA	GAA	TCAGATCG CTAC		GACTANACE TTCC	GAAGATATCG	TCAAAAA	TATCCTCCATA	AA	AAATG - 1	PCTCAACTAATCTTA	-CATCATTA	TCTATCA TTTT	TT T	GG AGT TATT CC CCAAI	4
36. ChLG3 1 R180293313 C11	GATTGA	GIGTTTCT	G TAAAATGAC	-CGGCGGAATC	CAA AT TTG CAA	AAA	TCAGATCG CTAC		GACTANACG TTCS	GAAGATATO	TCAAAAA	TAIGGTCTCGATA	A	AAA DG - 1	CTCARCTARACTTA	CGCTATTA	TCTATCAATTT	TTT	GG AGT CATT CACCTAL	é .
37. ChLG3_1_R180293313_C6	GATTGA	g ig ti t cear	g ta k aa tga.c	CGGCGAATC	CAR-AT CTG CAR	GAA	TCAGATCG CTAA		GACTARCOS TTOS	G AA <mark>G</mark> AT <mark>T</mark> TCG	TCRAARA	T AIGGT CTCGCTAC	A	A <mark>AA</mark> BG - 1	ect <mark>carg t</mark> aaactt a	-CATTA	t <mark>ctst</mark> caa <mark>t</mark> t t	TT T	gg agt tatt c cc <mark>c</mark> tat	4
38. ChLG3_2_R180294231_C5	AGTTGA	g tg tt t ctaa g tg tt t ctaa	G TAAAATGAC	CGGCGGAATC	AA AT CTG CAA	GAA	TCAGATCGCTAC		GACTAACCE TTCE	G AA <mark>G</mark> ATATOG KE BA <mark>G</mark> ATATOG	TCAAAAA	AATGGTTTCGTTA	A	AAATG - 1	PCTCARTTAAACTTA	-CGTCATTA	TCTGTCAATCT TCTGTCAATCT	TTT	GAAGTTATT-TCTTA CONTATT-TCTTA	
40. ChLG3_2_R180294231_C2	AGTTGA	GIGTTTCTAA	GTAAAATGAC		AA AT CTG CAA	GAA	TAGATCTCTAC		GACTAACOS TTO	GARGATATOS	TCAAAA	AAIGGTTTCGTTA	AA	AAATG - T	CTCARCTARACTT	-CGTCATTA	AT TG TCAATCT	TTT	GAAGTTATT TCTTA	A
41 ChLG3_2_R180294231_C6	AGTTGA	g tg tt t cfaa	GTAAAATGAA		AA AT CTG CAA	GAA	TCAGATCTCTGC		GACTAACCE TTC	BAAGATATCG	TCAAAAA	AATTATT TOG TTAK	AA	AAA'DG - 1	PCTCAACTAAACTTA	-CGTCATTA	TCIGTCAATCT	TT	AAAGTTATT-TCTTAC	A
42. ChLG3_2_R180294231_C8 43. ChLG3_2_R180294231_C4	AGTTGA ATTAM	g tg tt t ctam g tg tg tc tctam	G TAAAA TGAA	CGGCGGAATC	TAA - AT CTG CAA TAA - AT CTG CAA	GAA GAA	TCAGATCTCTGC		GACTAACOS TTC GACTAACOS TTC	SAAGATATCS SAAGATATCS	TCAAAAA-	AATTATT TOG TTAC AATTATT TOG TTAC		AAATG - 1 AAATG - 1	PCTCAACTAAACTTA PCTCAACTAAACTTA	-CGTCATTA -CGTCATTA	TCIGTCAATCT TCIGTCAATCT	TTT TTT	AAGTTATT-TCTTAC	A
44. ChLG3_2_R180294231_C9	AGTTGA	GTGTTTCFAA	GTAAATGAC		AA - AT CTG CAA	GAA	TCAGATCG CTAC		GACTAACOS TTO	g Tag atatog	TCAAAAA	TAIGATC TCG TTA	AA	AATG - 1	PCTCAACTAAACTCA	-CGTCCTTG	TCTGTCAATTT	TTT	AACTTAATT-TCTTAC	G
45. ChLG3_2_R180294231_C3	AGTTGA	g tig tit t ctaa	GTAAAATGAC		AA AT CTG TAB	GAA	TCAGATEG CTAC		GACTAACCATTCG	g tag atatog	TCRARRA-	TATEGTCTCGTTA	A	AAATG - 1	PCTCARCTRARCTT	-CGTCATT	TCTGTCTATTG	TTA	GG AGCTATTGTCTTAT	6
47. ChLG3_2_R180296434RC_C6	AATTGA	g to tt t ctam	G TAAAATGAC		CAA AT TTO CAA	GAA	TCAGATCG CTAT		GACTAACOS TTC	SAAGATATOS	TCAAAAA	TAICGTATOGT	A	ACTG - 1	CTCAACTAAACTT	-CGTCATTA	TTT <mark>GT</mark> CAA <mark>T</mark> TT	TTT.	GG AGATAG T TTCTTA	á –
48. ChLG3_2_R180296434RC_C4	AATTGA	g tg tt t ctam	G TAAAATGAC	CGG <mark>A</mark> GG AATC	AA - AT TTG CAA	GAA	TCACATCG CTAT		GACTAACOS TTC	SAA <mark>G</mark> ATAT <mark>T</mark> G	TCAAAAA-	T AIG CT C T C G T T A	AA	AAA TG - 1	PCTCAACTAAACTTA	-C <mark>G</mark> TCATTA	t Cigtcaatt t	TTC	gg agt ta <mark>g</mark> t t <mark>t</mark> cttat	4
49. ChLG3_2_R180296434RC_C7 50. ChLG3_2_R180296434RC_C5	AATTGA	g 19 TT T CPAM G 19 TT T CPAM	GTANAATGAC		BA-AT TIG CAA	GAA	TCAGATOG CTAT		GACTAACOS TTC	A A A A TATT	TCAAAAA-	TAIG CTC TCG TTAI TAIG CTC TCG TTAI	A	A AA 119 - 1 A AA 119 - 1	CTCARCTAAACTTA	-CGTCATTA	TOTOTCAATTT	TTC	GG AGT TAG T TTCTTAT GG AGT TAG T TTCTTAT	
51. ChLG8_R180289124RC_C5	AATTAA	ar g tt <mark>c</mark> ct <mark>c</mark> ak	g ta a aa tga t	CGGCGAAATC	CAA - AT TTG TAA	AAA	TCAGATCG CTAC		GACTAAC <mark>T</mark> E TTO	GAAGATATCG	TCAAAAA	TTT TGTCIG GT TA	AA	A AA DG - 1	ATCAACTAAACTTA	TG TCATTA	t <mark>ct<mark>g t</mark>caa<mark>t</mark>t t</mark>	TT	gg ag <mark>c</mark> tatt t tt tt oc	
52 ChLG3 2 R180296434RC_C8	ARTIGA	g ts tt t ctam s ts tt t ctam	G TAAAATGAC		CAA AT TTG CAA	GAA	TCAGATCG CTAC		GACTAACCE TTCC	G AAG ATAT <mark>T</mark> G X2 TAG A TATCC	TCACAAA	TATAGTCTCGTTA	A	AAATG - 1	PC TCAACTAAA CTTA	-CGTCATTA	TCTGTCAATTT TCTGCCAATTT	TTT TTT	GG AG <mark>A</mark> TATT T TT AG GG AG A TATT T TT AG	-
54. ChLG7 R180286742 C3	ATTAA	GIGTTTCTAM	GTAAATGAC		CAA ATCIG CAA	GAA	TCARG TCG TFAC		CACTAACOS TTO	G TAG ATATOS	TCAAAA	TAIGGTCTCGTTA	AA	AAA IG - I	CTCAACTAATCTT	-CGTCATTA	TCGGTCTAATT	TTT	AGAGTTATTTCTTA	G
55. ChLG7_R180286742_C5	ATTAA	g tg t <mark>o</mark> t ctak	GTAAAATGAC		CAA AT CIG CAT	GAA	CAGATOS CTAC		GACTAACCTTTC	s t ag a ta tog	TCAAAAA	TATTGTC TCG TTAC	AA	AAA DG - 1	PCTCAACTAAACTTA	CATCATTA	TCTATCAATTT	TTC	GGAGTTATTTCCTTA	G
57 Chi G8 R180287672RC C13	GTTAM	g 15 TT T CTAA G 15 TT T CTAA	G TAG AT TGAC		AT AT CTG CAA	GAA	TCARG TOG CTAC		GACTANCOS TTOS	g a rg ata tos G a rg ata tos	TTAAAAA	TATAGTCTTG TAA	A	AAADG - 1 AAADG - 1	TTCAACTAATCITA	-CGTTATTA	TCIGCAAATTT	TTT	GG AGCTATTCTGCTAT GG AGCTATTCTGCTAT	â
58. ChLG8_R180287672RC_C4	GTTAM	g ig ti t ceaa	g tag a <mark>t</mark> tga.c	T GGCGG AATC	Fat C IG CAR	GAA	TCARG TOG CTAC		GACTARCOS TTOS	g ar <mark>g</mark> atat cg	TTAAAAA	TATAG <mark>T</mark> C TTG TAA	2a.A ;	A AA IIG - 1	e t tcaac <mark>t</mark> aa t ctt a	-C <mark>G</mark> T <mark>T</mark> ATTA	T <mark>C</mark> T <mark>G CA</mark> AA <mark>T</mark> T T	TT	gg ag <mark>c</mark> t att <mark>ctg c</mark> t at	A
59. ChLG8_R180287672RC_C3	GTTAA	g tig tit t ctaa	G TAG AT TGAC		AT AT CTG CAR	GAA	TCARG TCG CTAC		GACTAACCE TTCG	g aa <mark>g</mark> atatog	TTAAAAA	TATAGTCTTGTAA	A	AAATG - 1	TCAACTAATCTTA	- CGTTATTA	TCTGCAAATTT	TTT	GG AGCTATTCTGCTAT	A
61. ChLG8_R180287672RC_C5	GTTAM	GIGTTTCTAM	G TAG AT TGAC		AT AT CTG CAA	GAA	TCAAG TOG CTAC		GACTAACOS TTO	GARGATATOS	TTAAAAA	TATAGTC TTG TAA	A	AAATG - 1	TTCARCTARTCTT	-CGTTATTA	TCTCCAAATTT	TTT.	GG AGC TATT CCTCTAL	c .
62. ChLG8_R180287672RC_C16	GTTAA	GTGTTTCPAN	G TAG AT TGA.C		AT AT CTG CAA	GAA	TCARG TCG CTAC		GACTAACCE TTO	GAAGATATCG	TTAAAAA	TATAGTC TTG TAA	AA	AAA TG - 1	PTCAACTAATCTTA	-CGTTATTA	TCTGCAAATTT	TTT	gg ag c tatt c c tc tat	G
64 Chi G8 R180287672RC C-7	GTT AM	g tg tt t ctaa g tg tt t ctaa	G TAG AT TGAC		TAT AT CTG CAA	GAA	TCAGGTCGCTAC		G AG - AACOS TTOS G ACT AACOS TTOS	G AAG ATATOS IS AAG ATATOS	TTAAAAA	TAIGGTC TCTTAA TATAGTCTTGTAA		A A - 11G - 1 A A A 11G - 1	PTCAACTAATCTTA PTCAACTAATCTTA	-CGTTATTA -CGTTATTA	TOTOCCARTTT	TTT TTT	GAGCTATTCTAT GGAGCTATTCTGCTAT	G
65. ChLG8_R180287672RC_C12	ATTAA	g tg tt t ctam	G TAAAATAAC		AA -AT CTG CAA	GAA	TCAC TCG CTAC		GACTAACOS TTO	GAA <mark>G</mark> ATATOG	TTAAAAA	TATAGTC TTG TAA	A	AAA IG - I	TTCAACTAATCTTA	-CGTTATTA	T <mark>C</mark> T <mark>C</mark> CCAA <mark>T</mark> TT	TT T	gg ag <mark>c</mark> tatt ctg c ta t	A
66. ChLG8_R180287672RC_C7	GTTAA	GTGTTTCTAM	GTAAAATGAC	CGGCGG AATC	AA AT CTG CAA	GA <mark>G</mark>	TCAGG TCG CTAC		GACTATCOSTTCO	GAAGATATOG	TTAAAAA-	TATEGCCTCGTAA	A	AAATG - 1	PTTCARCTARTCTTR	AGTCATTA	TCTGCCARTTT	TTT	GG AGCTATTCCTAT	
68. ChLG8_R180287672RC_C6	GTTAM	g ig it i ci t a	G TAAAATGAC		AA AT CIGCAA	GAA	TTAGG TTG CTAC		GACTAACOS TTO	GARCATATOS	TCAAAAA	TAIGGECTEGTAA	A	AAABG - 1	TTCGACTAATCTTA	-CGTCTTA	TATCCCARTT	TTT.	GG AGATATTTC CTAT	G
69. ChLG8_R180287672RC_C17	GTTAM	g tg tt t ct <mark>t</mark> ak	g ta a aa tgac		TAA - AT CIG CAA	GAA	T TAG G T T G CTAC		GACTAACCE TTCE	GAAGATATCO	TCAAAAA	TAIGGTCTTGTAA	AA	AAA IIG - I	e <mark>t teg</mark> ac <mark>t</mark> aatctt a	-C <mark>G</mark> TC T TTA	T AIG CCAR <mark>T</mark> TT	TT	gg ag <mark>a</mark> t att to <mark>g e</mark> t a <mark>t</mark>	G
70. ChLG8_R180287672RC_C8 71_ChLG8_R180287672RC_C19	GTTAA GTTAA	g 115 TT T CTAM 6 TC TT T CTAM	GTANARTGAC		AA AT TGCAR	GAA	TCAGG TCG CTAC		GACTARCOS TTOS GACTARCOS TTOS	GARGATAT <mark>R</mark> G GARGATAT	CAAAAA	TATGGTCTTGTAA TATGGTCTTGTAA	A	A AA TG - 1 A AA TG - 1	TCARCTRATCTTA	-CGTCATTA -CGTCATTA	TCIGCCARTT TCIGCCARTT	TTT TTT	GG AGCT ATTCCTTTAT GG AGCT ATTCCTTTAT	G C
72. ChLG8 R180287672RC C-8	GTTAM	GIGTTTCTAM	GTANATEAC	TG TCGG AATC	AA-AT CTG CAA	GAA	TCAG TOG CTAC		GACCAACCE TTO	GARGATATCS	TTAAAAA	TAIGGTCTCGTTM	AA	AAA DG - 1	TCAACAAAACTTA	-CGTCATTA	TETECEAATTT	TTT	GCC GTATTCC TGTA	6
73. ChLG8_R180287672RC_C-5	GTTAA	g Tatt t CPAM	GTAAATGAC		AA AT CIG CAA	GAA	TCAGG TCG CTAC		GACTAACCAFFC	GAAGATATOG	TTAAAAA	TAIGGTCTCGTTA	AA	AAATG - 1	PTCAACTAATCTTA	AGTCATTA	TCTCTCAACTT	TT T	GG AGCTACT TCTTA	GG
75. ChLG8_R180287672RC_C-8	GTTAM	g is titician g is titician	NG TAAAA TGAC		AA ATCIGCAA	GAA	ACAGG TC CTAC		GACTAACOS TTCS	SAR ATATOS	CAAAAA	TAIGGTCTCGTTA	AA	A AA DG - 1	TCAACTAATCITA	- AGTCATTA	TCTCAACTT TCTCTCAACTT	TTT	GGAGCTACTTCTTA	G
76. ChLG8_R180287672RC_C9	GTTAA	g tg Ct t ct a a	GTAGAATTAC	GGCEBAATC	TAC AT CTG CAA	GAA	TGAGG TOG CTAC-		GACTAACCE TTC	GAZGATATOG	TCAAAAA	T AIGGT CTCGT T A	AA	A AA DG - 1	TCAACTAATCTT	AGTCATTA	TCTCTCAACTT	TT	gg ag <mark>c</mark> t act tc t tt a	G
77. ChLG8_R180287672RC_C20 78. ChLG8_R180287672RC_C14	GTTAA GTTAA	G TG CFT CFAX	G TAG ART AC	GGC BAATC	ACAT CTG CAR	GAA	TGAGG TCG CTAC		GACTAACCETTCE	GAAGATATCG	TCRAAAA-	TATCGTCTTGTTA		AAATG - 1 AAATG - 7	ETCARCTRATCTT	-CGTCATTA	TOTOCAATTT	TTT TTT	GG AGC TATT CTTCTAT GG AGC TATT AT CTTCTAT	Ģ
79. ChLG8 R180287672RC C-4	GTTAM	GIGTTTCTAA	g ta a aa t at c		AA AT CIG CAA	GAA	TCAGG TCG TRAC		GATTAACOS TTO	GARGATAT	TCAAAAA	TAIGGTCTTGTTA	AA	AAA DG - 1	PCTG A AGT AAACTT	CATCATTA	TCTCCCARCTT	TTT	GGAGCTATTCCTCTA	G

80. ChLG8 R180287672RC C-2	G TT A AG IG IT I CTAROG IA R AA T AT C	- TGGCGGAATCTAA - ATCTG CAAGAA	-TCAGG TCG TRAC	G AT TAACOS TTOGG AR <mark>G</mark> A TAT <mark>T</mark> S TCAARAA - T AIG C TTG T T A CAA	AAATG	- TOT <mark>G ANG T</mark> ARACTTA-CATCATTAT CTCCCAACT IT T	GGAG <mark>C</mark> TATT <mark>C</mark> C TC TA <mark>T</mark> G
81. ChLG8 R180287672RC C10	GTTARG IG TTTCTARCG TARAATATC	T GGCGG AATC T AA -AT C TG CAAGAA	-TCAGGTCGTCAC	GA <mark>T</mark> TARCES TTEGE AA <mark>G</mark> ATAT <mark>T</mark> E T ERAAAA -T A IG G T ETTE T TAE A <mark>A</mark>	- AAA IG	- TCICARCTARACTTR-CATCATTATCTCCCARCTTTT	GG AGCTATTCC TCTATG
82. ChLG7 R180286742 C4	ATTGAG TG T <mark>C</mark> T <mark>T</mark> TA ACG TAG AA T <mark>A</mark> A <mark>T</mark>	CGGCG R AATC CAA - <mark>G</mark> T CTG TAAGAA	TCAGATCG CTAC	G AC TAR <mark>G</mark> OF TTCGE <mark>T</mark> ARA TATOS <mark>T</mark> CRA <mark>G</mark> AR - T RIG G T C TOG T T R CAR		-TCTCAACTAATCTTA-CGTCATTATTTGTCTAATTTTT	EGAGTTATTTCTTATG
83. ChLG7 R180286742 C6	AT TGAG IG TT I CT <mark>G</mark> ACG TAG AA TGA <mark>A</mark>	CGGCGAAATCCAA GTTTGCAAGAA	TCAGATTG CTG C	G ACTARCOS TECGS TAG ATATOS TCARAAA - TATG G TC TOG TTACAA	AAADG	-TCTCAACTAATCTTA-CGTCATTATCTGTCTAATTTTT	A GAGTTATTTC T TTA T G
84. ChLG7 R180285670RC C4	GATTAAG TG TT T CTAACG TAG AA TGAC		-TCGGATCACTAC	GACTARCOG TTC <mark>A</mark> GAA <mark>G</mark> ATATOGG <mark>G</mark> AAAAA -T A TAG AAAAC T <mark>TT</mark> A <mark>CA</mark>		-ATTCAACTAAATTTT-CAACATTGACAAGCAATTTTTT	GGAGTTATTT <mark>T</mark> CTTAC
85. ChLG7 R180285871 C30	GATTAAG TG TT T CTAACG TAG AA TGA C	OGGCGG AATC CA <mark>G</mark> - ATCTG CAAGAA	-TCIGATOGCTAC	GACTAACCETTC <mark>A</mark> SAA <mark>G</mark> ATATCEGG <mark>G</mark> AAAAA-T AC AG AAAACT<mark>TT</mark>ACA		-ATTCAACTAAATTTT-CAACATTGACAAGCAATTTTTT	GGAGTTATTT <mark>T</mark> CTTAC
86. ChLG7 R180285871 C25	GATT AG TO TT T CTAACG TAG AA TGAC	CGGCGG AATC CAG - ATCTG CAAGAA	TCAGATCG CTAC	GACTAACOS TTCASAAGATATOSGGAAAAA-TATAGAAAACTTTACA		-ATTCAACTAAATTTT-CAACATTGACAAGCAATTTTTT	G R AGTTATTT TTAT TTA T
87 Chi G7 R180285871 C11	GATTARG TO TT T CTARCE TRE RATGAC	CGGCGGAATCCAG ATCTGCAAGAA	TC TG ATCG CTAC	GACTAACOS TTCASAAGATATOSG CAAAAA TAGAGAAAACTTTACA	ATTS	ATTCAACTAAATTTT-CAACATTGACAAGCAATTTTTT	GAGTTATTTCTTAT
88 Chi G7 R180285871 C20	GATTANG STTTCTAACG TAG AATGAC		TC TG ATCG CTAC	GACTARCONTCANA AND ATATONG CAAAAA TAGAGAAAACTTTACA	ATTG	-ATTCAACTARATITT-CAACATTGACAAGCAATTTTTT	GGAGTTATTTTCTTAT
89 Chi G7 R180285871 C12	ATTA AG TO TT T CT A ACG TAG AB TGA C		TC TE ATCS CTAC	GACTARCE TTO A RAGATATOR CRAAAA TAGAGAAAACTTTACA		ATTCARCTARA TTTT-CARCATTCACARCARTTTTT	- GG AGT TATT TO CTT AC
00 CH C7 D190295670DC C6	CREW BAC WATT TOT A BOO THE BRUCK C	COCCOC BOTCCOC ATCTCCO BOD	TC BC ATCC CT & C	CACTARCOS TTCAS ROCATATOCCCCR RARR TACACARA ASCTTTRACA	A TTTC	ATTCARCTAR ATTTT CAACATTCACABCCAATTTTT	
01 CHLG7 D190285971 C7		-OCCOCCARCOAR - ATOTOCARA	TOTO A ACC OT A C		- B PTT	- ATTOA SCHAR STOTT - CASC ATTOA CASC C & ATTOTT	
02 CHLO7 D190295974 C1E					2 100		
92. ChLG/_K1002030/1_C13	ATT ANY IN TT CLARKA THIS AN IGAC	CAUCUS ANTO CAA ATO TO CAASAA	TO CARGO CIAC	GACTARCOSTICAS ANA ATATONG CARAAA TAGAGAAAA TITAAA		ALIGARCHARTITI CHAGATIGACAMBCAATITIT	
83. CALG7_K160263671_C4		COOCOGARICORA AILIOCARA	TO BE ARUS CIAC	GALTARUG TICH AN ATATON CARAAR TAYASAAAATTITATA		ALL CARGE AND ALL CARGE TO A CARGE AND CARE TITLE	GGAGITATTI CTIAL
94. ChLG7 K100203071 C13	GATTANS IS IT I CIARGE INS ARTSKC	COBCOGARICCAR ANCISCRASAR	IC IS AND CIAC	GACTARCOSTICASAAGATATOGGCAAAAA TAGAGAAAACTITACA	AN 1 103	ALIGNACIANATITI CAACATIGACAASCAATITIT	GGAGITATTICTIAG
95. ChLG/_R1802858/1_C22	GATTAAG IG ITTCTAACG TAGAATGAC	- OGGODG AATCURA - ATCIG CAAAAA	-ICIGAACGEFAC	GACTAACCE TFCASAAGATATOGG CAAAAA - TATAGAAAACTTTACA	- A PBs	-ATTLAACTAAATTTT-CAACATTGACAAGCAATTTTTT	GGASTTATTTCTTAC
96. ChLG/_R1802858/1_C26	GATTAAG IG ITT CTAACG IAG AATGAC	- CGGUGGAATCCAA ATCIGCAABAA	TC IGAAUG CTAC	GACTARCOS TTUAS ARGATATOSO CARRAR - TATAGRARACTTTAUR	- ATTS	-ATTCAACTAAATITT-CAACATTGACAAGCAATITTTT	GGAGTTATCTTAT
97. ChLG/_R180285871_C24	GATTAAG IG TTTCTAACG IAG AATGAC	CGGCGGAATCCAG ATCIGCAAGAA	TC IG AADG CTAC	GACTAACOS TTCAS AAGATATOSG CAARAA TATAGAAAACTTTACA	AAT D9	-ATTUARCTAAATITT-CAACATTGACAAGCAATTITTT	GGAGTTATTTTCTTAC
98. ChLG/_R1802858/1_C6	GATTAG IS ITTCFAACG IAG AATGAC	OGGCGGAATCCAA -AACIG CAAGAA	TC IG AADG CTAC	GECTAACOG TTCAS AAG ATATOGG CAAAAA -TAGAGAAAACTTTACA	- A TBS	-ATTCAACTAAATITT-CAACATTGACAAGCAATTTTTT	GAAGTTATTTTTTAT
99. ChLG7_R180285871_C21	GATTA AG IG IT I CTAACG IAG AA IGAC	CGGCGGAATCCAA -AACTGCAAGAA	TCTGAACGCTAC	GCTARCOSTICAS AAGATATOSG CAAAAA -TAGAGAAAACTTTACA	- ATTG	-ATTCARCTARATITT-CAACATTGACAAGCAATTTTTT	GAAGTTATTT TT TTAT
100. ChLG7_R180285871_C29	GATTAAG IG TTTCTAACG TAG AATGAC	CGGCGGAATCCAA ACTGCAAGAA	TC TG AACG CTAC	GCTARCOS TTCAS AAG ATATOS G CRABAA - TAGAGAAAAC T <mark>TT</mark> ACA	AATTG	-ATTCAACTAAATTTT-CATCATTGACAAGCAATTTTTT	GAGTTATTTTAT
101. ChLG7_R180285871_C18	GATTANG TO TT T CTARCO TAG RATGAC	CC C C C A ATC CAA -A AC TC CAAGAA	-TCTC AACG CTAC	GCCTAACOG TTCAGAACATATOGG CAAAAA-TAGAGAAAACTTTACA		-ATTCAACTAAATITT-CATCATTGACAAGCAATITTTT	C A AGTTATTT TT TTA T
102. ChLG7_R180285871_C32	GATTARG IG IT I CTARCE IAG RATGAC	- CGGCGGAATCCTA - AACTGCAAGAA	TCTTAACG CTAC	GC TAACCE TTCAS AAC A TATCEG CC AAAA - TAGAGAAAAC T TT ACA	- ARTIG	-ATTCAACTAAATITT-CATCATTGACAAGCAATTTTTT	GAAGTTATTT TT TTAT
103. ChLG7_R180285871_C14	GATTA AG TG TT T CTA ACG TAG AA TGA C	CGGCGG AATC CAA -A <mark>AC</mark> TG CAAGAA	TC TG AACG CTAC	G <mark>G</mark> CTARCOS TTC A S AR <mark>G</mark> ATATOS G CRARAR - T AG AG RARAC T <mark>TT</mark> A <mark>CA</mark>		-ATTCAACTAAATTTT-CAACATTGACAAGCAATTTTTT	GG AGT TATT TTCTTAT
104. ChLG7 R180285871 C31	G ATT N AG IG IT I CTAACG IAG AATGAC	CGGCGGAATCCAA AACTGCAAGAA	TC TG AACG CTAC	g <mark>g</mark> c taac og ttc <mark>a</mark> g an <mark>g</mark> a tatog g caaaaa - t ag ag aaaac t tt a <mark>cc</mark>	ATTG	-ATTCAACTAAATTTT-CGACATTGACAAGCAATTTTT	- GGAGTTATTT T CTTA T
105. ChLG7_R180285871_C17	GATTANG IG TTTCTANCG TAG AATGAC	CGGCGG AATC CAA -A <mark>AC</mark> TG CAAGAA	TC ICAACG CTAC	G <mark>c</mark> ctaacos tec a s aa <mark>s</mark> ata tosg caaaaa -t a tag <mark>aaaacttt</mark> a ca		-ATTCAACTAAATTTT-CAACATTCACAACCAATTTTTT	GGAGTTAT <mark>C</mark> T <mark>T</mark> CTTA T
106. ChLG7_R180285871_C28	GG TT A AG TG TT T CTAACG TAG AATGAC	CE G CEE AAT C CAA -A AC TE CAAGAA	-TC IG AACG CTAC	G <mark>S</mark> CTAACCETTC A E AA <mark>G</mark> ATATCEG CAAAAA-T A TAG <mark>AAAAC</mark> T <mark>T</mark> A CA	- A TIG	-ATTCAACTAAATTTT-CAACATTGACAAGCAATTTTTT	GG AGT TATCTTAT
107. ChLG7_R180285871_C3	GG TT N AG TO TT T CTAACG TAG AA TGAC	CGGCGG AATC CAA -A <mark>AC</mark> TG CAAGAA	TC TG AACG CTAC	G <mark>G</mark> CTARCOS TTC <mark>A</mark> S AA <mark>G</mark> ATATOSG CAARART A TAG <mark>AAAAC</mark> T TT ACA	ATTG	-ATTCAACTAAATTTT-CATCATTGACAAGCAATTTTTT	GGAGTTATTT <mark>T</mark> CTTA T
108. ChLG7_R180285871_C23	GATTARG TO TTT CTARCG TAG RATGAC	CGGCGG AATCCAA AACTG CAAGAA	TC TG AACG CTAC	G <mark>G</mark> CTARCOS TTC A S AA <mark>G</mark> ATATOSG CAARAR T AG AG <mark>AAAAC</mark> T T ACA	AATT	ATTCARCTARATITT-CATCATTGACAAGCAATTTTTT	GGAGTTATTTCTTAT
109. ChLG7 R180285871 C8	GATTARG IG TTTCTARCG TAG AATGAC		-TCICATCG CTAC	G <mark>c</mark> ctarccettc a s ar <mark>s</mark> atatogg caaaaa-t ag ag <mark>araac</mark> t <mark>tt</mark> a ca	- A TIG	-ATTCAACTARATITT-CATCATTGACAAGCAATTTTTT	GGAGTTATTT <mark>T</mark> CTTA T
110. ChLG7 R180285871 C9	GG TT A AG TG TT T CTAACG TAG AA TGA C	CGGCGG AATC CA <mark>G</mark> ATCTG CAAGAA	-TC TG AACG CTAC	G AC TARCOS TTC <mark>A</mark> S AA <mark>G</mark> A TATOS G CAAAAA -T <mark>AG</mark> AG <mark>AAAAC</mark> T <mark>TT</mark> A <mark>CA</mark>		-ATTCARCTRARTTTTCCATCATTGACAAGCARTTTTTT	GGAGTTATTT <mark>T</mark> CTTA <mark>T</mark>
111. ChLG7 R180285871 C5	GATTAAG IG TT I CTAACG IAG AA IGAC	CGGCGG AATC CAA ATCTG CAAAAA	TC TG AACG CTAC	g actar cos tec a s ra <mark>s</mark> atre cos <mark>s</mark> arrar - t as as rando t te as	AATT	-ATTCAACTAAATTTT-CATCATTGACAAGCAATTTTTT	- GGAGTTATTT <mark>T</mark> CTTA <mark>T</mark>
112. ChLG7 R180285871 C27	GATTAAG IG TT I CIAROG IAG AA IGAC	OGG OGG AAT CCAA - AT CTG CAA AA	-TCTG AACG CTAC	GACTAACOG TTCAGAAG <mark>AATATOGG</mark> AAAAA-TAGAGAAAACTTTACA		-ATTCAACTAAATITT-CATCATTGACAAGCAATTTTT	GGAGTTATTT <mark>T</mark> CTTA <mark>T</mark>
113. ChLG7 R180285871 C2	GATTA AG TO TT T CTA ACG TAG AA TGA C	- CGGCGGAATCCAA ATCTGCAA	TC TG AACG CTAC	GACTAACCETTC <mark>A</mark> SAA <mark>G</mark> ATATCEG <mark>G</mark> AAAAA-T AG AG AAAACT<mark>TT</mark>ACA		-ATTCAACTAAATTTT-CATCATTGACAAGCAATTTTTT	GG AGT TATT T <mark>T</mark> CTT A <mark>T</mark>
114. ChLG7 R180285670RC C7	GATT AG IG TT I CTAACG TAG AA IGA C	- CGGCGG AATC CAA - AT CTG CAABAA	TC TG AACG CTAC	GACTARCOSTTC <mark>A</mark> SAA <mark>G</mark> ATATOSG <mark>G</mark> AAAAA -T <mark>AG</mark> AG AAAAC T <mark>TT</mark> A <mark>CA</mark>		-ATTCARCTARATITT-CATCATTGACAAGCAATTTTTT	- GGAGTTATTT <mark>T</mark> CTTAT
115. ChLG7 R180285871 C16	GATTARG IG TT I CTARCG IRG RATGAC	CGGCGGAATCCAA ATCTGCAA	TC TG AACG CTAC	G ACTARCOS TEC <mark>A</mark> S RA <mark>G</mark> ATATOSG <mark>G</mark> AARAR - T AG AG AAAAC T <mark>TT</mark> ACA	AATT	-ATTCARCTAAATTTT-CATCATTGACAAGCAATTTTTT	GGAGTTATTTCTTAC
116. ChLG7 R180285670RC C5	GATTANG TO TT T CTANCE TAG AN TGAC		-TCAGATCG CTAC	GACTARCOS TTC <mark>A</mark> S AA <mark>G</mark> ATATOSG CAAAAA -T <mark>AG</mark> AG AAAACTTT A <mark>CA</mark>		-ATTCAACTAAATITT-CATCATT <mark>GACAAG</mark> CAATTTTT	GGAGCTATTTTCTTAT
117. ChLG7 R180285670RC C9	GATTAAG IG IT I CTAACG IAG AATGAC	CGGCGG AATC CA <mark>G</mark> - AT CTG CAAGAA	TCAGATCG CTAC	GACTARCOS TTC <mark>A</mark> S AA <mark>G</mark> ATATOSG CAAAAA -T <mark>AG</mark> AG <mark>AAAAC</mark> T <mark>TT</mark> A <mark>CA</mark>		-ATTCAACTAAATTTT-CATCATT <mark>GACAAG</mark> CAATTTTTT	GGAGCTATTTTCTTAT
118 Chi G7 R180285670RC C8	GATT AG IG IT I CTAACG IAG AATGAC	CGGCGGAATCCAG ATCTGCAAGAA	TCTGATCGCTAC	GACTARCOS TTCAS RAGATATOSG CRARAR TAGAGAAAACTTTRCA	ATT	ATTCARCTARATTTT-CATCATTGACAAGCAATTTTTT	GGAGTTATTTCTTAT
119 Chi G7 R180285871 CT9	GATTARG TO TT T CTARCO TAG AN TGAC	- CGGCGGAATCCAG ATCTGCAAGAA	TCAGATCACTAC	GACTARCOS TTCHS ARCATATOSG GARAAR TAGAGARARCTTTACA		ATTCAACTGAATTTT-CATCATTGACAAGCAATTTTTT	- GGAGTTATTTTCTTAT
120 Chi G7 R180285871 C10	GATTARG IS TT T CT ARCS TAS AATSAC		TCAGATCACTAC	GACTARCOS TTCAS AZGATATOGG CAAAAA - TAGAGAAAATTTTATA	ATTS	-ATTCAACTAAATTTT-CAACATTGACAAGCAATTTTTT	- GG AGTTATTTTCTTAC
121 Chi G7 R180285670RC C3	CARTTAR TO TT T CTARCE TAG AS TGAC		TCAGATCGCTAC	GACTARCOSTECHERAS ANTOS CARARA TEGASARCETTACA	- ATTS	- ATTCAACTAAATTTT-CAACATTGACAAGCAATTTTTT	- GG AGT TATT TTCTT AT
122 CH G7 P180285670PC C2	CARTTAR TO TTOTA BO TOG BE TO A C-	CGGCC BATCCAR ATCTGCARGAR	TCHENTOGCTAC	GACTARCONTEC ACARA ATATOSCONARA TABAGAAAACTTTACA		- ATTCASCTAAA TTTT-CATCATTCACTATCAATTTTC	CC 2 CT 2 TT TC TTT
122 CH C6 D180283422 CT	ATTAC STTTTT AND ANT AND A TO A		TORRETCO CTAC			- ATTRAACTAAATTTT-CATCATTCACTACAATTTTC	
124 CHICE P190294245PC C5			TCACA TCC CTAC				
125 CH C6 P180284245RC C7			TORNE TOC CTRC				
128 CH CE D190294245RC C7		- CCCCCC B B TCC B B - B TCCC B B B B	TO MAN TO GO CT AC		- BECT		
120. CILGO K 100204243KG C9		COCORDANCEAN ATTICCANAN	TOAL TOG GIAC				CO ACID ACID MC CO ACID
127. CILGO R 100204243RC CO	ATTAKS IS ITTOTAKS IN ANTON	CGGCGARATCLAA ATTIGCAAGAA	TOAGA TOG OTAC	GACTARCUS TICAS AMARTATUSG GAMAAA TAGAGAAAAUTTTAGA	And Day	- ITTCARCTARATITT-CRICTITGCCIRTCARTITTT	GG AGT TAT TTIG TTAT
120. CILGO R 100204243RC CO	ATTAK BITTCHARGE ACCOUNT AND A DOLLAR	COOLS ARTCOAR AT TO CAASA	TOACH TOS CTAC	GALTARUG TTUR ARAATATUG CARAAA TAYARAAA TT	ARC Da	- ITICASCIASA PTT-CETCTTIGCCIETCAAPTITT	GIG MATTATTTING TTAT
129. UILGO K100204240KU UZ	TO ATTAKS IS IT TO TAKOG IMA ATGAC	COGOGARATCICAN ATCIGCAAGAA	TCASA TOG CTAC	GACTARCOS TECAS ARRATATOS CARAAR TAGAGAAAACTTTACA	AACDS	-TITCARCTARATITT-CATCITIGCOINTCARTITTT	GARSTTATTTCTTAT
130. CILGO R100204245RC C3	TATTAN IS ITTCHARGE TAAATGAC		-TCARGTOGETGC	GACTARCOS TITAS ARRATATOSO CRAAAR TAS AGRAAGTTTACA	AACIDS	-TTTCAATTAA TTTT-CATCTTTCCCTATCAATTTTT	GASTIRTICTAT
131. CILGO_R180284245RC_C4	TATTGAS TO TT T CPARKS TAAATGAC	- CIGUISAATU CAA ATUTIS CAAGAA-	-TCAAG TOG CTG C	GALTARUGS TITAS AAAATATUSG CAAAAA TAYAG AAAAC T TTACA	- AAC 119	-TETCARCTARATITT-GATCTITACCTALCARTITTT	-GAASTTATTIC TTAT
132. ChLG10_R180276690_C2	AACTGAG COTCT CTAACG TAG AA TGAC	CGGCGGAATCCAA ATTTGCAAAAA	TCAAG TCG CTTC	GACTAACOS TTOSSAAAATATOS TCAA-AACTTTAGTCTOS TCACA	ATTE	-TCTAAACCAAACTTT-TATCATTATTTTTCAAATTTTT	ATAGTTATTTCTTAG
133. ChLG10_R1802/6690_C3	AATTGAG IG TTOCTARCG TANAA TGAT	G-OLG AATC CAA AT TTG CAAAAA	-TCAAG TCG CTAC	GAUTAAUG TTCGGAAAATATCG TCAA-AAATTTAGTCTCG TCACA-	ATTTA	- IUTAAACUAAACITT-CTTCATTATITTTCAAATITTT	ATAST TATT TOTTOS
134. ChLG6_R180285048RC_C10	AATTEAG TO TT T CTAACG TAG AATEAC	TACCEAAATC CAA ATTTC CAAGAA	TCAAG TTG CTAC	ACTACCE TFCGAAAAATATCE FCAA - AAATTTAGECTCE TCACA	-ATTTG	- TCICAACCAAACITT-CTTCATTATTTTCAACTITTC	- GG AGCTATT TTTAG
135. GREGE K180285048KC C13	AATTGAG IS TTTCTAACG TAS AATGAC	THE USARATC CAR AT TTG CAAGAA	TUARS TES CTAC	ACTACOS TECERARATATOS CAR ARTTTAS CTOS TCACA	ATTG	- TUTE AACUARACITT-CITCATTATITITAAACTITIG	GRANGETATTTTTAG
136. ChLG6_R180285048RC_C2	AATTAAG IG IT I CTAACG IAAAA IGG C	CGGTAAAATTTAA ATTTGCAAAAA	TCAATCACTAC	GACTAACOS TT TA S AARACATOS T CAA-AA R TT TA AT C TOS TCACA	ATTTA	-TCTTAACCAAACATT-CTTCATTATTTTTCAACTTTTA	- GGAGTTATTT TT TTAG
137. ChLG6_R180285048RC_C14	GATTARG IG TTTCTARCG TANAA TGAC		TCARATCG CTAG	GACTARCOS TE TA S AARACATOS T CAR-AA R TT TA RT C TOS TCACA	ATTE	-IUTAAACCARACATT-CTTCATTATTTTCAACTTTTA	GGAGTTATTTTT
138. GRLG6_R180285048RC_C11	AATTAAG IG IT ITTAACG TAAAATGAC	CGGCGARATCTRA ATTTG CAACAA	TCARATCG CTAC	G ACTARCOS TT TA S AAAA CATOS T CAA-AAATTTA AT CTOS TCACA	ATTT	-TCTAAACCAAATATT-CTTCATTATTTTCAAATTTTT	GG AGT TATT T TT TT AGG
138. ChLG6 R180285048RC C4	AATAGAG IG IT I CTAACG TAAAA TGAC	CGGCGARATCCAR ATTTGCARGAA	TCAAATCG CTAC	GACTARAGETTCAS ARRACATOS TRAA-ARATTTAATCTAS TCACA	ATTTG	-TCTAACCAAACATT-CTTATTATTTTCAAATTTTT	GGAGTTATTTCTTAGG
140. ChLG6_R180285048RC_C8	AATTGAG TATT T CTAACG TAAAATGAC	- CGGCAAAATCCAA ATTTGCAAGAA	CAAATCG CTAC	GACTAAROG TTCREARARACATOG TCAA-AARTT TARTC TOG TCACA	ATTEG	-TCTAAACCAAACATT-CTTCATTATTTTCAAATTTTT	GGAGTTATTTC T TTAGG
141. ChLG6_R180285048RC_C15	GATTARGIGTTTTARCGTARAATGAC	- OGGOGRAATCCAA - ATTTG CAAGAA	TCAN TCG CTAT	GACTARCES TTCTAAARATATAG TAAA-AAATTTAATCTCG TTATA	ATTE	- ITCAAACCAAACITT-CITCATTATITTCAACITTTC	- GGASTTATTTCTTAS
142. ChLG2_R180279754RC_C4	ARCTGRG IG TT CCTARCG TRARATGAC	- CGGCGAAATCCAA ATTCGCAAGAA	TCTARTCGCCAC	GACTARCOS TTOGARARATATOS T CRA-AR <mark>B</mark> TT TAG <mark>TCAC</mark> G TCACA	ATTTG	-TCTAARCCAAACTTT-CTTCATTGTTTTCCAAATTTTCC	- GGAGTTATTTCCTTAG
143. ChLG2_R180279754RC_C6	GATTGAG TATT I CTAACG TAAAATGAC	CGGCGRAATCCAA ATTCGCAAGAA	TCTANTCG CCAC	g ac taac of tech bara tatof t caa – arbit tag t cac	ATTE	-TCTAACCAAACTTT-CTTCATTCTTTCCAAATTTTT	
144. ChLG2_R180279754RC_C2	GATTGAG TO TT T TRACG TAAAA TGAC	CGGCGGAATCCAA -ATTCG CAAGAA	-TCTAATCG CTAC	A ac taa coe ttoge aaaa ta toe <mark>t</mark> oaa -aa <mark>a</mark> tt tag <mark>t</mark> o toe toa <mark>c</mark> a	- AT TIG	-TCTAAACCAAACTTT-CTTCATTATTTTTC	GGAGTTATTT <mark>TCA</mark> TAG
145. ChLG2_R180279754RC_C3	G ATTGAG TG TT T CTAACG TA <mark>A</mark> AATGAC	CGGCGG AATC CAA -AT TTG CAA <mark>A</mark> AA	TTAAATCG CG AA	G ACTAACC <mark>A</mark> TTCGG AAAATATCG <mark>T</mark> CAA -AA <mark>A</mark> TTTAG <mark>T</mark> CTCG TCA <mark>C</mark> A	- AT TTG	-TCTAAATCAAACTTT-CTTCATTATTTTTC	- GGAGTTATTTCCTTAG
146. ChLG9_R180290996_C7	gg t a gag 15 tt t ctaacg ta a aa tg <mark>g</mark> c	CGG CGG AAT <mark>A</mark> CAA -AT TTG CAAGAA	-TCAAATCG CTAC	G ac taa cos ttc <mark>o</mark> s abaa ta tos <mark>t</mark> caa -a a <mark>b</mark> tt tag <mark>t</mark> c tos tca <mark>ca cg t</mark> (CACA AT TTG	-TCTRAACCAAATTTT-CTTCAATATTTTCAACTTTTT	GG A AT TACT TC CTTC
147. ChLG9_R180290996_C9	gg ttgag ig it t <mark>g</mark> taacg ta a aa tgac	CAGCGG AATACAA AT TTG CAAGAA	TCAAA TCG CTAC	G ACTAACOS TTC <mark>O</mark> S AARATA <mark>S</mark> OS <mark>T</mark> CAA-AR <mark>A</mark> TT TAG <mark>T</mark> C TOS TCA CACOT (ACA AT TEG	-TCTAAACCAAATTTT-CTTCAATATTTTCAACTTTT	GGAGTTACTTAG
148. ChLG9_R180290996_C2	GG TT A AG IG TTTCTAACG TA A AATGAC	- AGG T EG AAT ACAA - AT TTG CA <mark>G</mark> GAA	-TCAAATCG CTAC	G ACTARCOS TTO <mark>O</mark> S A C RATATOS T CRA-AR <mark>A</mark> TT TAS T CTOS TCACACETO	laca at t tg	-TCTRAACCARACTTT-CTTCAATATCTTTCAACTTTT	GGAGTTACTTCCTTAG
149. ChLG9_R180290996_C4	gg ttgag ig tt <mark>a</mark> ctaacg ta <mark>a</mark> aa tgac	CGGCGGAAT <mark>A</mark> CAA -AT TTG CAAGAA	-TCAAAATCG CTAC	G ACTARCOS TTC <mark>O</mark> S AAAATATOS <mark>T</mark> CAA-AR <mark>A</mark> TTTAG <mark>T</mark> CT <mark>O</mark> S TCA <mark>CACOT</mark> O	ACA AT TIG	-TTTAAACCAAACTTT-CTTCTTATTTTTCAACTTTTG	GG AGT TA <mark>C</mark> T TC <mark>T</mark> TT AG
150. ChLG9 R180290996 C6	gg ttgag ig tt <mark>a</mark> ctaacg ta a aa tgac	- CGGCGG AAT <mark>A</mark> CAA - AT TTG CAAGAA	TCAA TCG CTAC	g ac taa cos tec <mark>o</mark> s aara ta tos <mark>e</mark> caa – ar <mark>a</mark> tt tas <mark>e</mark> ctos tca ca coto	ACAATTEG	-TTTAAACCAAACTTT-CTTCTTATTTTCAACTTTT	- GG AGT TACT TCT AG
151. ChLG9 R180290996 C8	gg attgag ig it i ctaacg ta <mark>a</mark> aatgac	OGGCGG AAT <mark>A</mark> CAA -AT TTG CAAGAA	-TCARATCG CCC	G AC TARCOS TTC <mark>O</mark> S AARA TA TOS <mark>T</mark> CAR - AR <mark>A</mark> TT TAS <mark>TCRO</mark> S TCA <mark>CACAT</mark> (CACATA TTG	-TCTRARCCARACTTT-CTTCATTATTTTTAACTTTT	GGAGTTA <mark>C</mark> TT <mark>T</mark> CTTAG
152. ChLG3 2 R180296862 C2	GATTAAG TATTTCTAACTAAAATGAC	OGG <mark>G</mark> GG AATC CAA -AT TTG CAAGAA	-CCARATCG CTAC	G ACTAACCE TTCGG AAAATATCG <mark>T</mark> CAA -AA <mark>A</mark> TTTAG <mark>T</mark> CTT <mark>C</mark> TCA <mark>GG</mark>	- ATTIG	-TCTAAACCAAACITT-CTTAATATTTTTAATTTTC	GGAGTTATTTCCTTAG
153. ChLG3 2 R180296862 C8	GATT AG IS IT I CTAACG ARAAGGAC	CGGCGG AATC <mark>G</mark> AA -ATTT <mark>TT</mark> AAGA <mark>G</mark>	-TCAARTCACTAC	GACTAACOG TTOGGARAATATOG TCCA-ARETTTAGTCTCAOG	- AT TTG	-TOTRARCCARACITT-CTTRATATTTTTAATTTTTC	GGAGTTATTTCCTTAG
154. ChLG3 2 R180296862 C16	GATTARG TO TT T CTARCE TRANATGAC	CGGCGGAATCGAA ATTTTAAGAA	TCAAATCACTAC	G ACTAACOS TEOGGAAAATATOS TCAA-AAATTTAGTCTTG TTACA	ATTTC	TCTAAATTAAACTTT-CTTCATTATTTTTAAAATTTTC	GCAGTTTTTTTTTTTT
155. ChLG3 2 R180296862 C3	GATTARG TO TT T CTARCE TRAATGAC	CTCCASAATCCAA GTTTG CAAGAT	TCANATOG CTG C	GACTARCOS TTOSS AARATATOS TCAR-ARATTTASTCTOCTCA CA		-TCTAAACCAAACTTT-CTTOCTTATTTTTAAATTTTC	GGAGTTTTTTTTTTTAG
156, ChLG3 2 R180296862 C9	GTTTARG TO TTT CTAREG TRANSATGAC	-CTCCR AATCCAA ATTTG CAAGAT	TTAA TOG CTG C	GACTARCOS TECES ARATATOS TCAR-ARATTTAS TTRECTCA CA	ATTT	-TCTAAACCAAACTTT-CTTCCTTATTTTTAAATTTTC	- GGAGTTTTTTTTTTAG
157. ChLG3 2 R180296862 C6	GATTARG TO TTOCTAGOG AAAAATGAC	CGGCGARATCTAA ATTTGCTARAA	TCAAG TTG CTG C	G ACTANTOS TECGE ARAATACOS TCAA - ARATT TAGTC TCCTCAGA	ATTTA	CTAAACCAAACTTG CTACATTATTTTCAAATTTTC	GGAGTTTTTTTCTTAG
158. ChLG3 2 R180296862 C14	GATTANG COTTOCTO ACO TAAAA TGA C	OGGCOG AATOGAA AT TTO CAAGAA	TCAAATCG CTG C	G ACTARCOS TTOGE ARAATATOS TCAAGARATT TAGTC TCA CA	ATTE	-TCTAAACCAAACTTG-CTTCATTATTTTCAAATTTTT	AGAGTTTTTTTTTT
159 Chi G3 2 R 180296862 C7	GRETARG TO TT TTARCE TARAATEAC	-CGGCCGAATCGAA ATTTG CAAGAA	TCATG TCACTAC	GACTARCE TECH AARATATCE CAR ARATTTRE CTCCCCAR	ATTS	-TCTAATCCAAACTTT-CTTCTTATTTTCAATTTT	GGAGTTTTTGCCTTAG
160 Chi G3 2 R180296862 C15	GRETARS TO TTT TRANCG TAKAN TGAC	CGGTGGAATCGAA ATTTACAAGAA	TCAAG TCG CTAC	GACTARCOS TTOSS ARAATATOS TCAR-ARATTTAS TO TCA CA	ATTE	TCTAN CCAAACTTT CTTCATTATTTG CAAATTTTT	GGAGTTTTGCCTTAT
161 Chi G3 2 R180296862 C13	GATTANG TO TTTTCARCO TAAAA TCAC	OCACCG ARTOCAA AT TTC CAACAA	TCAAG TOG CTAC	GACTARCOS TTOSS ARAATATOS CAA - ARATTTRC CTCACA	ATTS	-TCTAATCCAAACTTT-CTTCATTATTTTCAAATTTC	GGAGTTTTTTCCTCC

162. ChLG3 2 R180296862 C4	GATTAAAIG TTTTCAACG TAAAAIGAC	- CGGCGGAATC <mark>G</mark> AA - AT TTG CAAGAA	TCAAG TCG CTAC	GACTAACOG TTOG R AAATATOG T CAA-AA A TTTAG T CT CC TCA C A	
163. ChLG3_2_R180296862_C12	CATTAG IS IT I TCAACG TAAAA TEAC	- CGGCGGAATO <mark>G</mark> AA - AT TTC CAAGAA	-TCARG TCG CTAC	GACTAACCE TTCGE AAAATATCE TCAA-AAATTTAGTCTCACA	at TTECGAETTATTCCTTAG
164. ChLG3_2_R180296862_C10	G ATT A AG IG IT T TC AACG TA A AATGAC	CGGCGG AAT C <mark>G</mark> AA -AT TTG CAAGAA	TCAAG TCG CTAC	G ACTAACCE TTCGE ARAATATCE CCAA AA <mark>A</mark> TTTAG <mark>T</mark> CTT CTCACA	attt <mark>a</mark> -tctaaaccaaacttt-cttcattatttt t caa <mark>a</mark> titt <mark>t</mark> ggagttatttccttag
165. ChLG3 2 R180296862 C11	g att a ag te tt t <mark>tc</mark> aacg ta a aa tgac	- CGGCGG AATC <mark>G</mark> AA - AT TTG CAAGAA	TCAAG TCG CTAC	G ACTAACOS TTOSG ARAATATOS COAA AA <mark>A</mark> TTTAS <mark>T</mark> OTOACA	ATTTA TCTAAACCAAACTTT-CTTCATTATTTTCCAAATTTTT GGAGTTATTTCCTTAG
166. ChLG3 2 R180296862 C5	GATTAG IG IT T <mark>TC</mark> ACCG TA A AATGAC	CGG CGG AAT O <mark>G</mark> AA - AT TTG CAAG <mark>C</mark> A	-TCARG TCG CTAC	G ACTAACOS TTOGE AAAATATOS <mark>T</mark> CAA - AA <mark>A</mark> TT TAG T C T <mark>CC</mark> TCA <mark>C</mark> A	atte-tetaaaccaaacttt-cttcattattt ta aa t tttcggagt <mark>gta</mark> tccttag
167. ChLG8_R180288782RC_C4	AATTGAG TATT T CTAACG TAAAATGAC	CG TCGE AAT C <mark>G</mark> AA - AT TTG C <mark>T</mark> AGAA	TCARATCS CTAC	G ACTAACCE TTCEE AAAATATCE <mark>T</mark> CAA -AA <mark>G</mark> TTT <mark>T</mark> G T CTEE TCA C A	
168. ChLG8 R180288782RC C5	ARTTGAG T <mark>A</mark> TT T CTARCG TR <mark>A</mark> RR TGAC	CG TCGG AAT C <mark>G</mark> AA -AT TTG C <mark>T</mark> AGAA	TCAR TCG CTAC	G AC TAAC OF TTCGE ARAATATOF T CAA - AA <mark>G</mark> TTT <mark>TG T</mark> C TOG TCACA	
169. ChLG8 R180288782RC C3	AATTGAG TATT T CTAACG TAAAA TGAC	- CGGCGGAATO <mark>G</mark> AA - AT TTG C <mark>T</mark> AGAA -	TCAR TCG CTAC	G ACTAACOS TTCGS AAAATATOS <mark>T</mark> CAA AA <mark>G</mark> TTT <mark>T</mark> GTCTOS TCA <mark>C</mark> A	AG TES - TCTCAACT AAACTTT - CTTCATTAT CTCTCAACTTTTC
170. ChLG8 R180288782RC C2	AATTGAG TATT T CTAACG TAAAA TGAC	CG T CGE AAT O <mark>G</mark> AA - AT TTG C <mark>T</mark> AGAA	-TCAAATCG CTAC	G actracce troge agaa ta toe t caa -a G tt t t e t cae	
171. ChLG2 R180279754RC C5	AA <mark>C</mark> TGAG TG TT <mark>C</mark> CTAACG TA <mark>A</mark> AA TGAC	CGGCGGAATCCAA-ATTTGCAAGAA	TCTARCECTAT	G AC TAAC CE TTCGE AAAA TA T <mark>TCT</mark> CAA - AA <mark>A</mark> TT TAG <mark>T</mark> C T <mark>CA</mark> TCA <mark>C</mark> A	CTTTA-TCAAACTTAACTTT-CTTCATTATTTTTCAAFTTTTTGGAGTTATTTCCTCAG
172. ChLG10 R180276690 C1	ARCTGAG TO TOT CTARCO TAG AR TARC	CGGTGG AATC CAA AT TTG CAA	TCAAG TTG CTAC	GACTAACCATTCGGAAAATATCGTCAAAAA-TTTAGTCTCGTCACA	
173. ChLG3 Z R180295754RC	AATTGAG TG TT T CTAAOG TAG AA TGAC		TCARG TOG CTAC	GACTARC TA TTC T ; GAAATATCAS CAAAAA-TTTAG TCTCS TCACA	at TTCTCTAAACCAAACATT-CTTCATTATTTTCAACTTTTCGGGCTTATCTCCTTAG
174. ChLG10 R180277145 C4	AATTAAG IG IT I CI <mark>G AG</mark> G IAG AA IGAC		TCARCTCG CTAC	G A <mark>T</mark> TAA <mark>G</mark> CE TTCGE AAAA TA TCGE CAAAAA TT TAGC <mark>T</mark> TTG TCAAA	
175. ChLG10 R180277145 C8	ARTT RATIGTTTCT<mark>G</mark>AGGTAGARTGAC	- CAGCGG AAT CAA - AT TTG CAAGAA	TCARCTCG CTAC	G A <mark>T</mark> TAA <mark>G</mark> OF TTOSE ARAA TA TOSE CAARAR TT TAEC <mark>T</mark> TTE TO ARA	
176. ChLG10 R180277145 C10	AATTGAG TO TT T CTTACG TAG AATAAC-	- CGGCGGAATCCAA ATTTGCAAAAA	TCAACTCG CTAC	G ATTAN <mark>G</mark> OF TTOSG ARAA TA TOSG CAARAR - TT TAGO <mark>T</mark> TTG TO ARA	
177. ChLG10 R180277145 C8	AATTGAG IG TT I CT <mark>T</mark> ACG IAG AAT A AC	- CGGCGGAATCCAA - ATTTG CAAGAA	TCARCTOG CTAC	G A <mark>T</mark> TAACCE TTCGE AAAA TA TCGG CAAAAA TT TAGCC TTG TCAAA	at tt <mark>a</mark> -tc <mark>g</mark> aaaccaaa <mark>tag</mark> t-ct <mark>g</mark> cattat t tt ug t tt tat t t cadagt cacgtccttag
178. Chi G10 R180277145 C3	ARTTGAG TO CT A CO TAG ARTGAC		TCARCTCG CTAC	GACTAACCE TTCEE ABAATATCE G CAABAA-TT TAGCT TTG TCABA	
179 Chi G10 R180278257 C7	AATTAAG TO TT T CTAACG TAG AA TGAC	CGGTGG AATCCAA ATTTG CAAGAA	TCAAG TCG CTAC	GACTAACOS TTOGG ABAATATOSG CAABAA TT TAGCCTTG TOABA	
180. ChLG10 R180278257 C11	AATTAAG TO TT T CTAACO TAG AATGAC	CGG CG AAT C CAA -AT TTC CAAGAA	TCARG TCG CTAC	GACTARCOS TTOOS ARAATATOS GOAARAA-TT TAGOC TTO TOARA	
181 Chi G8 R180289798RC C3	AATTAAG TO TT T CTARCO TARAA TGAC		TCARG TCG CTAC		
182 Chi G8 R180289798RC C6	AATTAAG TG TT T CTAACG TAG AA TAAC	AGGCGGAATCCAA ATTTGCAAGAA	TCAAG TCTAC	GACTANCOS TECOS ABAATATOS GCAABAA TETAS CCTTG TCABA	ATTA TCAAACCAAATAGT CTTCATTATTTCATCTATTC GGGGTCATGTCTTAG
183 Chi G8 R180289798RC C4	AATTAAG TO TT T CTAACO TAG AA TGAC	CCCCCCC AATCCAA ATTTC CAAGAA	TCARG TOG CTAC	GACTANCOS TTOTO ABAA TA TOS S COABAA - TT TASCO TTO TO ABA	
184 Chi G8 R180289798RC C5	AATTAG TO TT TCT AACO TAG AATAAC-	ACCCCCAATCCAA ATTECCAACAA	TCARATCTCTAC	CACTARCCE TTOPE AARA TATODE CAARAA	
185 CH G8 R180289798RC C2	ABTTERS TO TT T CT A ACG THE ROTES	CGGCGE AATCCAA - ATTTG CAAGAA-	CARGING CTAC		
186 Chi G3 2 R180297342 C5	AATTGAG TO TT T CTAACG TAG AN TGAC	CGGCGAAATCCAA ATTTGCAAGAA	CAAGTCACTAC	GACTAACOS TTUTE AAAATATOGG CAAAAA TTTAGCCTTGTCAAA	ATTTA TEGAAACCAAATAGT CTTCATTATTTCTTTCTGTTC GAAGTTATGTCCTTAG
187 Chi G3 2 R180297342 C17	AATTGAG TO TT T CT A ACC TAG AN TCAC	-CEECE AATCCAA ATTECAACAA	CAAG TCACTAC		
188 Chi G10 R180277145 C7	AATTAAG TO TT T CT A CG TA AAA TCAC	CGTCSAATCCAA ATTTS CAASAA	CAR TOS CTAC	GACTAACCE TTORE AAAATATOE CAAAAA TTTACCETTE AAAA	
189 Chi G10 R180277964RC C2	ARTIGAS IS IT I CLARCE THE ARTICLE	CGGCGGAATCCAA ATTTGCAAGAA	TCAAG TCG CTAC	GACTARCOS TTOSS ARAATATOS GCARAAA TTTAGCC TTG TCARA	
190 Chi G10 R180277964RC C3	AATTGAG TO TT T CTARCE THE ATTGAC	CGGCGGAATCCAA ATTTGCAAGAA	TCAAG TCG CTAT	GACTAACOS TECGGARAATATOSG CAARAA TETRACCETIG TCARA	ATTTA TEGAAACCAAATAGT CTTCATTATTTTCCTTTTC GGGACTER
101 CH C10 P180278257 C2	A ATTEAC TO TT TOT A ACC TA A A TEAC		TORRETOR CTO COM		ATTTA TEGA ACCAA BEACT CONCAPT ATTICCOPTINETC - CAS ACTATICCOPT
192 CH G10 P180277964PC C7	A BETTER AG TE TETA ACC THE BETER C	CGCCCE BETCCAB-BTTTCCABGBA	TCAR TCC CTAC		
193 Chi G10 R180277964RC C9	ABTTGAG TO TT T CTAACG TAG BB TGAC	CGGCGG BATCCBA ATTTGCBBGBB	TCARS TOS CTAC	GACTARCOS TECOS BARA TRECOS CRARAS - TETROCOTES TORAS	MATTA TAGA A SCCAA A TAG T COTCATT AT TITCCA ACTATTC GG A ACTATT COTTAG
194 CH G10 R180277964RC C6	A ATTGAC TO TT TOT A ACC TAC AS TCAC		TO ARG TOG OT TO	- CACTABOC TTOSCARAATATOSCOARAA - TTTRCCCTTCTCRAA	
105 CH C10 D180279257 C15	A APPRAGES DE LES ACCEAC AS DES C	COCOCCA AND CAA AND CAACAA	TOTALS TO STAC		A THE MECHANICAL CONCERNMENT OF A CARDEN AND A CONCERNMENT OF A CARDEN AND A CONCERNMENT OF A CARDEN AND A CA
106 CH CO D10000000000 CO	A REF AG TO TO TOTAL OF THE ACTION	CACCO BARCCA - ATTIC CANANA	TOPRO TOS OTAC		
107 CH C17 D190292040RC C0	A BUT AC TO TO TO TA BOO TAC BATCAC	COCCOS ANTOCA ATTIC CAASA	TO BBG TOS CIAC	C 3CT 33 CT TTCCC 3 33 3 TA CCC TA 3 3 3 5 TTTSCCCTTC TC 3 35	ATTA TO AN CANCENE AND TO ATTATT TO ATTATT A A A A A A A A A A
109 CH C10 D190279257 C12	A ATT AC TO TT TOTA BOO TAG BATCAC	- COOCCE ATCCEA - ATCCC CAREAR	TCARS TOS CIAS	C ACTARCE TTOS ANN INCOS MANNE TTERCETTO TONE	ATTA TOTAL COMMENSI CITCATATITO CITCATATITO CASTA CONSCIONA
190. CILG IU KIOUZ/020/ CIZ	ARTING TO TO TOTALOG TAG ARTONC	COCCERTS AND CONTRACTOR OF THE CARDINA	TCARS TOS CIAS	CACENCCE TO COMMANY A CONTRACT OF THE CONTRACT. THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT. THE CONTRACT OF THE CONTRACT OF THE CONT	
200 CH C40 D400270237 C2	A REPART OF THE REPART AND THE REPORT	CIGCOG BARCCBB ATTIG CARGAA	TCARGING CTARTER	C 3C T 22 COT THE COLOR RANK TRUCES CARAAR TT TRUCE THE TO ARE	ATTIA TOMATCAATAA TOTOCATATATTICA TOTTTIC AGAINT AND TOTTA
200. CHLG10 K1802/623/ C8	AATTAAS IS IT ICTAROS INS AATGAC	CASCES ARTCOAK AT THE CAREAR	TCARG TOS CTAR	G AC TARCOS TECES RAMATATOS CARAMA TETRACO TOS CARA	ATTA TOPA CONSTRUCTION TO CONSTRUCT AND TO CONST
201. CILG10 R180278257 C13	ARTTANS IS IT TOTANOS INS ARTSRC		TCARS TOS CITAR	C ACCARCOS TITOSS AMARTATOSS CARAGA TITIASCO TIS TOARA	
202. ChLG10_R180278257_C16	ARTIGAS IS IT I CTARGE TAB ARTICL	- OGGUGAATCCAA AT TIG TAAGAA	-ICARGING CIAR	GAUTRACUS TTURS ARRATATUSS CRAARA TTTASCUTTS TURRA	- ATTA TORATCARATA TO TOTATATTITO TESTATTO- OGO ANTAN INCOTTAS
203. ChLG10_R180278257_C10	AATTGAG IS ITTUTACOS TAS AATGAC		TCARGTOS CPAR	ALTACOS TTOS ARAATATAS COARAA TTTAS COARAA	ATTTA TAGAAACCAAATAG T- CTTCATTATTTPCTTIS TATTC- AGG ACTATG TCCTTAG
204. CILG10 R1802/825/ C14	AATTGAS IS IT TCTACOG IAGAATGAC	COOCAAAATCCAA ATCIGCAAGAA	TCANG TOG CTAN	ARCTARCOS TECOS AMARTATAS CCARARA TITAS CON CONSTRUCTION CON	ATTA INGRACIAR IST CITATIATITICTES INTO ASGATING ICCITAS
205. ChLG10_R180278257_C17	ARTIGAG IG ITTCTACOG IMGAATGAC	- CGGCAAAATCCAA AT TG CAAGAA	TANG TOG CIXA	ARCTARCES TTOSS AMARTATAS CLARARA TTTAS TOTIS TTARA	
208. ChLG10_R180278257_C4	AATTGAG IG ITT CPACCG TAG AATGAC	CGGCAAAATCCAA -ATCIGCAAGAA	TCARG TCG CPAC	GACTAACCE TTUES AAAATATAG CCAAAAA-TTTAG CTTG TCAAA	ATTTA-TAGAAACCAAATAGT-CTTCCTTATTTTCTTGTAITTC-AGGACTATGTCCTTAG
207. ChLG10_R180278257_C5	AATTAAS IS ITTCTAACS TAS AATSAC-	- CGGUGGAATCCAA ATTIG CAAGAA	TCARG TUS CPAC	GAUTAACOS TTUSS AAAATATUSG CAAAAA TTTAGCUTTG TUAAA	- ATTTA TAGAACCAAATAS T CTTCATTATTTPCTTIS TATTC - ASS ACTAIS TCCTTAS
208. ChLG10_R180278257_C6	AATTAAG IS ITT CFAACG IAG AATGAC	- CGG GG AATCCAA - ATTTG CAAGAA	TCARG TOG CPAC	GAUTAACOG TTOGGAAAATATOGGCAAAAA -TTTAGECTTG TCAAA	ATTTA TAGAAACCAAATAGT-CTTCATTATTTCCTTG TATTC- AGGATTANGTCCTTAG
209. ChLG6_R180283422_C4	AATTAAG TO TTTCTAACG TAG AATGAC		-TCARG TELS CPAC	GACTAACCE TTCSE AAGATATCSE CAAAAA-TTTAACCTCG TCAAA	ATTTA TTAAAACCAAATAAT - CTTTATTATTTTCCTTTTATTC - AGG CT CATG TC - TTAG
210. ChLG6_R180283422_C7	AATTAAG TO TT T CTAACG TAG AATGAC	CGACGGAATCCAA-ATTTGCAAGAA	TCARG TCG CTAC	GACTAACCE TTCSE ARGATATCSE CAARAA-TTTAACCTCE TCAAA	AT TTA TTARAACCAAATAAT - CTTTATTATTTTCCTTTATTC AGG CTTATG TCCTTAG
211. ChLG6_R180283422_C3	AATTAAG TIS TT T CTAACG TAG AATGAC	CGGCGGAATCCAA ATTTGCAAGAA	TCAAG TCG CTAC	GACTAACCE TTCGGARCATATCGG CAARAA TTTAACCTCG TCAAR	- ATTTA TTARAACCAAATAAT CTTCATTATTTCCTTTATTC AGGCTTATGTCCTTRG
212. ChLG8_R180283422_C5	AATTAAG TO TT T CTAACG TAG AATGAC	- CGGCGGAATCCAA ATCTGCAAGAA	-TCARG TCG CTAC	GACTA-CCETTCEEA-GATATCEE CAAAATTTAACCTCETCAAA	TTTA - TTARAACCAAATAAT - CTTCATTATTTTCCTTT
213. ChLG6_R180283422_C6	AATTAAG TG TT T CTAACG TAG AA TGA C	- CGGCGGAATCCAA ATCTGCAAGAA	TCARG TCG CTAC	GACTAACCE TTCGE AR <mark>G</mark> ATATCGE CAAAAA-TTTA <mark>A</mark> CCT <mark>C</mark> G TCAAA	ATTTA TTARAACCAAATAAT-CTTCATTATTTCCTTTATTC- AGGCTTATG
214. ChLG6_R180283422_C8	AATTAAG IG IT T CTAACG IAG AA IGAC	CGGCGGAATCCAA ATTTGCAAGAA	TCAAG TCG CTAC	GACTAACOS TTOSSARSATATOSS CAARAA TTTAACCTOS TCARA	ATTTA TTARAACCAAATAAT-CTTTATTATTTTCCTTCTAFTC
215. ChLG8_R180283422_C2	ATTAG IG IT T CTACCACAG AATGAC	- CGGCGGAATCCAA ATCTGCAAGAA	TCAAG TCG CTAT	G ACTAACOG TTOGG AAAATATOG G CAAAAA-TTTAG CTTAG TOAAA	AT TTA - TCCRARCCRARTS T- CTTCATTAT TTTCCTTCTATTC AGC CTTATG TCCTTAG
218. ChLG3_2_R18029/352RC_C2	AATTGAG TG TT T CTAACG TAG AATGAC	- CGGCGGAATCCAA ATTTG TAAGAG	TCARG TCG CFG C	GACTAACCE TTCEE AAAATATCEE CAAAAA-TTTAGCCTCATCAAA	ATTTA TCCAAACCAAATAAT - CTTCATTATTTTCCTTCTAFTC GGGCTTATGTCCTTAG
217. ChLG3_2_R180297352RC_C4	AATTAAG TO TT T CTG ACG TAG AATGAC	CGGCGGAATCCAA-ATTTGTAAGAA	TCARG TCG CTG C	GACTARCOS TTUSS ARAATATUS CAARAA-TTTAGCCTOATCAAA	AT TTA - TCGAARCCAARTAG T- CTTCATTAT TTTCTTTCTATTC GGGGT CATG TC CTTAG
218. ChLG10_R180277964RC_C8	AATTGAG TO TT T CTAATG TAG AATGAC	CGGCGAAATCGAA AT TTG CAAGAA	TCAAG TCG CTAC	GACTAACCE TTCGG ARAATATCGG CTARAA TTTAGCCTTG TCAAA	
219. ChLG10_R18027/964RC_C12	AATTGAG IS TTTCPAACATAG AATGAC	- CGGCGGACTCCAA ATTTGCAAGAA-	-ICARG TOG CTAC	GASTARCONTOUS AGAATA TOGO CAAGA - TT TASCC TTG TCAAG	- ATTIA IUBAAACCAAACAST UTTCATTATITTCTTCTATTC-GGGGTCATGACGTTAG
220. ChLG10_R180277964RC_C5	AATTGAG TO TT T CTAACG TAG AATGAC	CGGCISE AATC CAA -AT TTG CAAGAA	TCARG TCG CTAC	G ACTAACCE TTCEE ABAATATCEE CEABAA -TTTAGCCTTE TCABA	AT TTA - TEGAARCEARATAG T- CTTCATTAT TTTC TT CTATTC GGGGTCATGACCTTAG
221. CnLG10_R18027/964RC_C11	AATTGAG IG TTTCTAACATAG AATGAC	COULSE A CTCCAA AT TTG CAAGAA	TUANG TOG CTAC	GAUTAAUGS TICGGAAAATATIGG CAAAAA TITAGIC TIG TCAAA	- ATTTA TUBAAACCAAATAG T CTTCATTATTTTCG TTCTATTC GGGGGACATGACCTTAG
222. CnLG10_R18027/964RC_C4	AATTGAG TE TT T CTARCE TAG AATGAC	- CGGCGGAATCCAA ATTTGCAAGAA	TCAAG TCG CTAT	GAUTAAUG TICGGAAAATATOGG CAAAAA - TITAGCCTTG TCAAA	- ATTIN INVAAACGAAACNGT-CTTCATTATTTTCTTCTNTTT-GGAGTCATGACCTTNG
223. ChLG10_R1802/7964RC_C10	AATTGAG IS ITTCTAATS TAG AATGAC		TCARG TOG CTO C	GACTARCES TTUES AAAATATUES CAAAAA-TTTAGECTIG TUAAA	ATTTA - TEGRAACCAAACAG T- ETTCATTATTTFCCTTETATTC GGGET CATE TCETTAG
224. ChLG10_R180276782_C3	AATTAATIG TTTCTAACG TAAAATGAT	CGTCGAAATCCAA-ATTTGCAAGAA	TCARG TCG CTAC	GACTAACCE TTC T E ARAATATC AAT AARAA TTTAG T C G TG C CAAA	AT TTA - TCGAAACCAAATAG T- CTTCATTAT TTTCC TTCTAT TT GGGGT TATG CTCTTAG
225. ChLG10_R180276782_C4	AATTGAG TO TT T CTAACG TAG AAT AAT	CGGCGGAATCCAA ATTTGCTAGAA	TCAGATCG CTAC	AACTAACOG TTCTAARAATATOG ACAARAA TTTAGCOG IG CCAAR	ATTTA TCGRARGCRARTAGT - CTTCATTRTTTTCTTCTTATTT - GGGGTCATGGCCTTRG
226. ChLG10_R180276782_C5	AATTAAG TE TT T CTAATE TE G AATEAC	- CGGCGGAATCCAA ATTTGCAAGAA	TCARG TCACTAC	GACTAACCETTCE CAAACATCEG CAAAAA-TTTAGCCCTG CCAAA	
227. ChLG10_R180276782_C2	AATTAAN IG IT I CIAACG IAG AATGA	GGCGGAAT CAA AT TTG CAAGAA	TCARG TCG CTAC	GACTAACCE IGCTE AAAATATCEG CAAAAA-TTTT	ATTTA - TCGAAACCAAATATT-CTTCATTATTTTCTTCTATTTC-GGGGTTATGGCCTTAG
228. CnLG3_2_R180295754RC_C1	AATTGAG TO TT T CTAACG TAG AATGAC	CGGCGGAATCTAA ATTTGCAAGAA	TCAAG TCG CTAC	GACTAACOS TTC SAAAS TATEGG CAAAAA TTTAGCCTTG TCAAA	- ATTTA TOGARACCAARTAG T-CTTCATTATTTTCCAACTATTT -GGGGTCATGTTCTTAG
229. ChLG3 2 R180295754RC CB	AATTGAG TI TT T CTAACG TAG AATGAC	CGGCGGAATCTAA AT TTG CAAGAA	TCAAG TCG CTAC	GACTAACCE TTCE ARAC TATCEG CAARAA TT TAGCC TTG TCAAA	ATTTA TCGAACCAAATAGT - CTTCATTATTTCCAACTATTT - GGGGTCATGTTCTTAG
230. CnLG3 2 R180295754RC C2	AATTGAG TO TT TCO AACG TAG AATGAC	- CGGCCSAATCCAA ATTTGCAAAAA	-1 AAG TOG CTAC	gactaacorffC saar tatege caaaa - TT tagec ttg teara	- ATTIN IUGAAACCAAATAG T-CTTCATTATTTTCCAACTATTT -GGGGTCATGTTCTTMG
231. CnLG3 2 R180295754RC C4	AATTGAG TO TT T CTAACG TAG AATGAC	CGGC AATCCAA ATTTG CAA AA	TTAAG TCG CTAC	GACTAACCUTCUE AAAG TATGGG CAAAAA TTTAGCCTTG TCAAA	- ATTR-TCGARACCARATAGT-CTTCATTATTTCCARCTATTTGGGGTCATGTTCTTAG
232. CnLG3 2 R180295754RC C3	AATTGAG TO TTTCCAACG TAG AATGAC	CGGC CAATCCAA ATTTG CAA	TTAAG TCG CTAC	G ACTAACOS TÉC T E AAA <mark>G</mark> TA T G GG CAAAAA - TT TAGCC TTG TCAAA	- ATTTA TUGAAACCAAATAGT CTTCATTATTTTCCAACTOTT GGGGTCATGTTCTTAG
233. CnLG3 2 R180295754RC C7	ARTIGANTS IT T CEARCE TAS ARTGAC	CGGCGGAATCCAA ATTTGCAA	TTAAG TCG CTAC	G ACTAACCE TECTE AAA <mark>G</mark> TA T <mark>E</mark> GE CAAAAA - TT TAC <mark>G</mark> C TTE TCAAA	
234. CnLG3 2 R180295754RC C9	AATTGAG TO TT T CPAACG TAG AATGAC	COGUES AATCTAA ATTTE CAAGAA	TCARG TOG CTAC	GACTAACCE TTCE AAAATATCEG CAAAAA TTTAGCCAIG TCAAA	- ATTTN-TOGAAACCAAATAGT-CTTCATTATTTTCCAACTAFTT -GGGGTCATGTTCTTAG
235. CnLG3_2_R180295754RC_C8	AATTGAG TO TT T CTAACG TAG AATGAC	- CGGCGGAATCTAA ATTTG CAAGAA	TCARG TCG CTAC	G ACTAACOS TECGE AAAATATEG CAAAAA - TTTAGCCTTG TCAAA-	- ATTTA TUGAAACCAAATAGT CTTCATTATTTTCCAACTATTT GGGGTCATGTCCTAAG
236. CnLG3_2_R180295754RC_C5	AATTGAG TI TT T CTAACG TAG AATGAC	CGGCGGAACCTAA ATTTG CAAGAA	TCAAG TCG CTAC	G ACTAACOS TFCTS AAAATATOGG CAAAAA TTTAGCCATG TCAAA	ATTTA TOGARACCARATAGT GTTCATTATTTTCTATCTATTT GGGGTCATGTCCTTAG
237. CnLG9_R180292048RC_C4	AATTGAG TO TT T CTO ACG TAG AA TAA C	OUGOLE AATCCAA ATTTE CAAGAA	TCAATTOG CTAC	GACTAACCUTTATEAAAATATCEGCAATAA-TTTAGCCTTGTCAAA-	- ATTTA TUGAAACCAAATTTT-CTTCATTATTTTTCAACCATTT -GAGATTATGTTCTTAA
Z38. GILG9_K180292048RC_C6	AATTAAG TO TT T CTAACG TAG AATGAC	- COUCES AATC CAA AT TTG CAAGAA	TCARG TOS CTAC	SALTAACOS TTCTS ABAATATTGG CAABAA TTTAGCCTTG TTABA	- ATTTA TOGARACCRARTETT-CTTCATTATTTTCARCONTT - GAGATTATGTTCTTA
Z39. ChLG3_2_R180297352RC_C5	AATTGAG IG TTTCIGACG TAG AATAAC	GGCGG AATCCAA ATTTG CAAGAA	TCAAG TOG CTG C	GALTAACOS TECTS ARAATA TOGG CAAGAG TT TAGCC TIG TCAAR	ATTTA TOGARACCARA TAG T CTTCATTATTTTCATCTNTTC GAG TTTATG TTCTTAG
240. ChLG3 1 R180292427 C2	AGTTGAG TO TT T CTARCE TAG AR TGAC	CUGCEG AATCCAA ATTTE CAAGAA	TCAAG TCG CTAC	G ACTAACOS TECGE AAAATA TOSG CAAAAA - TT TAGCC TEG TCAAA	
241. ChLG3 2 R180296218RC C1	AATTGAG TETT T CTAACG TARAATGAC	CAGTGG AATC CAA AT TTG CE AGAA	TCARG TCG CTAC	G ACTAACCIS TT <mark>AT</mark> S AAAATA TOSG CAAAAA - TT TAGCC TTG TO <mark>S</mark> AA	
242. CnLG3_2_R180297332RC_C4	ARTIGAG IS ITT CTARCE IAG ARTAC	CGGCGGAATCCAA ATTTGCAAGAA	TCAAG TCG CTAC	GACTARCOS TTCT BARAATATOGG CGARAA TTTRGCCTTG TCARA	ATTTA TCGAAACCAAA TAG T-CTTCATTATTTTCG TTACG TTCGG <mark>G</mark> GTTAT <mark>G</mark> TTCTTAG
243. ChLG3 2 R180296909 C3	AATTGAG TE TT TO <mark>G</mark> AROG TAG AATGAC	- CGGCGG AATCCAA - ATTTG CAAGAA	TTAACTCG CTAC	GACTAACCOTTCTCGAAATATCGGCAAAAA-TTTAGCCTTGTCAAA	

244 Chi G3 2 R180296909 C4
245. ChLG3 2 R180296909 C2
246. ChLG3_2_R180296909_C5
247. ChLG3_2_R180296909_C14
249 Chi G3 2 R180296909 C0
250. ChLG3 2 R180296909 C11
251 ChLG3 2 R180296909 C9
252. ChLG3_2_R180296909_C1
253. ChLG3_2_R180296909_C8
255 ChLG3 2 R180296909 C12
256. ChLG3 2 R180296909 C13
257. ChLG3_2_R180297332RC_C9
258 ChLG3 2 R180297332RC C7
259 ChLG3 2 R180297332RC C5
261 Chi G3 2 R180296216RC C5
262. ChLG9 R180291738RC C3
263. ChLG3_2_R180296218RC_C5
264. ChLG3_2_R180296216RC_C3
265. ChLG3 2 R180296216RC C4
267. Chi G9 R180291738RC C4
268. ChLG9 R180291738RC C5
269. ChLG3_2_R180296216RC_C6
270. ChLG3_2_R180296218RC_C3
271. CHLG3_2_R180287352RC_C3
273. ChLG3 2 R180296218RC C4
274. ChLG3 2 R180297342 C6
275. ChLG3_2_R180297342_C9
276. ChLG3_2_R180296216RC_C1
277. ChLG3_2_R180297342_C8
279 Chl G3 2 R180297342 C7
280. ChLG3 2 R180297342 C2
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282. ChLG3_2_R180297342_C16
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284. CHLG3 2 R18029/342 C15
286 Chl G3 2 R180297342 C3
287 ChLG3 2 R180297342 C12
288. ChLG3_2_R180297342_C14
289. ChLG9_R180291738RC_C6
290. ChLG9_R180292003RC_C7
292 Chi G9 R180292003RC C10
293. ChLG9_R180292003RC_C4
294. ChLG9 R180292048RC C5
295. ChLG9_R180292048RC_C7
296. ChLG9_R180292048RC_C3
297. ChLG10_R180277145_C5
299. Chi G10 R180277145 C2
300. ChLG3 T R180292427 C4
301. ChLG3_1_R180292427_C6
302. ChLG3_1_R180292427_C3
303. ChLG10_R180277145_C11 204_ChLG10_R180277064DC_C12
305 Chi G9 R180292048RC C2
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309. ChLG9_R180292045RC_C/
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318 Chi G9 R180292045RC C4
319, ChLG9 R180292045RC C8
320. ChLG9_R180292045RC_C13
321. ChLG9_R180292045RC_C10
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	АТТІС САЙДАА АТТІС САЙДАА АТТІС САЙДАА АТТІС САЙДАА АТТІС САЙДАА АТТІС САЛДАА АТТІС САЛДАА	TCAME TOO CEAC TCAME TOO CEAC	CALTAACGT CACTAACGT
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326	ChLG9_R180291738RC_C2	AATTGA <mark>O</mark> TG TT T CT <mark>G</mark> ACG TAG AATGAC	- GGCGG AATC CAA - AT TTG CAAGAA	-TCAAG TTG CTGG	G AC TAACOG TT <mark>AT</mark> G AAAA TA TOGG CAAAAA TT TAG <mark>A</mark> C TTG TCA	AAAT TT	-TCARAACCAAATTTT-CTTCATTATTTTCCAACTATTC	
327	. ChLG9_R180291738RC_C7	AATTGANIG TT T CTG ACG TAG AATGAC	TGGCGGAATCCAA -ATTTGCAAGAA	TCARCTOG CGAC	G ACTAACCE TT <mark>AT</mark> E AAAATATCEG CAAAAA-TT TAGCC TTG TCA	AAAT TTA	TCGAAACCAAATTTT-CTTCATTATTTTCCAACTATT	
328	. ChLG3_2_R180297332RC_C3	ARTT AG TG TT T CCAACG TAG ARTGAC	-CGGCGGAATCCAA-ATTTGCAAGAA	-TCAAG TOG CTAC-	GACTARCOS TTC <mark>I</mark> G RARATATOGG CRARAR-TTTAGCCTTG TCR	AAATTTA	-TTGRARCCAARTTTT-CTTCATTATTTTCCARCTCTTC	
329	. ChLG3_2_R180297332RC_C8	AATTGAG TG TT T CFAACG TAG AATGAC	-CGGCGGAATCCAA ATTTGCAAGAA	-TCAAG TTG CTAC-	GACTAACOS TT AT S AAAATATOS <mark>A</mark> CAAAAA - TT TAGCCTTG TCA	AA ATTTA	-T TG RAACCAAR T TTT-CTTCATTATTTTCCAACT C ITC	GTTACTATGTCCTTAG
330	. ChLG9_R180292003RC_C2	AATTGAG IG IT I CTAACG IAG AATGAC	-OGGOOGAATCCAA -ATTTGCAAGAA	-TCARG TCG CTAC-	GACTAACCTTTCGGAAAATATCGGCAAAAA-TTTAGCCTTGTCA	AAAT TTA	-TCGARACCARATITT-CTTCATTATTTTCCRACTATTC	GGARTTATC TC CTT AG
331	. ChLG6_R180284364RC_C7	AATGAG IG TT I CFAACG IAG AATGAC	-OGGOGGAATCCAA -ATTTGCAAGAA	-TCARG TOG CTAC-	G ACTAACCE TTCEE AAAATATCEE CAAA <mark>G</mark> A-TTTAGCCTCE TCA	AAATTIG	-TTGAAACCAAACTTA ATTAATTATTTCCAACTATTC	GGGATAATGTCCTTAG
332	. ChLG6_R180284364RC_C9	AAATGAG TG TT T CTAACG TAG AATGAC	-CGGCGGAATCCAA-ATTTGCAAGAA	-TCAAG TOG CTAC-	GACTAACOS TEOSGAAAATATOSG CAAM <mark>G</mark> A-TETAGCCT <mark>O</mark> G TCA	AAATTIG	-TTGAAACCAAACTTA ATTAATTATTTTCCAACTATTC	GGGATAATS TCCTTAG
333	. ChLG6_R180284364RC_C8	AAATGAG TG TT T CTAACG TAG AATGAC	CGGCGGAATCCAA ATTTGCAAGAA	TCAAG TCG CTAC	g actaacos teos raaatatoss caaa <mark>s</mark> a - te tascet <mark>o</mark> s tea	AA AT TD3	-TIGAAACCAAACTTA ATTAATTATTTTCCAACTATT	CTGGGATAATG TCCTTAG
334	. ChLG6_R180284364RC_C1	ATTGAG IG TT I CTAACG TA A AA TG <mark>C</mark> C	-CGGCGGAATCCAA -ATCTGCAAGAA	-TCARG TOG CTAC-	GACTAACCE TTCEE AAAATATCEE CAAM <mark>G</mark> A-TTTAGCCTCE TCA	AAATTIG	-TIGAAACCAAACTTA-ATTAATTATTTTCCAACTATTC	AG <mark>G AT A ATG</mark> TCCTT AG
335	. ChLG6_R180284364RC_C6	AATTGAG TG TT T <mark>A</mark> TAACG TAG AATGAC	-CGGCGGAATCCAA-ATTTGCAAGAA	TCARG TCG CTAC	<mark>A</mark> AC TAAC OF TTOEG ARAA TA TOEG CAARAA - TT TAGC <mark>T</mark> TO <mark>G</mark> TC A	ARATTIG	-T <mark>TG</mark> AAACCAAACTT A A TT A ATTATTTTCCAACT A TTC	GG <mark>GATA</mark> AT <mark>G</mark> TCCTTAG
336	. ChLG6_R180284364RC_C12	AATTGAG TG TT T CTAACG TAG AA TGAC	CGGCGGAATCCAA GTTTGCAAGAA	TCAAGGCG CTAC	GACTAACOS TTOSGAAAATATOSG <mark>G</mark> AAAAA - TTTAGC <mark>T</mark> TOG TCA	AAATTTG	-TTGAAACCAAACTTA-ATTAATTATTTTCCAACTATTC	GGGATAATG TC CTT AG
337	. ChLG6_R180284364RC_C3	AATTGAG TG TT T CTAROG TAG ARTGAC	-OGGCGG <mark>G</mark> ATCCAA ATTTGCAAGAA	-TCARG TCG CTAC-		AAAT TT <mark>A</mark>	-TCCAAACCAAACTTA ATTAATTATTTTCCAACTATT	GG AGT TAT <mark>G</mark> TC CTT AG
338	. ChLG6_R180284364RC_C5	AATTGAG TG TT T CTAACG TAG AATGAC	CGGCGG <mark>G</mark> ATC CAA -ATTTG CAAGAA	-TCARG TCG CTAC-	G ACTAACCE TTCGG AAAATATCGG <mark>G</mark> AAAAA-TTTAGC <mark>T</mark> TCG TCA	AAATTTA	-TCCAAACCAAACTTA-ATTAATTATTTTCCAACTATT	GGAGTTAT <mark>G</mark> TCCTTAG
339	. ChLG6_R180284364RC_C10	ARATGAG TG TT T CTARCG TAG ARTGAC	-CGGCGGAATCCAA-ATTTGCAAGAA	-TCARG TCG CTAC-	G ac taa coe ttogg abaa ta togg caabaa -tt tagc <mark>t</mark> tog tob	AAAT TTG	- T <mark>TG</mark> AAACCAAACTT A A TT A ATTATTTTCCAACT A IT	GGAGTTAT <mark>G</mark> TCCTTAG
340	. ChLG6 R180284364RC C13	AATTGAG TG TT T CTAACG TAG AATGAC	CGGCGGAATCCAA ATTTGCAAGAA	TCAAG TCG CTAC	g actaac <mark>g</mark> e tto <mark>a</mark> s aaaa tatoge caaaaa - tt tago <mark>t</mark> toe toa	AR AT TIG	-TIGAAACCAAACTTA ATAAATTATTTTCCAACTATT	- GGAGTTAT <mark>G</mark> TCCTTAG
341	. ChLG6_R180283958_C16	A <mark>C</mark> TTGAG TG TT T CTAACG TAG AA T <mark>C</mark> A <mark>T</mark>	-CGGCGGAATC TAA -AT TTG CAAGAA	-TCARG TOG CTAC-	G act <mark>g</mark> acos tross aga tatos <mark>t</mark> orada a -tt tago <mark>t</mark> tos tea	aa at tt <mark>a</mark>	-TECAAACCAAACTTA-ATTAATTATTTTCCAACTATTC	GG <mark>C A</mark> TTAT <mark>C</mark> TC CTTAG
342	. ChLG6_R180284364RC_C2	AATTGAG TG TT T CTAACG TAG AATGAC	- T GGCGGAAT <mark>A</mark> CAA -ATTTG CAAGAA	-TCARG TCG CTAC-	Gactaac <mark>s</mark> e TTC <mark>a</mark> s Abaatatce <mark>T</mark> CAAbaa-TTTAG <mark>T</mark> CT <mark>C</mark> ETCB	AAATTTA	CCAAACCAAACTTT-ATTAATTATTTTCCAACTATTC	RGCATAATC TTAG
343	ChLG6 R180284364RC C4	AATTGAG IG IT T <mark>A</mark> FAACG IAG AATGAC	-CGGCGG AATC CAA -AT TTG CAAGAA	TCAAG TCG CTAC	G ACTAAC <mark>G</mark> G TTC <mark>A</mark> G AAAATATCG <mark>T</mark> CAAAAA - TTT <mark>T</mark> G T C T C G TCA	AA AT TT <mark>A</mark>	-TCGAAACCAAACTTT-ATTAATTATTTTCCAACTATTC	- Ag g a t a at g tc c tt ag
344	. ChLG10_R180276690_C4	AATTGAG IG TTTCTAACG TA <mark>A</mark> AAT <mark>A</mark> AC	-CGGCCGAATCO <mark>G</mark> A - AT TTG <mark>T</mark> AAGAA	-TCAAG TCG CTAC-	<mark>C</mark> actaacos TTOSS Aaaat <mark>t</mark> Tos <mark>T</mark> CAAAAA <mark>a</mark> tt tas <mark>T</mark> CTTS TCA	AAAT TIG	-TETRAACCAAACTTT-CTTCATTATTTTCCACCTTTTC	ATAGCTATTTTAG
345	. ChLG6_R180283958_C18	aattgag te <mark>c</mark> tt ctaace tae aate <mark>e</mark> c	-CGGCGGAATC CAA -ATTTG CAAGAA	-TCARG TCG CTAC-	G actaacos ttogg aaaatatog <mark>t</mark> caaaaa - tt ta <mark>at</mark> c t <mark>o</mark> g tca	AAATTTC	-TCTAAACCAAACTT <mark>C</mark> -CTTCATT <mark>G</mark> TTTTCCAA <mark>T</mark> TTTT	AT AGTTATTT T CTTA A
346	. ChLG10_R180276690_C5	AACTGAG IG TOT COAACG TAG AA TGAT	-CCGCGGAATCCAA ATTT <mark>A</mark> CAAGAA	TCAAG TCG CTAC	GACTARCOS TTOGGRAAATATOG <mark>T</mark> CRAAAA TT TAGCC T <mark>O</mark> G TCA	AA AT T <mark>AT</mark>	CT-AAACCAAACTTT-CTTCATTATTTTC	AT AGT TATT TC T TT AG
347	. ChLG10_R180276690_C7	aa <mark>c</mark> tgag ig it t c <mark>c</mark> aacg iag aa tga <mark>t</mark>	-CGGCGGAATCCAA-ATTT <mark>A</mark> CAAGAA	-TCAAG TCG CTAC-		AAAT TT <mark>T</mark>	- T <mark>T</mark> TRANCCARACTT <mark>R</mark> -CTTCATTATTTTCCAACTTTTC	CATAGTTATTTCTTAG
348	. ChLG6 R180283958 C9	AATT <mark>C</mark> AG IG IT I CI <mark>C</mark> ACG IAG AA IG <mark>C</mark>	- CGGCGGAATCCAA - ATTTGCAAGAA	-TCARG TCCC TAC-		AATTTG	-TTIGAACCAAATTTT-CTT-ATTATTTTCCAACTTTTC	AT AGTTATT <mark>C</mark> CCTTAG
349	. ChLG6 R180283958 C12	AATT CAG IG IT I CI <mark>G</mark> ACG IAG AA IG <mark>G</mark> C	-CGGCGGAATCCAA ATTTGCAAGAA	-TCAAG TCCGTAC-	G AC TAAC OF TTOGG AAAA TA TOG <mark>T</mark> CAAAAA - TT TAG <mark>T</mark> C T <mark>O</mark> G TC A	AATTTG	-TTTGAACCAAATTTT-CTT-ATTATTTCCAACTTTTC	RT AGTTATT C CCTTAG
350	. ChLG6 R180283958 C15	AATTCAG IG IT I CI <mark>G C</mark> CG IAG AATG <mark>G</mark> C	CGGCGGAATCCAA ATTTGCAAGAA	-TCAAG TCCGTAC-	g ac taa cos teoss aaaa tatos <mark>t</mark> caaaaa - tt tas <mark>t</mark> c t o s tca	AR TTG	-TTTGAACCAAATTTT-CTT-ATTATTTTCCAACTTTTC	- ATAGTTATTCCCTTAG
351	ChLG6 R180283958 C6	AATT <mark>C</mark> AG IG IT I CI <mark>G</mark> ACG IAG AA IG <mark>G</mark> C	-OGGOGGAATCCAA -ATTTGCAAGAA	-TCARG TCCC TAC-	G ac taacog ttogg aaaa ta tog <mark>t</mark> caaaaa - tt tag <mark>t</mark> c t <mark>o</mark> g tca	AAATTIG	-TTIGAACCAAATTTT-CTTTATTATTTCCAACTTTTC	AT AGT TATT CCTTAG
352	ChLG6 R180283958 C2	AATTGAG TG TTT CTAACG TAG AATGAC	- OGGC AGAATC CAA - AT TTG CAAGAA	-TCARG TCCGTAC-		AAAT TTG	-TTTGAACCAAATTTT-CTTTATTATTTCCAACTTTTC	AT AGTTATT C CCTTAG
353	. ChLG6 R180284364RC_C11	AATTG <mark>G</mark> G TG TT T CTAACG TAG AATGAC	-CGGCGGAATCCAA-GTTTGCAAGAA	-TCAAG TOG CTAC-	G AC TAAC OS TTOGG AAAA TA TOGG CAAAAATT TAG <mark>T</mark> C T <mark>O</mark> G TC A	AAAT TTG	-TTTAAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	RT AGTTATTTCCTTAG
354	ChLG6 R180283958 C3	a <mark>g</mark> ttgag tg tt t ctarcg tag artgac	CGGCGGAATCCAA ATTTGCAAGAA	TCAAG TCG TAC	g ac tarcos ttogg rara tatogg craara 🔒 tagce tog ter	AA AT TES	-TTTAAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	AT AGTTATT <mark>C</mark> CCTT <mark>GA</mark>
355	. ChLG6 R180283958 C7	A <mark>C</mark> TTGAG IG TT I CTAACG IAG AATGAC	-CGGCGGAATCCAA ATTTGCAAGAA	-TCAAG TCG TRAC-		AAAT TIG	-TTTRAACCARACTTT-CTTCATTATTTTCCARCTTTTC	AT AGTTATT <mark>C</mark> CCTT <mark>GA</mark>
356	. ChLG6 R180283958 C10	a <mark>g</mark> ttgag tg ttt ctaacg tag aa t <mark>c</mark> a <mark>t</mark>	-CGGCGGAATCCA <mark>T</mark> -ATTTGCAAGAA	-TCAAG TCG TAC-	G AC TAAC OF TTOGG AAAA TA TOGG CAAAAA - <mark>A</mark> T TAGCC T <mark>O</mark> G TC A	AAAT TTG	-TTTAAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	C <mark>AT</mark> AGTTATT <mark>C</mark> CCTT <mark>GA</mark>
357	. ChLG6 R180284279RC C10	AATTGAG TG TT T CTAACG TAG AATGAC	CGGCGGAATCCAA ATTTGCAAGAA	TCAAG TCG TAC	GACTAACOS TTOSGAAAATATOSG CAAAAA - TTTAGCCT <mark>CC</mark> TCA	AA AT TIG	-TTTAAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	At agttatt c ctta a
358	ChLG6 R180283958 C8	AATTGAG IG IT I CTAACG IAG AATAAC	-OGGOGGAATCCAA -ATTTGCAAGAA	-TCAAG TOG CTAC-	G AC TAACOG TTOGG A <mark>C</mark> AATATOGG CAAAAA-TT TAG <mark>T</mark> C T <mark>O</mark> G TCA	AAAT TIG	-TCTRARCCARACTTTTTCATTATTTTCCARCTTTTC	AT AGTTAT <mark>ACTT</mark> TTA <mark>A</mark>
359	ChLG6 R180283958 C11	AATTGAG IG ITT CTAACG TAG AATAAC	-OGGCGGAATCCAA ATTTGCAAGAA	-TCARG TCG CTAC-	G ac taa coe troeg a <mark>c</mark> aa ta togg caaaaa - tt tag <mark>e</mark> c t <mark>o</mark> g toa	aaaa tite	-TCTAAACCAAACTTTTTCATTATTTTCCAACTTTTC	AT AGT TAT <mark>ACTT</mark> TT A <mark>A</mark>
360	. ChLG6 R180283958 C5	AATTGAG TG TT <mark>G</mark> CTAACG TAG AATGAC	-CGGCGGAATCCAA -ATTTGCAAGAA	-TCARG TOG CTAR-	G AC TAAC OF TTOGE ACAA TATOF G CAAAAA TT TAG <mark>T</mark> C TOG TC A	ARAT TTG	-TCTRARCCARACTTTTTCATTATTTTCCARCTTTTC	AT AGT TAT <mark>ACT T</mark> TT A <mark>A</mark>
361	. ChLG6 R180283958 C14	AATTGAG TG TT T CTAACG TAG AATGAC	CGGCGGAATCCAA ATTTGCAAGAA	TCAAG TCG	g actaacos ttoss raaatatoss caaara - tt tagcc t <mark>o</mark> s tca	AR ATTEG	-TTTAARCCAAACTTTTTCATTATTTTCCAATTTTTC	- At agt tat <mark>act t</mark> tta <mark>a</mark>
382	ChLG6 R180284279RC C12	AATTGAG IG TT I CTAACG IAG AATGAC	-OGGOGGAATCCAA -ATTTGCAAGAA	-TCARG TCG TRAC-	G AC TAAC CE TTCEE AAAA TA TCE G CAAAAA TT TAG CC T <mark>C</mark> E TCA	AAATTIG	-TTTAAACCAAACTTT-CTTCATTATTTCCAACTTTTC	C <mark>AT</mark> AGTTATT <mark>C</mark> CCTTAG
363	. ChLG6 R180284279RC C17	AATTGAG IG TT I CTAACG TAG AATGAC	-CECCE AATC CAA -ATTTE CAAGAA	-TCARG TCG TAC-	G AC TAAC CE TTCEG AAAA TA TCEG CAAAAA - TT TAGCC T <mark>C</mark> E TC A	AAAT TTG	-TTTAAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	RT AGTTATT C CCTTAG
364	. ChLG6 R180284279RC C3	AATTGAG TG TT T CTAACG TAG AATGAC	CGGCGG AATC CAA AT TTG CAAGAA	TCAAATCG CTAC	GACTARCOS TROGG CARATATOS GCARAAA TTTAS CCTCC TCA	ARATTES	-TTTAAACCAAACTTT-CTTCATTATTTTCCAACTIC	
365	. ChLG6 R180284279RC C4	AATTGAG IG IT <mark>G</mark> CTARCG IAG AATGAC	-OGGOGGAATCCAA -ATTTGCAAGAA	-TCAAG TOG CTAC-	G AC TAACOG TTOGG <mark>C</mark> AAA TA TOGG CAAAAA TT TAGCC T <mark>CO</mark> TCA	AAATTIG	-TTTRAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	AT AGT TATT CCTTAG
366	. ChLG6 R180284279RC C8	AATGAG IG TT I CCARCG IAG AATGAC	-OGGCGGAATCCAA ATTTGCAAGAA	-TCARATCG CTTC-		AAAT TTG	-TTTAAACCAAACTTT-CTTCATTATTTTCCGACTTTTC	AT AGTTATT C CCTTAG
367	. ChLG6 R180284279RC C11	AAATGAG TG TT T CCAACG TAG AATGAC	-CGGCGGAATCCAA -ATTTGCAAGAA	TCAAATCG CTTC-	GACTARCOS TEOGGAAAATATOGG CAAAAA TEAGCCTCC	ARAT TIG	-TTTAAACCAAACTTT-CTTCATTATTTTCCGACTTTTC	
368	. ChLG6 R180284279RC C5	AAATGAG IG TT I CCAACG IAG AATGAC	CGGCGGAATCCAA ATTTGCAAGAA	TCAAG TAG CTAC	G ACTARCOS TEOSS ARARTATOSS CRARAR TETROSCOT <mark>CO</mark> TCA	AR ATTES	-TTTAAACCAAACTTT-CTTCATTATTTTCCGACTTTTC	- ATAGTTATTCCCTTAG
369	. ChLG6 R180284279RC C15	AATTGAG IG IT I CTAACG IAG AATGAC	-OGGCGGAATCCAA -ATTTGCAAGAA	-TCARATCG CTTC-	G actaa coe ttoeg aaa a ta toeg caaaaa -tt tag cc t <mark>oo</mark> tca	AAATTIG	-TTTAAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	AT AGTTATT C CCTTA A
370	ChLG6_R180284279RC_C13	AATTGAG IG IT I <mark>G</mark> TAACG TA A AATGAC	-CAGCEG AATC CAA -AT TTG CAAGAA	-TCARG TOG CTAC-	G act aa coe trogg <mark>c</mark> aaa ta togg caaaaa tt tag cot <mark>o</mark> g to a	AAAT TTG	-TTTAAACCAAACTTT-CTTCATTATTTTCCGACTTTTC	AT AGTTATT CT CTTAG
371	. ChLG6 R180284279RC C18	AATTGAG IG IT T <mark>G</mark> TAACG TA R AATGAC	-CAGOGG AATC CAA -AT TTG CAAGAA	-TCAAG TOG CTAC-	GACTARCOS TEOGS CARATATOS GCARARA-TETAS CCTOS TCA	AAAT TTG	-TTTAAACCAAACTTT-CTTCATTATTTTCCGACTTTTC	AT AGT TATT CT CTT AG
372	. ChLG6 R180284279RC C7	AATTGAG IG IT I CTAACG IAG AATGAC	-OGGOGGAATCCAA -ATTTGCAAGAA	-TCAAG TOG CTAC-	G AC TAACOG TTOGG CAAATATOGG CAAAAA TT TAGCC T <mark>O</mark> G TCA	ARATTIG	-TTTRAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	AT AGTTATT C CCTTAG
373	ChLG6_R180284279RC_C9	AATTGAG TG TT T CTAACG TAAAATGAC	- CGGCGGAATCCAA - ATTTGCAAAAA	-TCAAG TCG TAC-	G actaa coe troge <mark>c</mark> aaa ta toge caaaaa - tt tag cct <mark>o</mark> g tc <i>a</i>	AAATTIG	-TTTAAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	AA AG <mark>G</mark> TATT <mark>C</mark> CCTTAG
374	. ChLG6 R180284279RC C16	ARTGAG TG TT T CCAACG TAG AA TGAC	-CGGCGGAATCCAA ATTTGCAAAAA	-TCAAG TOG TAC-	GACTAACOS TTOGG CAAATATOGG CAAAAA-TTTAGCCTOG TCA	ARAT TTG	-TTTAAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	ARAGG TATT CCTTAG
375	. ChLG6 R180284279RC C6	AATTGAG TG TT T CTAACG TAG AATGAC	CGGCGARATCCAR AT TTG CAAGAA	TCARG TAG CTAC	g actaacog teogg caaatatogg caaaaa - tetagcetog tea	AR ATTES	-TTTAAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	- MAAG <mark>G</mark> TATT <mark>O</mark> CCTTAG
376	. ChLG6 R180284279RC C2	AATTGAG IG IT I CTARC <mark>A</mark> TAG AATGAC	OGG CGG AAT C CAA - A T CTG CAAGAA	-TCARG IGG TFAC-	G actaa coe tto <mark>t</mark> e aaa a ta toeg caaaaa - tt tagec t <mark>o</mark> e tea	ARAT TIG	-TTTRAACCARACTTT-CTTCATTATTTTCCAACTTTTC	AA AG <mark>G</mark> TATT <mark>C</mark> CCTTAG
377	ChLG6_R180284279RC_C14	AATTGAG TG TT T CTAACG TAG AATGAC	-CGGCGG AATC CAA -AT TTG CAAGAA	TCARG TCG CTAC	GACTAACCE TT <mark>TA</mark> G AAAA TA TOGG CAAAAATT TAGCC T <mark>CC</mark> TC A	AAAT TTG	-TTTAAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	AAAGG TATT CCTTAG
378	. ChLG6 R180284279RC C19	ARTTGAG TG TT T CTARCE TAG ARTGAC	CGGCGGAATCCAA ATTTGCAAGAA	TCAAG TOG CTAC	GACTAACOS TI <mark>TA</mark> S AAAATATOSG CAAAAA - TTTAGCCT <mark>CC</mark> TCA	ARATTIG	-TTTAAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	
379	. ChLG6 R180284279RC C20	AATTGAG IG IT I CTAA <mark>T</mark> G IAG AATGAC	-OGGOGGAATCCAA -ATTTGCAAGAA	-TCAAG TOG CTAC-	G AC TAACOG TI <mark>TA</mark> G AAAA TA TOGG CAAAAA - TT TAGCC T <mark>O</mark> G TCA	AAATTEG	-TTTRAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	AT AGT TATT CC CTT AG
380	ChLG6 R180283958 C17	AATTGAG TG CTT CTAACG TAG AATGAC	-CGGCGGAATCCAA ATTTGCAAGAA	-TCARG TOG CTAC-		AAATTTA	-TTTAAACCAAACTTT-CTTCATTATTTTCCAACTTTTC	AA AGTTATT <mark>C</mark> CCTTAG
381	. ChLG5_R180282757_C6	aat <mark>a</mark> gag <mark>b</mark> g tt t c <mark>c</mark> aacg tag aatga c	CAGCE AATC CAA -AT TTG CAAGAA	-TCARG TCG CTAC-	G ACTAACOS TTOSS ABAATATOS <mark>T</mark> CAABAA-TT TAGCC T <mark>O</mark> S TCB	CR AT TTG	-TCTAAACCAAATTTT-CTTCATTATTTTCCAACTTTTC	AA AGTTATT CCT TTAG
382	. ChLG5_R180282757_C10	aat <mark>a</mark> gag <mark>a</mark> g itt t c <mark>c</mark> aacg tag aatgac	-CAGCGARATCCAA AT TTG CAAGAA	TCAAG TCG CTAC	g actaacos trogs aaaatatos <mark>t</mark> caaaaa - tt tagcc t <mark>o</mark> s tca	CA AT TIG	-TCTAAACCAAATTTT-CTTCATTATTTTCCAACTTTTC	- AA AGTTATT <mark>CCT</mark> TTAG
383	. ChLG5_R180282757_C5	AATAGAG AG TT TOCAROG TAG AATGAC	-CAGCGAAATCCAA ATTTG CAAGAA	-TCARG TOG CTAC-	G AC TAACOG TTOGG AAAA TA TOG <mark>T</mark> CAAAAA TT TAGCC T <mark>O</mark> G TCA	CAATTIG	-TETRAACCAAATTTT-ETTCATTATTTTCCAACTTTTC	
384	. ChLG5_R180282757_C7	AAT <mark>A</mark> GAG <mark>A</mark> G TT T C <mark>C</mark> AACG TAG AATGAC	-CAGCGAAATCCAA -ATTTG CAAGAA	-TCARG TCG CTAC-	Gactaacos TTCG <mark>a</mark> aaaatatos <mark>T</mark> CAAAAA-TTTAGCCT <mark>O</mark> S TCA	CA AT TTG	-TCTAAACCCAATTTT-CTTTATTATTTTTCAACTTCTC	ACAGTTATTCCTTTAG
365	. ChLG5_R180282757_C11	AATAGAG AG TT T CCAACG TAG AA TGAC	CAGCGAAATCCAA ATTTGCAAGAA	TCAAG TOG CTAC	GACTARCOS TTOS RAAATATOS TCRAAAA TTTAGCCTOS TCA	CA AT TIG	-TCTAAACCCAATTTT-CTTTATTATTTTTCAACTTCTC	ACAGTTATTCCTTTAG
386	. ChLG5_R180282757_C13	AATTAAGAG TTTCTAACATAAAATGAC	-GGCGGAATCCAA AT TTG CAGGAA	-TCAAG TOG CTAC-	G A <mark>t</mark> taacog TTC <mark>O</mark> G AAAATATOG <mark>t</mark> caaaaa - TT tagcc tog TCA	CAAT TIG	-TCTRARCCORATITT-CTTCATTATTTTCAACTTCTC	ATTOCTTTAG
387	. ChLG5_R180282757_C2	AATAGAG AG TTTCCAACG TAG AATAAC	-OGGCAAAATCAAA ATTTGGACGAA	-TCARG TOG CTAC-	G ACTARCOS TTOSS AARATATOS <mark>T</mark> CRAAAA TTTAGO <mark>S</mark> TOS TCA	CAATTIG	-TCTAAACCAAATTTT-CTTCATTATTTTTCAATTTTTC	
368	. ChLG5_R180282757_C3	AATTAACTG TTT CTAACG TAG AATGAT	-CGGAGAAATTCGA ATTTG CAAGAA	-TAAAG TCG CTTT	GACTAACC <mark>CITCC</mark> FAAAATATCG <mark>T</mark> CAAAAA-TTTAGCCTCGTCA	CAAT TTG	-TCTAABCARGATTTT-CTTCATTATTTTTCAATATTTC	AAAGTTATTCCCTTAG
389	. ChLG5_R180282757_C8	AATT AAAA G TTT CTAACG TAG AATGA T	CGGAGAAATTOGA ATTTG CAAGAA	TAAAG TCG CTTT	g actaaccottog baaatatog <mark>t</mark> caaaaa - TT tagcotog toa	CA AT TIG	-TCTAARCANGATITT-CTTCATTATTTTCAATATTTC	- AAAGTTATTCCCTTAG
390	. ChLG5_R180282757_C12	AATTAAAAG TTTCTAACG TAG AATGAC	-OGGCAAAATCCAA ATTTG TAAGAA	-TCARA TOG CTAC-	GACTAAC <mark>I</mark> G TTC <mark>O</mark> GAAAATATOG <mark>T</mark> CAAAAA-TTTAGCCT <mark>O</mark> G TCA	CAATTIG	-TCTRAATCRAATTTT-CTTCATTATTTTCCAACTTCC	ATAGTTGTTCCCTTAG
391	. ChLG8_R180289124RC_C7	AATT AAAA G TT <mark>C</mark> CTAACG TA A AATGA T	-CGGC SAATCCAA -ATTTG CAAGAA	-TCAGGTCGCTTC-	A ACTAACOS TTOSS AAA <mark>C</mark> TATOS <mark>A</mark> CAAAAA	CAATTIA	ACTAAACTAAACCAAAATTTCCAAGATTC	ATAGTTATTCCCTTAA
392	. ChLG5_R180282757_C4	AATTAACIG TOT CTAACG TAG AATAAT	-CGGAGARATCCAA ATTTGCAAGAA	TCAAG TOG CTAA	GACTAACOS TTOSG AAAATATOS <mark>T</mark> CAAAAA -TTTAGCCT <mark>O</mark> S TCA	CAATTIG	-TCTAAACCAAATTTT-CTTCATTATTTTCCAACTTTTC	ACAGTTATT CCTTTAG
393	ChLG5_R180282757_C9	AATTAACTS TOT CTAACG TAG AAT AAT	CGGAGAAATCCAA ATTTGCAAGAA	TCAAG TCG CTAA	G ACTAACOS TTOSS AAAATATOS TCAAAAA TTTAGCCTOS TCA	CA AT TOS	-TCTARACCARATTTT-CTTCATTATTTTCCARCTTTTC	- ACAGTTATTCCTTTAG
394	. ChLG8_R180289124RC_C8	AATTGAG TOTT T CTAACG TAG AATGA <mark>T</mark>	-CGGTGAAATCOGA ATTAGCAAGAA	-TCARG TAG CTAC-	GACTAACCE TTCEGAAA-TATCE <mark>T</mark> CRAAAA -TTTAGCCT <mark>O</mark> G TCA	CA ATTIG	-TETRARCCARATITT-CTTCATTATTTTCCARCTITTC	ATAGTCATTCCCTTAG
395	ChLG8_R180289124RC_C3	<mark>g</mark> att a ag a g tt <mark>c</mark> ctaacg ta a aa t aa t	-CAGCEG AATCAAA AT TTG CAAGAA	-TCAAG TCG CTA <mark>G</mark> -	GACTAACCE TTCGGAAAATATCGGCAAAAA-TTTAGCCTCGTCA	CAATTIG	-TTTAACCAAATTT-CTTCATTGTTTTCAAACTTTTC	
396	ChLG8_R180289124RC_C4	GATTAAGAG TTTCTAACG TAAAATAAT	CAGCEG AATCAAA ATTTE CAAGAA	TCAAG TCG CTAC	GACTAACC <mark>T</mark> ITCGG AAAATAT <mark>G</mark> G T CAAAAA TTTAGC T TOG TCA	CA ATTIG	-TCTAARCCAAATTTT-TTTCATTATTTTCCAACTITTC	
397	ChLG8_R180289124RC_C2	AATTGA AA G TT T CTAAOG TAG A <mark>G</mark> TGAC	-OGGC AATCCAA ATTIG CAAGAA	-TCARG TOG CTAC-	G AC TAA CO T ITOGG AAAA TA T <mark>O</mark> G T CAAAAA TT TAGO TI OG T T A	CAAT TIG	-TETRARCCARA TTT-CTTCATTATTTCARACTITTC	ATAGTTATTCCCTTAG
398	. ChLG8_R180289124RC_C6	AATTGAG IG TOTATAACG CAG AG TGAC	-OGGOEGAATCCAA-ATTEGCAAGAA	-TCARG TOG CTAC-	GACTAACCE TTCGG AAAATAT <mark>G</mark> G <mark>T</mark> CAAAAATTTAGC <mark>T</mark> TGG TCA	CAATTIG	-TCTAAACCAAATTTT-CTTCATTATTTTCAAACTTTT	ACAGTTATTCCCTTAG
399	ChLG6_R180284722RC_C6	ARTTARTIGA A GTTT CTARCE TAG ARTGAC	-CGGCGARATCTAA-ATTTTCAAGAA	-TCAAG TOG CTAC-	GACTAACOS TTOGGAAAATATOS <mark>E</mark> CAAAAATTTAGC <mark>E</mark> TOG TCA	AAATTIG	-TCGRAACCAAAGTTT-CTTCATTATTTTTCAACTITTC	MTAGTTATTCCCTTAG
400	ChLG6_R180284722RC_C10	AATTAATTGA AA GTTTCTAACGTAGAATGAC	CGGCGAAATCAA ATTTCAAGAA	TCAAG TCG CTAC	g ac taacos ttogs aaa ata tos <mark>t</mark> caa aaa - tt tago t tos tca	AAATTBG	-TCGAAACCAAAGTTT-CTTCATTATTTTCAACTTTTC	- ATAGTTATTCCCTTAG
401	ChLG6_R180284722RC_C14	AATTAATTGA AG TT T CTAACG TAG AATGAC	-CGGCGAAATCTAA ATTTTCAAGAA	TCARG TOG CTAC	GACTAACCE TTCGE AAAATATCE TCAAAAA-TTTAGCTTCG TCA	AAATTTG	-TCGAAACCAAAGTTT-CTTCATTATTTTTCAACTTTTC	ATAGTTATTCCCTTAG
402	ChLG6_R180283958_C4	AATTGAG IG TT I CTAACG IAG AAT CAT	CATAGGAATC CAT AT TTG CAAGAA-	TCAAG TOG CTA-	AGA TAACOS TTOSS AAAATATOSS CAAAAA TTTT	AAATTIG	-TCGAAACCAAACTTT-CTTCATTATTTTCCAACTTGTC	
403	ChLG6_R180283958_C13	A <mark>G</mark> TTGAG IG TT T CTAACG IAG AA T <mark>CA</mark> T	CGGCGGRATCCAT ATTIG CAAGAA	TCAAG TOG CTA-	AGA TAACOS TTOGG AAAA TATO3G CAAAAA TTTTGCC TOG TCA	AA AT TIG	-TCGAAACCAAACTTT-CTTCTTATTTTCCAACTTCTC	C ATAGTTATTCCTATAG
404	ChLG6_R180284722RC_C3	AATTGAG IG TT <mark>C</mark> CTAACG IAG AATGA <mark>A</mark>	CGGCCGRATCCAR ATTE TAAGAA	-TCAAG TOG CTAC-	GACTAACOS TTC <mark>A</mark> SAAAA <mark>A</mark> ATOS <mark>T</mark> CAAAAA-TTTAGECT <mark>O</mark> S TCA	AAATTE	-TEGRARICARACTTT-CTTCATTATTICCCARCTTTTC	ATAGTTATTCCCTTAG
405	ChLG6_R180284722RC_C7	aattgag tg tt <mark>c</mark> ctaacg tag aatgac	GGCGGAATCCAA ATGTGCAAGAA	TCARG TCG CTAC-	GACTAACOS TTC <mark>AA</mark> AAAA <mark>A</mark> ATOS <mark>T</mark> CAAAAA-TTTAGCCT <mark>O</mark> G TCA	AAATTIG	-TCGAAATCAAAGTTT-CTTCATTATTTCCCAACTTTTC	AT AGT TATT CC CTT AG
406	ChLG6_R180284722RC_C2	AATTGAG IG TT T CTAACG IAG AA IGA <mark>A</mark>	CGGCGAAATCCAA ATTTGCAAGAA	CAAG TOG CTG C	AACTAACOS ITCE AAAATATOS CAAAAA TITAGCCTOGCA	AA ATTIS	-TCGAAACTTT-CTTCATTATTTCCCAACTITTC	C ATCGTTATTCCTTTAG
407	. ChLG6 R180284722RC C8	AATTGAG TG TT <mark>C</mark> CTAACG TAG AATGAC	-CGGCGGAATCCAA -ATTTGCAAGAA	-TOGAG TOG CTAC-	AG CTAACOG TTC T G AAAATATOG <mark>T</mark> CAAAAATTTAGCCT <mark>O</mark> G TCA	AAAT TIG	-TCGRARCCARACTTT-CTTTATTATTTCCARCTTTTC	AT AGTTATT O CCTTAG

408. ChLG6 R180284722RC C12	AATTGAG TË TT <mark>C</mark> CTARËË TAG AATGAË	- CCCCCCG ARTCCAR AT TTC CAAGAA	-TOGAG TOG CTAC	ACCTARCOS TTCTS ARAATATOS TCAARA	- AT TEG -	-TC <mark>GRARCCARACTTT-CTT</mark> A	TTATTTTCCAACTTTTC	AT AGTTATT <mark>C</mark> CCTTAG
409 Chi G6 R180284722RC C4	AATTGAG IG IT CCTARCE TAG AATGAC	COGCOG AATCCAR - ATTTG CAAGAA	TOGAG TOG CTAC	AGCTARCOS TTO TE AARATATOS TOAAAA	- ATTIG	TCGAAACCAAACTTT-CTTTA	TTATTTCCAACTTTTC	AT AGT TATT CCTTAG
410 CH CG D100204722DC C11			TO DO TOO OT & C			TOTAR BRICAR SCHOOL COMON		
410. GILGO R 100204722RC GTT		COOCCERTATION ATTICCERTAR			P11 1 1.07	TGARA CARACTIC CITCA		
411. ÇhLĢ6_R180284722RÇ_Ç15	AATTGAG TO TTOCTARCG TAG AATGAC	CGGCGGAATCCAA AT TTG CAAGAA	TOGAG TOG CTAC	AGCTARCOS TTC SAARATATOS CARARA - TT TAGCTTOS TCARA	ATTB	TCGAAACCAAAGTTT-CTTCA	TTATTTTCCAACTTTTC	AT AGT TATT CCTTAG
412. ChLG6 R180284722RC C17	AACTGAG TG TT T CTAR T G TA R AATGAC		-TCARG TCG CTAC	AATTAACOS TTOGSAAAATATOS TCAAAAA	- AT TIG -	-TCCAAACCAAACTTT-CTTCA	TTATTTC	AT AGT TATT CCTT AG
413. ChLG6 R180284722RC C18	AACTGAG IG IT I CPAACG IAAAATGAC	- CGGCGAAATCCAA ATTTACAAAAA	TCARG TOG CTAC	AATTAACCE TTCES AAAATATCE TCAAAAA-TTTAGCCTCG TCAAA	- ATTIG -	-TCGAAACCAAACTTT-CTACA	TTATTT <mark>C</mark> CCAAC <mark>A</mark> TTTC	ATAGT TATT CCCTTAG
414 Chi G6 R180284722RC C19	A RETEACTO TO THE ACCIDE AS TO A C		TO MAG TOS OTAC			TREABLE CATACTER - CTTCA	PTATTTCCAACTTTC	T AGTTATT C CC
445 CHLOG D190394732DC C18	A ADDO ACIDO DO COLA ROCIDA DO CIDA DE LA CIDO		THE R OF THE OWNER OWNER OF THE OWNER OWN		N TO TO TO TO	TOGA & BOORA & COURT OFFICAL		A CIT TO A CIT OF COME AC
415. GILGO K100204722RC C10	AAT TGAG DE TT OCTAALS TAAAATGAL	COSCOGRATCCAR ATTICCARAGAR	TCAAG TOG CTO	GACTARCOS TICOS ANRATATOS I CAAAAA TITTASCONOS TCAAA	ATTT	REGRAACCARACITI CIICA	TTATTTCCCARCTITIC	ALMST TATTOC CTTAG
416. ChLG9_R180290695RC_C4	AATTGAG TG TT T CTAACG TAAAATGAC		-TCTAG TCG CTAC	GACTARCOS TTOGGAARATATAG TCRAARA-TG TAGCCTOG TCARA	ATTT	-T <mark>TG</mark> AAACCARACTTT-CTTCA	TTATTTTCCAACTTTTC	AT AGT TATTOCTTAG
417. ChLG9_R180290695RC_C6	AATTGAG TG TT T CTAACG TA <mark>A</mark> AATGAC	CGGCAGAATACAA AT TTG CAAGAA	TCAAG TCG CTAC	G ACTARCOS TTOSS AAAATATAS TAAAAAA	AT TT	-T <mark>TG</mark> AARCCAARCTTT-CTTCR	TTATTTTCCAACTTTTC	AT A AT TATT CCTT AG
418 Chi G9 R180290695RC C5	A ATTGAG TO TT T CTA ACG TA ABA TGA C-	CGGC A ATTACAA ATTTG CAAGAA	TCARG TES CTAC	- GACTAACCETTCESSAAAATATAS TCAAAAA - TTTAGCCTCESTCAAA	ATTT	TTGAAACCAAACTTT-CTTCA	TTATTTCCAACTTTC	AT A BT T AT T C C TTT AG
440 CH CO D10020000000000					10 CD CD CD			
413. CILOS KIOU230030KC C3	HALL MADE IN THE CLAMES AND A DECK	COCOS HALCONS AT THE MARKAN	ICHIGIOG CLAC				111111100110111110	
420. ChLG6_R180285048RC_C3	GATTAAG IG ITTICAACG TAAAATGAT	- CGGCGAAATCCAA ATTTGCAAAA	TCAAATTGCTAT	GACTAACCATTTAAGAAATATCATCAAAAA-TTTAGTCTCGTCACA	- AT T'IG -	-CAAAACAAAACIGT-CTTCA	TTATTTTCCAACTTTTC	AT AGT TATTOC TTTAG
421. ChLG6 R180285048RC C7	AATTGAG T <mark>A</mark> TT T CT <mark>G</mark> ACG TA <mark>A</mark> N <mark>G</mark> TGA C	CGGCGAAAT <mark>T</mark> CAA -AT TTG CAA <mark>A</mark> AA	TCAAAT GCTAC	G ACTAACOS TT TAAG AAATATC <mark>AT</mark> CAAAAA-TTTAG T CTTGTCA <mark>C</mark> A	AT TTG -	CARARCARARCTTT-CTTCR	TTATTTCCAACTTTTC	RT AGT TATT TO <mark>G</mark> TT AG
422 Chl G6 R180285048RC C6	AATTGAG TO TT T CTAACG TAG AATGAC	TAGCGARATCCAR AT TTG CRAGAR	TCAAG TEG CTAC	GACTAACOS TT TAAS AAATATO <mark>AT</mark> CAAAAA TTTAG T CTTG TCACA	ATTEG	-CARARCARARCTTT-CTTCA	TTATTCTCCAACTTTTC	ATATT TACTCCTTT AG
423 CH C6 P180285048PC C5	ACT TA TTO TO TOT A ACC TO A A TAA C	CCCC AA A BTCC B & A TTTC AA ACA A	TOBACTECOTAC	CARTESCONTROLASS STRTMY TO A SA A		CTCS & SCCSS & TTTT CTTCS	PT &T T T PCC & &CT TT PC	STATT TATT OT THE ME
423. CHLOG R 100203040RC 03								
424. ChLG6_R180285048RC_C9	ACTATISTICIARSSIA AATAAC		TCARS TES CPAC		- AT 113	GIGARACCARA PTT-CTTCA	PPATTPPCCARCTTTC	ATATT TATT C. TTTAS
425. ChLG6 R180285048RC C12	ACTTACTS TTTCTAACG TAAAATAAC	- CGGCAAAATCCAA ATTTGCAAGAA	TCAAG TTG CTAC	g actaa <mark>t ca</mark> ttcg <mark>a</mark> rara ta tog t craara – tt ta <mark>r</mark> cc ttg tcara	ACTIG	GTGRARCCARACTTT CTTCA	TTATTTTCCAACTTTTC	ATAT T TATT C C T TT AG
428. ChLG9 R180290695RC C2	AACTGAG CTTTTCTARCGTARAATGAC	- CGGCGGAATCCAA - ACTTGCAAGAA	-TCAAG TOG CTAC	G ACTAACOS TT A SG AAAATA TOSG CAAAAA - TT TA AT C TOS TCAOA	- ATTES -	-TCCAAACCAAACTTT-CTTCA	TTATTTTCCAACTTTTC	ATAGTTATTCCCCTAG
427 Chi G6 B180284722BC C9	A ATTGAG TO CTTCTA ACG TAG AATGAC	- COGCOG BATCCBB - AT TTG CAAGAA	TCARG TOS CTAC		- ATTTG	TCGAAACCAAATTTT-CTTCA	TTATTTC	AGT TATT CC CTT AG
429 CHLC6 D180284722DC C12		0000003300033 300000033033	Include Inco other		A DE CHERC	TOTAL CONTRACTOR		
428. GILGO R 100204/22RC C13	AAT 1946 19 OF TUTAAL 9 199 AA 19AU	- USBUBBARTC CAR AT TIN CARBAA	TCARSTOS CERC	GAUTARUGS TIUTARRATATUST CARAGA TITASUUT GIUARA	ATTDa	TUGAAACCAAA TTT-CTTCA	TTATTTCCCAACTTTTC	ALMST TATT C CTTAG
429. ChLG6_R180284/22RC_C5	AATTGAG TG OF T CTARCG TAG AATGAC	OG G OGG AAT C CAA - AT TTG CAAGAA	-TCAAG TOG CTAC	G ACTAROCS TTC TARARATATCS TCAARA TT TAGCC TOS TCAAR	- AT T'BG -	TCGARACCARATTTCCTTCA	TTATTTCCCAACTTTTC	AT AGT TATT CCTTAG
430. ChLG9 R180292048RC C9	AATTGAG IG TTACTAACG IAG AATGAC	OGG OGG AAT C CAA - AT TTG CAAGAA	-TCARG TOG CTAC	G ACTARCOS TTO SAARATATOOS CRAAAR-TT TAGCO TO STCARA	- AT TTG -	- I <mark>gg</mark> aaaccaaacttt - Ctt <mark>t</mark> a	TTATTTTC <mark>T</mark> AACT N TTC	AT AGT TATT CCTT AG
431 Chi G8 R180289798RC C7	AATTAAG TO TT T CTAACG TAG AATGAC	CGGERGAATCCAA -ATTTGCAAGAA	TCAAGTOS CTAC	GACTARCONTERSABARATORS CRABBA-TTTAGECTERAA		TCGABBCCBABCTTT-CTTCB	TTATTTC	GTAGT TATT TO CTT OF
492 CH C0 D180202002DC CC	A BUTT ACCULTURE OF A ACCUTA BERTICA C		TO BROWCH CTRAC		NOTION AND ADDRESS	TOBARCCASECTUT COTO		CACT TATC W CTT AC
432. CILCOD R 100202003RC CO	ART ING 19 TI I CLARGE LANATORC	CONCORNATIONA ATTIC CHARAN	10/100 100 01/20	GALIARCO HE BRARANTE GARAGE HIMSOLIUS TEAR	AL 1 30	ICOMPOCIATION CITCO	LINI LII CANCINI LO	ASAGITAIG ICCITAS
433. ChLG9_R180292003RC_C8	AATTAG IG ITTCTAACG TAAAATGAC		-TCARG TCG CFAC	G AC TAACOG TTCT G AAAATATOAC CAAAAA -TTTAGCC TOG TCAAA	- AT T 13 -	TCDAAACCAAACITT-CTTCO	TTATTTTCAACTATTC	AGAGTTAIS TCCTTAG
434. ChLG10 R180276690 CB	AATTGAG TG TT <mark>C</mark> CTAACG TA <mark>A</mark> AATGAC	- CGGCGGAATCTAA ATTTTAAGAA	-ACAAG TOG CTAC	G ACTAACCE TTCE <mark>A</mark> AAAATATCE <mark>T</mark> CAAAAA TTT <mark>T</mark> G T CT <mark>C</mark> E TCAAA	- AT TTG -	-TCTAAACCAAATTTT-CTTAA	ttatttt t caa <mark>t</mark> tttc	gg <mark>g</mark> gttat <mark>g</mark> tc <mark>t</mark> ttag
435. ChLG10 R180276690 C8	AATTGAG IG IT CCTAACG TANAATGAC	-CGGCGGARTCCAR ATTTGCARGAR	-ACAAG TOG CTAC	GACTARCOS TTOSS ARAATAT <mark>S</mark> S TCAARA	ATT-A	TCTABACCBAACTTT-CTTCB	TTATTTTTAACTTTTC	gg <mark>g</mark> gt tat <mark>g tc <mark>t</mark>tt ag</mark>
436 Chi Go P180200006 C3	GATTGAG TO TT TOTA AGG TA ABATGAC	CGGCGG BATACBA AT TTG CBAGBB	TCARG TOS CTAC		- AT TTS	TOBAACCAAACTTT-CTTRA	TTATTTTCA ACT TTTT	GG AGT TACT TO TT AG
427 CH CO DI 80200008 CE					3 (1) (1) (1) (1)	TOOLS A A COLLEGE COLL		
437. CILCS R 100290390 CO	GGIIGMS ISTIICIMACE INAAAIGAC	COOCHS AND CAR AT THE CAREAR	TCARGING CIRC	GACTARCOL COSCARA TATO CARACTITIASCOLOGICARA	WIT D3	ICHARACCARACITI-CITCA	LINITI CARCITIT	GG MGI I MGI I CUII MG
438. ChLG6_R180284071RC_C3	AGTCGAG TG TT T CTAACG TAAAATGAC	- CGGCGAAATCCAA ATCTGCAAGAA	TCARG TCG CTAC	TACTARCOS TITOS ARAATATOS TCAARAC TITTAGTCIT CCTRGA	-ATTIG	TGATAAACAAATTTT-CTTTT	TTATTTTACAATATTTC	ACAAT TATT TCATTAA
439. ChLG6 R180284071RC C5	AGTOGAG TO TT T CTAACG TAAAATGAC	CGGCGAAATCCAA ATCTGCAAGAA	TCAAG TCG CTAC	TACTAACOS TTTCS AAAATATOS TCAAAAC TTTAG TC TT CCT AGA	ATTE	TGATAAACAAATTTTCCTTTT	ttattt <mark>a</mark> caa <mark>ta</mark> tttc	ACAAT TATT TCATT AA
440 Chi G6 R180284071RC C7	ACTOGAG TO TT T CTARCO TARAATGAC	- CCCCCCAA-ATCCAA-ATCTCCAACAA	TCARG TOG CTAC	TACTARCOS TETOS ARRATATOS TCARRE - TETRO TO CETRO A	- ATTTS -	TCATABACABATTTT-CTTTT	TTATTTACAATATTC	ACAAT TATT TO ATT AA
441 CH CG D100204071DC C4			THE R DEC STORE CTURE OF		200.0397			
441. CILGO R 10020407 IRC C1	AG 10 TI TOTAKO LAG AB INAC	CARGON ALCONA ALCONA	ICANS ICS CIAC	ACTACOL IT IN AASAIATO CAASAA TITASTCII COLAVA	ALLIG	ISALAACSAA IIII CIAII		A ALTALIA TALIA
442. ChLG6_R180284071RC_C4	AACCIGAG TO TTT CTARGE TARAATGAC	CGGCGAAATCCAA ATCIGCAAGAA	-TCARGTOS CPAC		MT T T \$	IGATAAACITT-CTTT	TTATTTTACAATATTTC	AGTTATTICCTTA
443. ChLG6 R180284071RC C6	AACCGAG IG IT I CTAACG IAAATGAC	CGGCGAAATCCAA ATCTGCAAGAA	TCARG TCG CTAC	TACTARCOS TTTC BARARTATOS TCARARA - TTTTGTCTT CGT ACA	ATTEG	- IGATAAACAAACTTT - CTT TT	CTATTTTACAATATTTC	ACAGTTATTTCCTTA
444. ChLG6 R180284071RC C2	AACCGAG IG IT I CICACG IAAAA IGAC		-TCARG TCG CTAC	TAC TAAC OF IT TOS AAAA TA TOS TCAAAAA TT IT GTC TT OGTA CA	- AT TEG -	TCATAAACAAACTTT-CTTT	TTATTTTACAATATTTC	ACAGTTATTTCCTTAA
445 CHIGE P180284071PC C12			GCARG TOS TAC			TCATARA TARA CONTRACTOR	THE SALE OF THE SEC. N. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2.	SCACT TATT W. TTT AS
446. OHLOG D480084074D0 042					3 10 10 10 10			
44b. ChLGo_K180284071KG_C13	AA	COGOGO ARTCIAA ATUR CAABAA	TCARG TUG	TAL TAAL US TITUS ABAATATUS CAABAA TITAS CITULTAS	-ATT 139	-16 AT AAAT AAACTTT CTTT	TTATTTTA, AATATTTC-	ACAGTTATTIC TITAA
447. ChLG6 R180284071RC C10	AACCGAG IG IT I CTAACG IA AATGAC	CGGCGGAATCCAA - ATCTGCAAAAA	TCAAG TCG TAC		- AT TEG -	- ICATAAATAAACTTT-CTT TT	TTATTTT AT AA TA TTTC	ACAGT CATT TO OTTAA
448. ChLG6 R180284071RC C8	AACCGAG IG IT I CTARCG TARAATGAC	- CGGCGGAATCCAA ATCTG TAAGAA	TCARG TOG CTAR	G ACTAACCE TT <mark>T</mark> EE AARATATCE <mark>T</mark> CAAAAA TTTAG <mark>T</mark> CTT CCT A <mark>G</mark> A	- ATTE-	- T <mark>GAT</mark> AAATAAACTTT-CTT TT	TTATTTTACAA <mark>TA</mark> TTTC	ACAGT TATT TO CTTAA
449 Chi G6 P180284071PC C9	A STOCIAG TO TT T CT A ACG TA BASTICA C	-CGGCGGBATCCAA -ATCTG BAAGAA	GCARGTOS CTAC	TACTARCOS TURAS A ARATATOS CORA ARA TTTA ARCTT CORAGA		TGATA SACAS SCITT T CTTTT	TATTTACAATATTC	AGT TATT TO CTT A
450 CHLCC D400004074DC C44			Incase management		3 (B) (B) (C)	TO MEAN CARAGE COMPANY		
430. GILGO K1002040/1KG_G11	ARCOMS IS ITTCTARGE IRRATION	COBCOGRATCIAN ATOIS TOBORA	ICANS I S CIAC	TACTARCOSTITUS AMARIATOS CAMAMA TITUS CITUCT MAR	VI TW3	BALAAACAAAGIII CIII	STATITIACASIATITIC	AGAGITATI ICCITA
451. ChLG9 R180290249 C2	CAC TGAG TG TT T CTAATG TANAA TGAC	- CGGCAGAATCTAA - ATCTG CAAGAA	-TCARG TOG CTAC	TCCTCACCETTTCEAAAATATCETCAAAAA-TTTAGTCTTTCAGA	- AT TTG -	- I <mark>CAT</mark> AAACAAACTTT-CTTCA	TTATTTTCCA TTA TTT T	ACAGT TATT CCTTTAG
452. ChLG9 R180290249 C8	CAG TGA A IG TT T CTAACG TA A AACGAC	- CGGCABAATCTAA ATCTGCAAGAG	TCARG TOG CTAC	TACT CACOS TITCS AAAATATOS TCAAAAA-TTTAS TCOS TTCASA	- AT TIG -	- T <mark>GAT</mark> AA <mark>A</mark> CAAACTTT-CTT TT	CAATTTCCCAGTATTTT	ACAGT TATT TT CTT AG
453 CHLCO P180200240 C3	CAPTCA SCATTER OF A ACC TA SAB TAA C		TCC CAG TOG TRAC			TCATABAAAACTETCA	PTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Carry are the carry ac
454 OHLOD D48000040 OF								
404. CILOS R 100290249 CO	CALIGNS IS III CLARCE LANARITA	COUCSS AGE COAR AIGIE CAREAR	IC CASICACIAC		NI 1 103	Lead BAR CLANCITI CITER		MONSTINIII CIINS
455. ChLG9_R180290249_C4	CATTGAG CG TTTCTAACG TAAAATTAC	- OG CIGRAATCCAA AT CIG CAAGAA	-TCARG TOG CTAC	TC CTAACCSTT TCTC AAATATCS TA AAAAA-TTT-G T CT T TCA G A	-ATTIG -	-I <mark>GAT</mark> AAACAAACPTT-CTTCA	TTATTTPCCAGTATTTT	ACAGTTATTTCTTAG
456. ChLG9 R180290249 C9	CATTGA RC G TT T CTAACG TA R AA T <mark>T</mark> A T	CGG <mark>A</mark> GG AATC CAAAT C TG CAAGAA	TTARG TOG CTAC	TG CTAACCETT TC EARAATATCE <mark>T</mark> CAARAA-T <mark>C</mark> TAG <mark>TT</mark> TT <mark>CC</mark> CR <mark>G</mark> A	- AT TTG -	-TGATAAACAAACTTT-CTTCA	TTATTTTCCAGTATTTT	AGT TATT CC TTT AG
457 Chi G9 R180290408 C2	TATTAAG TO TTT CCAACG TAAAAGGTC	CGGCGGAATCCAA ATCTGCAAGAA	TCAAG TCG CTAC	GACTARCOS TUTAS ARRATATOS CARARA TUTACUTACIA CAGA	ATTE	TTATAAACAAACTTT-CTTCA	TTATTTTCAGTATTTT	ACAGT TATT TC TTT AG
459 CH C0 D180200409 C5		COMPORANTICONA ATTOCCANCAA	CRACK THE CONTRACT		- B (P (P)(P))	TTATA ANCAS & CTUT COURCE	THE AST T WITE TO A C T & THE T	AC ACHT T ATT TAT TAT
400. CILCOS R 100280400 CO	ARE INNS IN TIT CARDON LAWAR LOAD		CANG TOO CLAC		AL 1 105			
459. ChLG9_R180290408_C4	TATTAAG IG IT CCCAACG IAAAAIGAC	- CGGCGG AATC CAA - ATCIG CAAGAA	TCARG TCG CTG C	ABCTAACCE TTTAE AAAATATOS TCAAAAA - TTTAGTCATTCCAGA	-ATTTG	TATAAACAAG CTTT-CTTCA	ATATTTT T CA GTA TTT T	TT AGT TATT TO CTT AG
460. ChLG9 R180290408 C9	AATTAAG IG IT I CTAACG TAAAATGAC	CGACGG AATC CAA ATCTG CAAGAA	CAAG TCG CTAG		ATTE	TCATABACAAATTTT-CTTCA	ATGT T TT <mark>T</mark> CAGTATT T	ACAGT TATT TC TTT AG
461 Chi G9 R180290408 C3	GATTGAG IG IT I CTARCG IR AATGAC	CGGCGGAATCTAA - ATCTG CAAGAA	TCAAG TOG CTAC	G AC TARACG TTTAS ARAA TA TOS TCAARAA	- AT TEG -	TTATAAACAAACTTT-CTTCA	TTATTTT TTAGAA TTT T	ACAGT TATT TO OTT AG
482 CHLC0 P190200408 CB	C A 1971 C A 12 17 C 17 P P C P A A 17 C 17 A A A 19 C A C	CCCCCC A ATCC A A TCCC A ACA A	- 90° 8.842 99°C2 C9P			TTATA ACCAS & CUMPLE CONCAS	արոր անդանությունը ու որ արանականությունը անորդությունը անդանությունը հարորությունը հարորությունը հարորությունը	SC ALSO IN A DISP OF THE ALSO
402. CHLC0 D490200400 CU					ALC: NO	THE AR CARACTER CHICK		
403. GILG8 R100280406 C/	CALL AND THE THE PARAMETER AND THE ARE THE COMPANY THE PARAMETER COMPANY THE PARAMETER AND THE PARAMET	A CORRECT OR ALL CORRECT OF A C	CARS TOS CIAL	COMPANYA II PANANATATA CARAGA TITAN CARA	PLI ING	LINGAR CITT-CIPCA	LINALTTING POPULATTTE-	TT AS
464. ChLG9_R180290408_C10	GATTGAG IG IT TATAACG TAAAATAAC	GGCGGAATCCAG ATCIGCAAGAA	CAAG TOG CTAC	GACTAACOS TT TA S AAAATATOS T CAAAAA TTTAS T CTA TO CASA	ATTB	TTAT AAACAAACTTT CTTCA	TTATTTT T CA GTA TTT T	ACAGTTATTTCTTAG
465. ChLG9 R180290408 C11	G ATTGAG IG TT T A FAACG TA A AAT <mark>AT</mark> C	- TGG CGG AATC CAC AT CTG CAAATC	CARG TCG CTAC	G AC TAA COS TT TA S AAAA TA TOS T CAAAAA TT T T S TT TT <mark>TC</mark> CA <mark>S</mark> A	-ATTTG-	-T TAT AA <mark>G</mark> CAAACITT-CTTCA	ttattt <mark>t</mark> ca <mark>gta</mark> ttt <mark>t</mark>	ACAGT TATT TC CTT AG
486 Chi G9 R180290408 C8	GATTCAG TO TT TATAACG TAAAATATC		CARG TCG CTAC	GACTARCONTURA AAAATATOS TCAAAAA-TTTAGTCTTTCCAGA	- ATTTG -	TTGTAAACAAACTTT-CTTTA	NTATTTT T-AGTA TTT T	ACAGT TATT TC CTT AG
467 Chi G9 R180292064RC C5	A ATTGAG TO TT T CTA ACG TA ABA TAAC	CGGCGGAATCCAA ATCTG AAGAA	TCAATTACTTC	GATTARCOS TUTES ARAATATOTS CRABAR TTTAGTCTTTCAR	AT TTA	TCATABACAAACTTT ATTCA	TTATTTTCAGTATTTT	ACAGT TATTGT CTT AT
400. UILU9 K100292004KU U0	ANI ISNS IS IT THIARAS TRAATGAC-	COSCOS ARTCCAR AT TIS AAGAA	-IGAAS TOACTAC	- GALIARCE II TA ARATATUS CAARA TITASTOTTTICAGA	- AT 135	ICAL NARCARACIO I ATTCA	LINI CTINGASTATTT	A STATISTICH A
469. ChLG9_R180292064RC_C2	GTTTAG IG TTTCTTACG TARAATGAC	- CGGCGGAATCCAA ATCIG TAAGAA	-TTARG TCACTAC	G ACTARCOS TT T EG AARATATOG G CAAAAA TTTAG T C TT T TCA <mark>G</mark> A	-ATTIG-	TCATAAACARACTTT-ATTCA	TTATTTT T CA GTA ITT T	ACAGT TATTGICTTAI
470. ChLG9 R180292064RC C8	AATTGAG TG TT T CTAACG TA R AATGAC	CGGCGGAATCCAA-ATCTGTAAGAA	TTARG TO CTAC	G ACTARCOS TT <mark>T</mark> SS ARAATATOS G CRARAA-TTTAG <mark>T</mark> C TT <mark>T</mark> TCR <mark>G</mark> A	- AT TTG -	TCATABAAAACTTT-ATTCA	TTATTTT <mark>T</mark> CA <mark>GTA</mark> TTT <mark>T</mark>	TCAGT TATTGT CTT AG
471 Chi G9 R180292064RC C4	GACTGAG TO TT T CTAACG TAAAA TGTC	CGGCGGAATCCAA ATCTGTAAGAG	TCARG TCACTTC	GACTARCOS TTUBS ARRATATONS CARARA TT TAGECTTUTCAGA	-ATTES	TCATATACAAACTTT CTTCA	TTATTTTCAGTATTTT	ACAGT TATTGT CTT AG
472 CHI CO D180202084DC CO		COCCCC B BECCB B - B FORC TB BC B B	THE R D C THE D CT D C			TO AREA AND AS A COUPLE TO THE A		AC ACTOR TO A THE TO THE TO THE D
472. CILOS R 100232004RC CS	HALIGHE IS III CLARGE INAAAI	Coocie and cona Alore Intern	ICHIG ICACIAC		AL 1 105	ICAL AND CASHOI I T		ACOUT INT THE THE
473. UNLOS R180282004RC C3	AATTAAS TO TT TURAAAS TAAAATGAC	CANCELARS ANTUGAR AT THE MAGAA	TURAS TURCEAG	GATTAAC IS TTERSAAAATATUSIS CAAAAA TTTISSECTTETCAGA	-ATT 13	TTALAAAUAAAGTTT-TTTCG	CIALTTINGTATTT.	ALAMATTATTTCTTAG
474. ChLG9_R180292064RC_C7	AATTAAG IG IT I CTAACG TANAA IGAC	CGGCGGARTCCAA -ATCTGTAAGAA	TCAAG TCACTAC	G A l TAAC i g TT TA G AAAA TATCEG CAAAAA TTTAG I C TT I TCA <mark>G</mark> A	AT TTG -	TCATA TACAAACTTT-CTTCA	ttatt tt ca <mark>gta</mark> ttt t	AC AGTTATT <mark>GT</mark> CTTAG
475. ChLG9 R180292064RC C1	ATTGANTS TT T CTANTG TANAATGAC	CGGCGAAATTCGA ATTTCTAAGAA	TCAACTCACTAC	AACTAACOS TETES AAAATATOS TAAAAA TTTTAS TCTTTCAGA	- AT TDG	TCATARACARACTTT-CCTCA	TTATTTT TCCGTA TTT T	ACAGTTATTGTCTTAG
476 Chi G9 R180292065RC C8	GATTACA TO TT T CT A ACG TA A BA TO A C	CCCCCCCARTCTAR ATCCCTARAA	CARG TOS CTAC		ATTO	TCATABACABACTTT TTCA	TTATTTT TACGTA TTT	ACAGT TATT TTAT MS
477 CH C0 D19020200010 00			TCARCINC CTA		- Mar many	TC ST 3 B C 33 2 CTUM COT C		C SCOTT STORMER STORE
411. UILUA KIOUZAZUOOKU UTU	CALIGNAR TTTUTARAS TRAATGAC	GOOLGS ARTURA ATURS AAAAA	TO PROTO TO STREET	BALIASCAS II DE BASSASTURS CASASA TITASTICI TICASA	WL 1.179	IL ALBANCASACITT-CTTCA	LIALTT RATIT T	A CHAIT TALT TALE AG
478. GREG9_R180292065RC_C4	GATTGANTG TT T CTAACG TANAATGAC	COUCHARTCHAR ATCIG TAAAAA	TCAAG TOG CTAC	GAUTAAUOS TITESTAAAAGATOGG CAAAAA TITAGTICITTCAAA	-ATTTS-	TUREAR CAAACTTT CTTCA	TTATTTTCCGTATTTT	GCALTTATTATA
479. ChLG9 R180292065RC C12	GATTGANIG TT T CTARCG TANAA TGAC		-TCARG TOG CTAC	G AC TAACOG TT <mark>T</mark> G T AAAA <mark>G</mark> A TOGG CAAAAA TT TAG <mark>TTO</mark> T T TCAAA	- AT TES-	TCATARACARACTTT-CTTCA	TTATTTT <mark>TCCCCA</mark> TTT <mark>T</mark>	G G AGT TATT T TA TAG
480. ChLG9_R180292065RC_CA	GATTGAG TO TTT CTAACG TAAAATCAC		TCARG TCG CTAC	GACTAACCE TTTETAAAAGATCEG CAAAAA-TTTAGTTCTTETAAA	-ATTT:	TCATAAACAAACTTT-C7TCA	TTATTTT TACGTA TTT T	ACAGT TATT TTAT AC
484 CHI CO D480303065DC CC		COCCCC BERCCER - BERCCER - COCCCE	TO BAC DESCRIPTION		- N TO CO.	TO AND RECARD COMPANY		
HOL CHLOB RIDUZUUORU UZ	ARLING BUTT TARAS TARAATGAC	WIGWIG ARLUWAR AI LIN BANKA	TO MAY THE OTHER	COLING THE TANALITY CAASA TITAT TO	AT 150	ICALANCANACITI-CITCA	LINA CITE OF THE TT	A A A A A A A A A A A A A A A A A A A
482. CHLG9_R180292065RG_C9	GATTARS IS IT TOTATTG TRAATGAC	COOCGAATCAA ATCIGTAAGAA	TOTAG TOG CTAC	GACTARCONTTENARATATOS CARARA TTTAGOTTTETCAGA	-ATTTG-	TUATAAACAAACITT CTTTA	TAITTTCTGTATTT	ALASTTAG TT TA TAG
483. ChLG9_R180292065RC_C11	GATTAAG TG TT T CTA TT G TA A AATGAC		-TCTRG TCG CTAC	GACTAACC <mark>A</mark> TT <mark>T</mark> EAAAATATCE T CAAAAA-TTTAGC <mark>T</mark> TT T TCA <mark>G</mark> A	-ATTTG	TCATAAACAAACITT-CTT	ttatttt tctgta ttt t	AC AGTTA <mark>G</mark> TT <mark>TTA</mark> TAG
484. ChLG9_R180292065RC_C3	GATT AG IG TT I CTAACG TA AATGAT	- CGGCTAAATCTAA ATCTGTAAGAA	TCTAG TTG CTAC	GACTARCONTETE ABAATATOS TCAABAA-TTTAGCTTTTCAGA	-ATTIG	TCATABACAAACTTT-CTTTA	TT <mark>G</mark> TTTT <mark>TCTGTA</mark> TTT T	ECAGTTATTTTATAG
485 Chi G9 R180292065RC C5	GATTAAG TO TT TATAACG TAABB TGAC	COGOGG AATCTAA ATCTG PARGAA	TCAAG TOG CTAC	GACTAACCATTEG AAAATATOS CAAAAA TTTAGCTTTTCACA	ATTT	TCATABACAAACTTT-CTTTA	TTATTTTTTTTTTTTTTT	ACAGT TATT TTAT 23
			IVI B BO INCIDOU A		The second	TO BA & A CLARK COURT COURT		
400. CILG9 R100292000RG_C/	CALLARS IS IT ICIALS INAMATGA	COOCGARATCIAN ATOIG AAGAA	-ICANS IGAGIAS	- GREINAGUS II ES ANARTATES CAANAA TITASECTTETTAAA	- AT 1 13	IGARACITI-CTIA	LINE CTING COLOUR TTE	A STATTIC AS
487. ChLG9_R180292065RC_C13	GATTARG TO TT TATAACG TAAAATGAC		TCAAGTCACTAG	GACTAACCE TTEGAAAATATEGG CAAAAA-ATTAGECTTECAAA	-ATTIG	TCARAR CARACTTT-CTT	TTATTTTCTTATTTT	ACAGTTATTT CTTAG
488. ChLG9 R180292065RC C14	GATTGAG TG TT T CTAACAAAAATGAC	CGGCGGAAT <mark>AT</mark> AA ATCTG TAAGAA	TTAAG TTG CTAC	CACTARCOS TTEGE ARAATATOGE CRAARA - TTTAGCCTTETAGA	ATTE	TCAAAACAAACTTT-CTTTA	TTATTTTCAA TA TTT <mark>T</mark>	ACAGT TATTGT CTT MG
489 Chi G4 R180280874RC C2	A ATTGAC TO TT T CTA ACC TA A AA TCAC	CGGCGARATCERATE TETACAACAA	TCACA TCACTAC	- GCT AACCS TTCSS ARCTTATTS TCAAAAA - AATGSTCTTS TTAAAA	ABAT	TOTO A ACRAA A CTTTT - COTCA	TTATOTOT ATTTT	AG AGT TATT TTCTT AT
	THE PARTY OF THE P				1.000			

b) alignment of cluster 2

0	1 10	20	30	40	50	6 <u>0</u>	70 80	90	10	> 110	12	0 190	140	150	160	170	180	190	200	209
Consensus	GGAACAAACCGCA-	-TTGCTCT ACG	a contraint ag interentin	GAGTT-ATGA				- TTTTCCAC	<u>TA</u>	TAGATATTGC-C	TBTC	T-TAATTTTTAG	C-RAAAAACTTT	ARAAG TTTA	CATCING TRAAAS	ST TGG T	-TTTATACSCAAJ	ATG-R	GCCGCTG AAT T CAAT	GA
1. ChLG10_R180277076_C9	GAACAAACOGCA	-TTG CTCTACS	ACTITIANTITI	GAG TT-AIGA	ATTTTTTGT		TGGATAAAA	- TTT TCCAC TA	TC -A	BAARTGG-C	TACT	C TAA A T T T AG G	C-AAAAAATTTT	AAATTTTTA	AT I CITG IG AAAA	AT IGAT	ATAATATC TAAL	LATG -A	GCCG <mark>TA</mark> GAAT T CAAT	C
2. ChLG10_R180277076_C14	GAACAAADOGCA-	-TIG CPCTADS	ACTIFICA. PTTTT	GAGTT-ALGA	A PTTTTTTG		TUGATASAS			GAAAT	T AGT		AAAAAA III	AAATTTTTA	ATTCTTG IG AAAA	AT 115 AT		ATG-A	GCCG TR GAATTCAAT	
4. ChLG6 R180284741 C4	GAACAAACOGCA	TIGCTCTAG	ACT TTT AG TTTT	GAGTT-ATGA	ATTTTTTTT		TGGATAAAA	TTTTCCACT	TG	AATGG-C	T ACC	C TAAATTTAGG	C AAAAAA TTTT	AAATTTTA	ATT CTTG IG AAAA	AT IGAT	ATAATATSTAAL	AATG A	GCOGTAGAATTCAAT	č
5. ChLG8_R180284691RC_C4	GAACAAACOGCA	-TTCCTACE	ACTITING TITT	GAGTT-AUGA	ATTTTTTT		-TGAATAAAA	- TTT TCCAC	TG	CacatG <mark>G</mark> C	TACC	C - TAAAT T TAGG	C-AAAAAATTTT	AAATTTTA	at f CTTG I <mark>G</mark> AAAA	at — IG at	ATAATATE TAAZ	AATG-A	g C C G TAB A G T T CA A T	.'G
6. ChLG6_R180284691RC_C6	GAACAAACCGCA	TTCCTCTAC	ACT TTTAG TTTT	GAGTT-ATGA	ATTTTTTTT		TG AA TAACA	- TTT TCCAC TA	TGA	CALATG <mark>G</mark> C	TACC	C-TAAATTTAGA	C-AAAAAA <mark>T</mark> TTT	AAA <mark>TT</mark> I <mark>G</mark> TA	AT CTTG TG AAAA	AT – IG AT	ATAATATSTAAJ	LATG - A	GCCGTAGAGTTCAAT	./G
7. ChLG6 K180284691KC C8	GAACAAACCGCA-	-TACCTCTAUS	ACTIFICAG TIFIC	GAGTT-AIGA			GAATAAAA	- TTTTCCACTA	TG -A	ACATGG-C	T ACC		C-BBBBBBBB	AAATTTTTA	ATTCTTG IGAAAA		ATAATATS TAAL	LATG - A	GCUG TA GAATTCAAT	G
9. ChLG2 R180279653 C4	GAACAAACCGCA	TIGATCAACE	ACTITIAS TITT	GAGTTATGA	ATTTTTTAA		TGAATAAAA	- TTT TTCAC TA	TG	CAAATGG-C	TACC	C TAAATTTAGG	C-AAAAAATTTT	AAATTTTA	ATT CTTG IG AAAA	AT IG AT	ATRACATS	AATG-P	GCCEC IG AAT T CAAT	.G
10. ChLG2_R180279653_C8	GAACARACCGCA-	TTGETCARCE	ACTTTTAGTTTT	GAGTT-ATGA	ATTTTTTTAA		TG BATABAA	- TTT T <mark>T</mark> CAC TA	TG -A	ARATARTGG-C	TBCC	C – TAAAT T T <mark>AG</mark> G	C-BBABB	ARATTTTA	<mark>at</mark> i citg i <mark>g</mark> aaaa	AT TG AT	- ATRACATS TAAJ	ARTG-R	GCCGC IG AAT I CAAD	.'G
11. ChLG2_R180279653_C12	GAACAAACCGCA	TTGATCAACG	ACTTTTAGTTTT	GAGTTATGA	ATTTTTTAA		-TG AA TAAAA	- TTTTTCACTA	TG -A	CANATANTGG C	T ACC	C TAAAT TIAGG	CAAAAATTTT	ARATTTTTA	ATT CTTG IG AAAA	AT IGAI	ATAACATSTAAJ	LATG A	GCCGC IG ANT I CAND	G
12. ChLG2 K1602/9653 C14 13. ChLG10 P180277076 C8	GAACAAABCOGCA-	-TIGETCIAG	ACTIVITAS TITTS	GAGTI-ATAA	Persper process		TG AA TAAAA	- TTT ITCRC IA			T-ATC	TAALTIII.	C-BARARA	AAATTITTA	ATTCTTG IGAAAA		- NTA A TA TO PAA 3	AATG-R	GCCGTAGAATTCAAT	NG
14. ChLG1 R180275527RC C4	GAACACACCGCA-	TTGCTCTACE	ACTTATAGTTTT	GAGTTATGA	A-TTTTTT	8	TTG AA TAAAA	TTTTCCACT	TA	AGARA-TACC-	TATC	T-TATTTTTT	CBARAAA-TGTT	ATAACTTTA	GATCTCGTTAAAT	T-IGGT	ATA ATACAG AAJ	AATG-A	GCCGCTGAATCCTAT	G
15. ChLG1_R180275527RC_C7	GAACACACCCCA-	-TTG CTCTACS	ACTENTASTTT	CACTT-ATGA	atttttt	N	TTG AA TAAAA	- TTT TCCAC	<u>чта</u> —	- AG A R A - T ACC -	TATC	T-TATTTTT	CAAAAA-TGT T	ATAACTTTA	<mark>g</mark> at et e g ttaaa <mark>t</mark>	st TGG T	-ATAATACAG AAZ	AATG-A	GCCGC IG AAT <mark>C</mark> CAAT	G.
16. ChLG1_R180275527RC_C6	GAACACACCGCA-	-TTG CTCTACE	ACATATAATTTT	GAGTT-ATGA	ATTTTTT	8	TTG AA TAAAA	ATTTCCACTA	ITA —	AGAAA TACC	TATC	T-TATTTTTT	CAAAAA-TGTT	ATAACTTTA	AATCTOS TTAAAT	GT-TEGT	-ATAATACAG AAZ	LATA A	GCCGC TAAAT CCAAT	G
18 Chi G1_R180275527RC_C5	GAACABACOGCA	-TGGCTCTACS	ACTINTAGTITI	GAGTT ATGA	ATTTTTT		TTG AA TAAAA	TTTTCCACT	TA	-2G AAAATACC-	T ATC	T-TAATTTTT	CARARAR-TGTT	ATAACTTTA	AT CTOS TLANA	ST ANGT	ATAATACAGAAJ	AATG-F	GCCGC IG ART CCARD	G
19. ChLG1 R180275527RC C8	GAACAAACCGCA	- TTG CTCTACS	ACTINTAGTIT	GAGTT-AIGA	ATTTTTT	A	TTG AA TAAAA	AFTTCCACTA	TA	AG AAA -TACC-	TATC	T-TAACTTTT	CARARAR	ATAACTTTA	TAT CTCS TTAAAT	T TEG T	ATAATACAG AA	AATG-A	GCCGC IG AAT CCAAT	G.
20. ChLG1_R180275527RC_C2	GCARACCGCA-	-TTG CTCTACG	ACTTATAGTTTT	GAGTT-ATGA	attttt t	8	TTG BA TABAA	TTATCCAC	ATA	-AAAA-TACC-	TATC	T-TAATTTTT	CBAAAAA-TGTT	AT AACTTTA	G AT CT <mark>C</mark> G TTAAA <mark>T</mark>	st— Iggt	- T T <mark>A</mark> ATAC <mark>AG</mark> AAJ	ATG-A	GCCGC IG ART CART	.G
21. ChLG6_R180283273_C5	GAACABACCACA	-TTG CTCTACS	ACT TTT AG TTTT	GAGTT ATGA	A-TTTTTTT	3	TTG AA TAAAA	TTTTCCTCT	TA	- NG ANA - TACT-	T ATC	T TAATT TTT	CARARA T-TGTT	ATAACTTTA	GAT CTCG TCAAAT	GG GGGT	ATAATACAG AAJ	LAAA A	GCOGCIGANT CCAND	G
23 Chi G6 R180283273 C4	GAACAAACCGCA-	-GIGCTCTAC	ACTIFFAGTITT	GAGTT-ATGA	9 - dated deficients		TTG AATAAAA	-TTTTTCCTCT		AGAAA - TACT	T-ATC	T-TAATTTTT	CAAAAAT-TGTT	ATAACTTTA	GATCTOS TOAAAT	BC GROT	-ATAATACAGAAJ	AAAA P	GCCGC TG A AT CCAAT	G
24. ChLG6 R180283273 C7	GAACARACCGCA	TIGCICTAG	ACTITIAG TITT	GAGTT-ATGA	a-tttttt	2	TTG AA TAAAA	- TTT TCCAC	TA	AGARA-TACT	TATC	T-TAATTTTT	CRAAAAT-TGTT	ATAACTTTA	GATCTOGTOAAAT	SC CGGT	ATAATACAG AAJ	ABAA R	GCCGC TG AAT CCAAD	'G
25. ChLG3 1_R180293178_C8	GAACAAACOGCA-	-TTG CTCTACS	ACTTTTAG TTTT	GAGTT-ATGA	<mark>G –</mark> TTT TTTT T	3	TTG AA TAAAA	- TTT TCCAC	173	-AGAAA-TACT-	TATC	T-TAATTATT <mark>T</mark> G	CARAAAAA TGTT	ATAACTTTA	GAT CTOG TTAAA	st – Iggi	ATAATATAGAAJ	LAAA A	GACGC IG AAT I CAAD	.G
26. ChLG3 1 R180293178 C6	GALCARACOGCA-	-TIG CTCTAG	ACTITIAS TITI				TTG AA TAAAA			-AGAAA-TACC-	T-ATC	T-TAATTTTT T-TAATTTTT	CAAAATA-TGIT	ATAACTITA	BATCING TPAAA	97	- ATAATACAGAAA		CCCCTC ANT TCARD	.G
28 Chi G3 1 R180293178 C9	GAACAAACCGCG	TIGCICIAG	ACCTTTAG TTTT	GOGTT-ATGA	A-TTTTTT	A	TTG AA TAAAA	TTTTTCCACTA	TA	-AGAAA-TACC-	T-ATC	T-TAATTTTTT	CRAAAA-TGTT	ATAACTTTA	GAT CTCG TTAAA	ST-IGGI	-ATAATACAG AAJ	AAAA P	GCCGC IG AAT I CAAD	G
29. ChLG3 1 R180293178 C4	GAACAAACOGCA	-TTG CTCTACS	ACT TTT AG TTTT	GAG TT-ATGA	<mark>6 –</mark> TTT TTTT T	3	TTG AA TAAAA	- TTT TCCAC	TA	-AGAAA-TACC-	TATC	T-TAATTTTT	CARAAAA-TGT T	ATAACTTTA	GAT CTCC TTAAA	ST TSG T	ATAATACAG AAL	AATG - A	GCCGC TG AAT T CAAT	:G
30. ChLG6_R180283273_C2	GAACAAAC	-TIG CTCTAC	ACT TTTAS TTTT	GAGTT-AUGA	A-TTTTTTT-	A	TTG AA TAAAA	- TTT T <mark>T</mark> CAC TA	ITA —	-AAAAA-TACG-	TTTC	T-TAATTTTT	CAAAAA-TTTT	AAAACTTTA	gat CTCS TCAAAT	5 C IG G I	ATAATACAG AAJ	AAA A	GCCECIGAAT CCAAT	.G
31. ChLG6_R180283273_C8	GAACAAACCACA-	-TTGCTCTAC	ACTIFF AGTIFF	GAGTT-A1GA 2 82 TT-A1G 8	9 — d. L.		TIG AA TAAAA	- TTTTTCAC TA		- ABABA TAU	T ATC	T TAATTTTT T TAATTTTT	CARAAAA TTTT	ARAACTITA	ATCING TOAAAT	5 C 116 G 1 5 M 10 C 1	- ATRG TACKG AAJ	19 88 7	GCCGCTGARTCCARD	AG AG
33. ChLG8_R180283273_C3	G TATARACOGCA-	-TIGCICIAG	ACTTIANSTITT	GAGTT-ATGA	A-TTTTTT-	a	TTG AA TAAAA	- TTT TTTAC TA	TA	-AAAA-TACT-	TATC	C TAATTTTT	CAAAAAA-TTTT	AAAACTTTA	GATCTOSTTAAA	T-TGGT	-ATAATACAG AAZ	AZAA P	GCOGC IG AAT T CAAT	G
34. ChLG6_R180283273_C10	GAATAAACCGCA-	-TIGCTACE	ACT TRAK TTTT	GAGTT-ATGA	A-TTTTTTT-	8	TTG AA TABAA	- TTTT TTAC TA		-AAAAA-TACG-	TATC	C-TAATTTTT	CAAAAA-TTTT	AAAACTTTA	<mark>g</mark> at ct <mark>e</mark> s teaaa <mark>t</mark>	GT TGG I	-ATAATACAG AAJ	sa <mark>aa</mark> a	GCCGC IG AAT T CA <mark>G</mark> T	/G
35. ChLG3_1_R180293178_C2	GGACARCCCTCA-	-TTG CTCTACS	ACT TTT AG TTTT T	GAGTT-ATGA		.	TTG AA TAAAA	- TTT TCCAC	TA	-AGARA-TACC-	TATC	T-TAATTTTT	CRAAAA-TTG T	AAAACTTAA	GAT CTCG TTAAA	ST-IGGI	-ACAATACAG AAJ	AAA A	GCGC TG AAT T CAAD	:G
37 Chi G3 1 R180293178 C3	GARGARACCGCA-	-TIGCTCTAG	AGT TTTAG TTTT	GAGTT ALGA	A-TTTTTT A-TTTTTT		TTG AA TAAAA	- TTTTCCAC	TA	-AGAAA-TACA-	T ATC	T-TAATTTTTT	CARARA - TTTT	AAAACTTTA	GATCICS TEAGAT	5 T - 16 G 1	-ATAATACAG AAJ	AATG-P	GCCGC IG AAT I CACP	.G ZG
38. ChLG8 R180289582RC C9	GAACABACCGCA	TTGCTCTAC	ACTTTTAGTTTT	GAGTT-ATGA	ATTTTT	2	TTG BATABAA	ACTT TCCAC TA	TA	GAAA-TACC-	TATC	T-TAATTTTAG	CBAAAA-ATTT	ABAACTTTA	GATCTCS TTAAA	ST	ATAATACAG AAJ	AATG -A	GCCGC TG AAT T CAAT	G.
39. ChLG8_R180289582RC_C11	GAACARACCGCA	TTGCTCTACS	ACTTTTAGTTTT	GAGTT-ATGA	ATTTTTT	3	TTG BATAAAA	ACTTTCCACTA	ATA	GGARA-TACC-	T-ATC	T-TAATTTTRAG	CARARAR-ATTT	AAAACTTTA	GAT CTCG TTAAAT	st - Igg I	ATAATACAG AAJ	LATG -A	GCCGC IG AAT I CAAD	G
40. ChLG8 K180289582KC CB	GAACAAABOGCA-	-TIG CPCTAG	ACTITIAS TITT	GAGTT-ANGA			TTG AA TAAAA	CPT TCCAC TA		GAAA-TACC-	T-ATC	T TAATTTTAS	CARAAAA-ATTT	AAAACTITA	ATCICS TRAAT	5T	- ATAATACAG AAA	LATG-R	GCCGC IG AAT T CAAD	.G
42. ChLG8_R180289582RC_C4	GAACARACCGCA	TTGCTCTAC	ACTTTAGTTTT	GAGTT-ATGA	A-TTTTTT		TTG AA TAAAA	-CTTTCCAC TA	TA	-GGARA-TACC-	TATC	T-TAATG TTTAG	CIGAAAA-ATTT	AAAACTTTA	GATTTCG TTAAAT	ST-IGGI	-ACAATACAG AAJ	ARTG-A	GCOGCIGANTICANT	.G
43. ChLG8_R180289582RC_C2	GAACAAACOGCA	TACTCTACS	ACTITIAGTITI	GAGTT-ATGA	ATTTTT	3 <mark>.</mark>	TTG AA TAAAA	CTTTCCAC	12A	-GGAAA-TATC-	TATC	T-TAATT TTTAG	CARAAAA-ATT T	AAAACTTTA	<mark>g</mark> at ct <mark>o</mark> g ttaaa <mark>t</mark>	AT IGGI	ATAATACAG AAI	LATG - A	GCCGCTGARTTCART	.'G
44. ChLG8_R180289582RC_C14	GAG CAAACCGTA-	-TTG CTCTACS	ACT TTTAG TTTT	GAGTT-ATGA	ATTTTTT	3	TTG AA TAAAA	-CTTTCCACTA	ITA —	-GGAAA-TACC-	TATC	T-TAATTTTTAG	CAAAAA-ATTT	AAAACTTTA	TATCTCETTAAAT	ST-IGGI	-ATGATACAGAAA	AATG-A	GCCGC IG AAT T CAAT	.G
45. ChLG8_R180289582RC_C15 46. ChLG8_R180289582RC_C13	GAACABACOGCA	-TTGCTCTAUS	ACTITIA	GAGTT ATAA	A-TTTTTT A-TTTTTT	* 2	TT AAAAA	- CFT TCCAC	TA	GGARA-TACC-	T ATC	T-TAATTTTTA	CARARAA-ATTT	AAAACTTTA	GAT CTOS TEASAT	st ling t	-ATAATACAG AAJ	AATG-A	GCOGC TEANT TOAND GCOGC TEANT TOAND	G
47. ChLG8 R180289582RC C3	GAACAAACOGCA	- TTG CTCTACS	ACTITIASTITT	AGTT-ATA	ATTTATT	a	TTTAA CAAAA	- TTTTCTACTA	TA	AGAA -TACC-	TATC	T-TAATTTTAG	CAAAAA-ATTT	AAAACTTTA	GATCACC TTAAA	T TGG T	ATAATACAG AAZ	AATG-A	GCCGC IG AAT T CAAT	G.
48. ChLG8_R180289582RC_C5	GAACAAACCGCA	TIGCTCTACE	ACTTTTAG TTTTT	ag tt-at <mark>a</mark> a	ATTTATT	3	TT <mark>T</mark> AA <mark>C</mark> AAAA	- TTT TC TAC TA	ITA	AGAAA - TACC	TATC	T-TAATTTTTAG	CBAAAA-ATTT	AAAACTTTA	<mark>g</mark> at c <mark>ac</mark> s teaaa <mark>t</mark>	ST – TGGT	ATAATACAG AAJ	LATG - B	GCCGC TG AAT T CAAT	.vG
49. ChLG8_R180289582RC_C10	GAACAAACCGCA-	-TTG CTCTACG	ACT TTT AG TTTT T	AAGTT ATAA AAGTT ATAA	A TTTXTT A TTTXTT	9 -	TTTAACAAAA	- TTT TCTAC TA		AGAAA - TACC-	T ATC	T TAATTTTPAG	CARAAAA-ATTT	ARAACTTTA	GATCACG TTAAAT	ST CGGI	-ATAATACAGAAJ	LATG - A	GCCGC IG AAT I CAAD	G
51. ChLG8 R180289582RC C7	GAACAAACOGCA	-TIG CTCTACE	ACT TTTAS TTTT	AAGTTATAA	ATTTATT	3	TTTAATAAAA	- TTT TCTACTA	TA	AGANA-TACC-	TATC	T-TAATTTTTAG	CARARAA-ATTT	AAAACTTTA	GATCACETTAAAT	ST-IGGI	ATAATACAGAAA	AATG-P	GCCEC IG AAT T CAAT	.G
52. ChLG10_R180277965_C5	GAATAAACCGTT	TTGTTCTAG	ACT TTT AG TTTT	GAGTT-ATGA	attttt	2	TTAAA TABAA	- TTT TCCAC		- AG ARA - TROC	TT	T - TAATT T TTAG	CBAAAA-TTTA	ARARCTTTA	<mark>g</mark> at et <mark>e</mark> g teaa <mark>g t</mark>	AT TG G T	- TT <mark>R</mark> ATAC <mark>RG</mark> AAJ	AATG-R	GCCGC IG AAT I CAAD	.'G
53. ChLG10_R180277965_C7	GAACAAACCGTT-	-TTG TCTAG	ACT CITAG TITT	GAGTT ATGA	ATTTTTT	5	TTG AA TAAAA	TTTTCCACTA	ITA	-AGABA-TACC-	T ATT	T TAATT T TEAG	CARARAR-TTTA	AAAACTTTA	GAT CTCG TTARG T	AT DEGI	TTATACAGAAJ	LATG A	GCCGC TG AAT T CAAD	;G
55. ChLG3 Z R180295674 C6	GGAACCGCA-	-TTACTCTACS	ACTTTTATTT	GAGTT-ATGA	A-TTTTT	3	TTG AATAAA	TTTTTCCAGTA	TA	-GGAAA-TACCI	ATC	T-TAATTTTTAG	CAAAAAA CTTT	AAAAG TTTA	GATCITG TTAATA	31	-TTAATACAG AAZ	AATG-P	GCCGC IG AAT T CAAT	.u .u
56. ChLG3_2_R180295674_C25	GG AACOGCA-	TTACTCTACS	ACTTTTATTT	gagtt-atga	ATTTTTT-	9	TTG AA TAAAC	- TTT TC CAG TA	1 TA	-GGARA-TACCT	ATC	T-TAATT T TTAG	CBAAAA-CTTT	AAAAG TTTA	G AT CITG TEAA TA	st — TGGT	-TTAATACAG AAJ	AATG-A	GCOGC IG AAT I CAAD	:G
57. ChLG3_2_R180295674_C8	GAC CARACCECA	TTG CTCTACS	ACTTTTAATTTT	GAGTT ACGA	ATTTTT	<u></u>	TTG AA TAAAC	TTTTCCAG TA	ATA	GAAA-TAOCI	A -TC	T TAATTTTAG	CAAAAA-CTTT	AAAAG TTTA	GAT CTTG TTAA <mark>T</mark> A	ST IGGI	TTAATACAG AAI	LATG A	GCCGCTGAATT CAAT	.G
58. ChLG3 2 R180295674 C2	GAACAAACOGCA-	-TIGCTCTAR	ACTITIATITI	GAGTT-ALGA			TTG AA TAAAC	TTTTCCAG T			A -TC	T - TAATTTTTAG T - TAATTTTTAG	CAAAAAA CIIII	ARAALI TITA	CATCITC TRATA	97	-TIARTACAGAAA -TTARTACAGAAA	LATC-A	GCCGC IG AAT T CARD GCCGC IIG AAT T CA AD	AG AG
60. ChLG3 2 R180295674 C20	GAGCARACCECA	TTGCTCTACS	ACTTTTATTT	GAGTT ATGA	ATTTTTT	9	TTGAATAAAA	TTTTCCACTA	TA -	GARA-TACCT	A -CC	T-TAATTTTAG	CAAAAA-CTTT	AAAAG TTTA	GAT CTTG TTAATA	ST-TGGT	TTAATACAGAA	AATG A	GCCGC TG AAT T CAAD	G
61. ChLG3_2_R180295674_C27	GA <mark>G</mark> CARACCGCA-	- TTG CTCTACG	ACTITTAATTTT	GAG TT-AIGA	ATTTTTT-	<mark>3</mark>	TTG AA TAAAA	- TTT TCCAC	TA	-GGARA-TROCT	ACC	T-TAATTTTRG	CARARA CTTT	AAAAG TTTA	<mark>g</mark> at citg teaa <mark>t</mark> a	GT NGGI	– T T <mark>A</mark> ATAC <mark>AG</mark> AAJ	AATG-A	GCCGC IG AAT I CAAD	:G
62. ChLG3_2_R180295674_C4	GAG CARACCECA-	-TTG CTCTACG	ACTTTTAATTTT	GAGTT-ATGA	ATTTTTT ATTTTTT	a	TTG AA TAAAA	- TTT PCCAC	TA	-GGAAA-TACCI		T-CAATTTTPAG	CAAAAA-CTTT	AAAAG TTTA	GATCTTG TTAATA	ST-TEGI	-TTAATACAGAA3	LATE - A	GCCGC IG AAT I CAAT	G
64 Chi G3 2 R180295674 C12	GAG CARACOSCA	-TIGCICIACS	ACTITTATITT	GAGTT ATGA	ATTTTTT	.	TTG AA TAAAA	TTTTCCAC		-AGAAA-TACCI		T TAATT TTTAG	CARARA CTTT	AAAAG TTTA	GATCING TRAATA	3T - 1661 ST - 1661	TTAATACAG AAJ	AATG P	GCCGC IG AAT I CAAD	3G
65. ChLG3 2 R180295674 C5	GAGCARACOGCA-	- TTG CTCTACS	ACTTTTAATTTT	GAGTT-ATGA	ATTTTTT-		TTG AA TAAAC	TTTTCCAC	TA	GAAA-TACCI	ATC	T-TAATTTTRAG	CAAAAA CTTT	AAAAG TTTA	GATCITG TTAATA	GTTGGT	TTAATACAG AA	AATG-A	GTCGC IG AAT TTAAT	7
66. ChLG3_2_R180295674_C24	GAGCARACCGCA-	TIGCTCTACE	ACTTTTAATTTT	GAGTT-ATGA	ATTTTTT	3	TTGAATAAA	- TTT TCCAC	чта. —	-GGAAA-TACCT	A -TC	T-TAATTTTAG	CARAAA-CTTT	ARAAG TTTA	<mark>g at cttg ttaa<mark>t</mark>a</mark>	ST	TTAATACAG AAJ	ATG-A	G T CGC IG AAT I <mark>T</mark> AAT	1
67. ChLG3_2_R180295674_C7	GAGCARACOGCA	-TTG CTCTACS	ACTTTTATTT	GAGTT ATGA	ATTTTTT	3	TTG AA TAAAC	TTTTTCCACTA	TA	-GGARA-TROCT	A -TC	T TAATT TTTAG	CARAAAA-CTTT	ARAAG TTTA	GAT CTTG TTAATA	ST IGGI	-TTAATACAGAAJ	LATG	GTCGC IG AAT TTAAD	G
69. ChLG3 2 R180295674 C10	GAGCAAACOGCA-	-TTGCTCTAC	ACTITTATTT	GAGTT-AUGA	ATTTTTT-		TTG AATAAAG	TTTTCCACTA	TA	GGAAA-TACCI	ATC	T-TAATTTTTAG	CAAAAA-CTTT	AAAAG TTTA	GATCTTG TTAATA	5 I 166 I	-TTAATACAG AAJ	AATG-P	GCCEC IG AAT T CAAT	G
70. ChLG3_2_R180295674_C18	GAGCARACCGCA	TIGCTCTAG	ACTTTTATTT	GAGTTATGA	ATTTTTT-	<mark>9</mark>	TTG AA TAAA	TTTTCCAC	1 TA	GGARA-TACCT	-TC	T-TAATTTTAG	CARAAA-CTTT	ARAAG TTTA	GAT CITG TEAATA	ST-IGGT	TTAATACAGAAJ	ARTG-R	GCOGCIGANTICAND	.'G
71. ChLG3_2_R180295674_C23	GAGCARACCECA	TTGCTCTAG	ACTITTAATTTT	GAGTTATGA	ATTTTTT	3	TTGAATAAAC	TTTTCCACTA	TA	GARA-TACCI	-TC	T-TAATTTTAG	CARARA CTTT	AAAAG TTTA	GATCITG TTAATA	ST TGGI	TTAATACAGAAJ	LATG A	GCCGCTGAATTCAAT	G
72. UNLG3 2 R180295674 C11 73. Chi G3 2 R180295674 C22	GAGCARADOGCA-	-TIGCTCTAG	ACTIFIANTITI	GAGTT-ATGA	ATTTTTT T	*	TTG AATAAAC	- TTTTCCACTA			A -TC	T = TAATTTTTAG T = TAATTTTTAG	CARAAAA-CTTT CARAAAA-CTTT	AAAAG TTTA	GATCITG TIAATA GATCITG TIAATA	81-1661 87-1661	-TIMATACAC AAZ	AATG-A	GCCGC IG ART T CARD GCCGC IG ART T CARD	an a
74. ChLG3 2 R180295674 C21	GAG CARACCOCA	TIGCTCTACE	ACTTTTATTT	GAGTT ATGA	ATTTTTT	5	TTGAATAAAC	TTTTCCACT	TA	GABA-TACCI	A -TC	TTAATTTTAG	CAAAAA-CTTT	AAAAG TTTA	GATCTTGTTAATA	ST IGGI	TTAATACAGAAJ	AATG P	GCCGC TG AAT T CAAT	.G
75. ChLG3_2_R180295674_C19	ga <mark>g</mark> caracogca-	- TIG CICIACE	ACTTTTAATTTT	GAGTT-ATGA	ATTTTTT	<mark>2</mark>	TTG AA T AAAC	- TTT TCCAC	1 TA	GARA-TACCI	ATC	T-TAATT T TEAG	CARAAA-CTTT	AAAAG TTTA	<mark>g</mark> at cttg ttaa <mark>t</mark> a	st—JGGI	-TI <mark>A</mark> ATAC <mark>AG</mark> AA2	LATG - A	g cogo ig aat i caat	G.
76. ChLG3_2_R180295674_C14	GAGCARACCECA-	- TTG CTCTACS	ACTTTTATTT	GAGTT-ATGA		3	TTG AATAAAG	- TTT PCCAC			A -TC	T-TAATTTTRAG	CRAAAA-CTTT	AAAAG TTTA	CATCING TRAATA	ST	-TTAATACAGAAA	LATE - A	GCCGC IG AAT I CAAT	.KG
78. ChLG3_2_R180295874_C13	GAGCARACOGCA-	TIGCTCTACS	ACTITIATIT	GAGTI ATGA	A-TTTTTT		TTG AA TAA AG	TTTTCCACT	TA	GANA-TAC	A -TC	T TAATT TTAG	CARARAA-CITT	AAAAG TTTA	GAT CITS CLARTA	ат — 11661 ат — 1166т	-TTAATACAG AAJ	AATG-P	GCCGC IG AAT I CAAD	.G
79. ChLG3 2 R180295674 C16	GAGCARACOGCA	TTGCTCTAC	ACTITIANTITI	GAGTT-ATGA	ATTTTTT-		TTG AAT AAAC	TTTTCCACT	TA	AGARA TACCI	A -TC	T-TAATTTTAG	CARARA-CTTT	ARAAG TTTA	GATCTTG TTAATA	ST	TTAATACAGAAJ	AATG - A	GCCGC IG AAT T CAAT	'G

80. ChLG3 2 R180295674 C26	GA <mark>G</mark> CARACOGCA-	- TTG CTCTACG ACTTTTANTTTT CG AG TT-ATG AA-TTTTTT	TTG AATAAAC - TTT TCCAC TATA	GGARA-TACCTA	TCT-TAATTTTTAG C <mark>A</mark> AAAAA-CTTTAAAAG TTTA <mark>G</mark> ATCTTG TT <mark>GAT</mark> AG T	IGG T T TAATAC <mark>AG</mark> AAAATGAGCCGC IG AAT T CAATG
81. ChLG3 2 R180295674 C3	GAGCAAACOGCA-	- TTG CTCTACG ACTTTTANTTTT CG AG TT-ATG AATTTTTT	TTG AA TAAAA - TTT TCCAC TA TA		– – ATCT– TAATT T TTAG C <mark>A</mark> AAAA – CTT TAAAAG TTTA <mark>G</mark> AT CTTG TTAA <mark>T</mark> AG T	IGG T T TA A TACAC AAAATG AGC CGC IG AAT T CAATG
82. ChLG9 R180291860RC C3	GAACAAACOGCA	- TTG CTCTACG ACT TTTAG TTTT IG AG TT-AIG AA- TT TTTT	TTG AA TAAAA - TTT TC CAC CATA		– – ATCT– TAATT I TT <mark>TT</mark> C <mark>B</mark> AAAAA– CTT TAAAAG TTTA <mark>G</mark> AT CT <mark>C</mark> G TTAA T A <mark>B</mark> T	IGG T T T <mark>A</mark> A TA C <mark>AG</mark> AA <mark>C</mark> ATG AG <mark>T</mark> CGC IG AAT T CAATG
83. ChLG5 R180282425 C3	GAACAAACCGCA	- TTG CTCTACG ACT TTTAG TTTT TA AG TT-ATG AATTTTTTT <mark>5</mark> T	TG AATAAAA TTTTCCAC TATA		– – ATCT – TAATTTTTAG C <mark>B</mark> AAAAA – <mark>T</mark> TT C AAAA <mark>TG</mark> TTA <mark>G</mark> ATCTCG CTAAAAG T	TG G T ATA ATA C <mark>AG</mark> AAA <mark>G</mark> TG AGC CGC TG AAT T CAATG
84. ChLG5 R180282425 C13	GAACAAACCGCA-	- TTG CTCTACS ACT TTTA <mark>T</mark> TTTT IS AG TT-AIS AATTTTTTT <mark>G T</mark>	TG AATAAAA TTT TCCA <mark>G TATA</mark>	CARA-TGC-T	ATCT-TRATTTTERS CARARA- T TT C ARAR TG TT RG AT CT C S TTARARS T	TEG T-ATAAACAG AAAG TE-AGCCEC TE AAT T CAATE
85. ChLG5 R180282425 C5	GAACAAACCGCA-	- TTG CTCTACG ACTTTTAG TTTTTG AG TT- ATG AA TTTTTTT <mark>G T</mark>	TG AATAAAA TTTTTCCACTATA	GAAA-TGGC-T	ATCT-TAATTTTTTAG C <mark>B</mark> AAAAA -T TT C AAAA <mark>TG</mark> FTA <mark>G</mark> ATCT <mark>C</mark> G TTAAAAG T	OSG T-ATAG TACAG AAAATG-AGCOGC IG AAT T CAATG
86. ChLG5 R180282425 C7	GAACAAACCGCA-	- TTG CTCTACG ACT TTTATTTT IG AG TT- AIG AA TTTT TTIG T	TGAATAAAA TTTTCCACTATA	GAAAA-TGCC-T	ATCT - TAATTT TTAG C A AAAA T TT CAAAA TG TTA <mark>G</mark> AT CTTG TTAAAAG T	
87. ChLG5 R180282425 C10	GAACAAACCGCA	- TTG CTCTACS ACT TTTATTTT IS AS TT-AIS AATTTT TTIS	-TG AATAAAA TTT TCCAC		- ATCT - TAATT T TTAG CAAAAA - TTT CAAAATG TTAG AT CTTG TTAAAAG T	
88. ChLG5 R180282425 C9	GAACAAACCGCA-	- TTG CTCTACG ACT TTTATTTT IG 2G TT-AIG AATTTTTTTG T	TG AATAAAA TTT TCCAC		ATCT- TAATT T TTAG C <mark>A</mark> AAAAA- <mark>T</mark> TT <mark>C</mark> AAAA <mark>TGA</mark> TA <mark>G</mark> AT CTTG TTAAAAG T	ISG C - ATAACACAG AAAATT - AGCCGC IG AAT T CAATG
89. Chi G5 R180282425 C14	GAACAAACCGCA-	- TTG CTCTACG ACT TTTATTTT IG 8G TT- AIG AATTTT TTIG T			ATCT - TAATTT TTAG CAAAAA - A TT <mark>C</mark> AAAA <mark>TG</mark> TTA <mark>G</mark> AT CTTG TTAAAAG T	
90 ChLG5 R180282425 C4	GAACAAACCGCA	TTG CTCTACG ACATTTAG TTTT IS AG TT ATG AATTTT TTTS	TG AATAAAA TTT TCCA <mark>G TATA</mark>		- ATCT - TAATTTTTAG CAAAAA - ATTG AAAATGTTAG AT CTCG TTAAAAG T	
91. ChLG5 R180282425 C12	GAACAAACOGCA-	- TTG CTCTACG ACT TTT AG TTTT IG AG TT-AIG AATTTT TTTG T	TG AA TAAAA - TTT TCCA <mark>G TATA</mark>		ATCT-TAATTTTTAG C <mark>R</mark> AAAAA -A TT C AAAA <mark>TG</mark> TTA <mark>G</mark> AT CT C G TTAAAAG T	TEG T-ATA TACAG AAAG TE-AGCCEC TE AAT T CAATE
92. ChLG5 R180282425 C6	GAACAAACCACA-	- TTG CTCTACG ACE TTTAG TTTTTG AG TT- ATG AA TTTTTTTG T	TG AATAAAA - TTTTCCA <mark>G TATA</mark>		- ATCT-TAATTTTTAG C <mark>R</mark> AAAAA -A TT <mark>G</mark> AAAA <mark>TG</mark> TTA <mark>G</mark> ATCT C G TTAAAAG T	
93. ChLG5 R180282425 C2	GAACAAACCGCA	- TTG CTCTACG ACT TTTAG TTTT TAG AT T- ATG AAT TTT TTTG T	TG AATAAAA TTT TCCAC TATA		- ATCT - TAATT T TTAG CRAAAAATT TT CAAAATG TTAG AT CTOG TTAAAAG T	TEGT-ATAGGAAAATG-AGCCGCTGAATTCAATG
94. ChLG6 R180284741 C8	AACAAACOGCA	TTG CTCTACG ACT TTT AG TTTT CG AG TT - ATG AA TTTT TTTG T	TG AATAAAA TTTTCCAC		- ATTT - TAATT T TTAG CARAAAA - TTT TAAAATG TTGG AT CTCG TTAAAAG T	
95 Chi G6 R180284741 C11	AACAAATCGCA-	- TTG CTCTACS ACTTTTRS TTTT	TGANTANA-TTTTCCACTATA		ATT - TAATT T TENS CAAAAA - TTT TAAAA TG T TOO AT C TC TTAAAAG T	TEGT-ATATATATAGAAAATE-AGCCECTEAATTCAATE
96. Chi G6 R180284741 C13	GAG CARACCECA-	TTG CTCTAGE ACT TTTAG TTTT IG AG TT-AIG AATTTTTTTG	TG AATABAA TTT TCCAC	GAAAA-TGTT-T	ATTT-TAATTTTTAG CRAAARA-TTTTARAATGTTGG ATCTOG TTARAAG T	
97 CH G8 R180289275RC C7	GAACAAACCGCA	- TTG CTCT A CG A CTTTTA TTTT CA AG TT- A TG AA TTTTTTTTTTTTTTTTTTTTTTT	-TGAATAAAA TTTTCCACTATA		- ATGT - TAATTT TTAG CAAAAAA - TTT TAAAA TGT CAG AT CTOG TTGAAAGG	- TEAT ATA TACAS AAAATE - AGCCGC TEAATT CAATE
98 Chi G8 R180289275RC C16	GAACAAACCGCA	-TTG CTCTACE ACT TTTANTTTTC AG TT-ATE AATTTTTTTC	TG AA TAAAA - TTT TCCAC TATA		ATGT-TAATTTTTAG CARAAAA-TTTTTAARATGTCAG AT CTCC TTGRAAGG	TE AT-ATAATACAG AAAATE - AGCCGC TE AAT T CAATE
99 Chi G8 R180289275RC C9	GAACAAACCGCA-	- TTG CT CT A CG A CT TTT A TTTT G AG TT - A TG AA TTTT TTTG T	TG AATAAAA TTTTCCACTATA		ATGT-TAATTTTTTAGCAAAAA-TTTTTAAAATGTCAGATCTCGTTGAAAGG	
100 Chi GB R180289275RC C12	GAACAAACCGCA	TTG CTCTACS ACT TTTANTTTT CS AG TT ATG AATTTT TTTG T	TGATAAAA TTTTCCACTATA		ATGT TAATTTTTAG CAAAAA-TTTTAAAATGTCAG ATCTCG TTGAAAGG	TGAT ATAATACAG AAAATG AGCCGC TGAAT T CAATG
101 Chi G8 R180289275RC C8	GAACAAACCGCA	- TTG CTCTACG ACT TTTAATTTT CG AG TT-ATG AATTTTTTTG T		GABAT-TGOT-T	- ATGT - TAATTTTTAG CAAAAAA - TTTTAAAATGTCAG AT CTCG TTGAAAGG	TGAT-ATAATACAG ABAATG-AGCOGC TGAAT TCAATG
102 Chi G8 R180289275RC C3	GAACAAACCGCA-	-TTG CTCTACE ACT TTTAG TTTT			- ATGT-TAACTTTTAGCAAAAA-TTTTTAAAATGTCAGATCTCGTTGAAAGG	
103 Chi G7 R180285737 C4	GAACAAACCGTT	TTG CTCTATE ACT TTT AG TTTT TE AG TT-ATAAA TTTT TTTAT	TGATAAA TTTTCTAC		- ATGT - TACTT TTTT CAAAAA - TTT TAAAATGT CAG AT CTCATTGAAAGT	GAT-ATAATACAG AAAATG - AGC CGC TG AAT T CAAT
104 Chi G8 R180289244RC C2	GAACAAACCGCA	TIG CTCTACE ACT TTTAG TTTT IG TO TT AIG AATTTTTTTGT	TGAATAACA TTTTCCACTATA	GARAT-TGCC-T	ATGT TAATTTTTAG CAAAAA TTTTAAAATGTCAG AT CTCG TTGAAAG T	- IG TT-ATAATACAG AAAATG - AGCCGC IG AAT T CAATG
105 Chi G8 R180289244RC C4	GAACAAACOGCA	- TTG CTCTACC ACT TTTAG TTTTTG TG TT-ATG AATTTTTTTG T	TG AA TAACA - TTT TCCAC TATA		- ATGT - TAATTTTTAG CAAAAAA - TTTTAAAA TGTCAG AT CTCG TTGAAAG T	
106 Chi G8 R180289244RC C9	GAACAAACCGCA	-TTG CTCTACG ACT TTTGC TTTTTG AG TT-ATG AATTTTTTTG	TGATACA TTTTCCACTATA		- ATGT-TAATTTTTAG CAAAAA-TTTTAAAATGTCAG ATCTCG TTAAAAG T	
107. Chi G8 R180289244RC C7	GAACAAACCGCA	TTG CTCTACG ACT TTTAG TTTT IG AG TT-AIG AATTTTTTTG	TG AAG AAAA TTT TCCTCTATA		ATGT-TAATTTTTAGCHAAAAA-TTTTAAAATGTCAGATCTTGTTGAAAGT	
108. ChLG8 R180289247RC C6	GAACAAACOGCA	TTG CTCTACS ACT TTTAS TTTT IS AS TT-AIS AA TTTT TTIS	-TG AAG AAAA TTTTCCTCTATA		ATGT TAATTTTTAGCAAAAA-TTTTAAAATGTCAGATCTTG TTGAAAGT	TET ATATACAGAAAATG AGCCGCTGAATTCAATG
109 Chi G8 R180289247RC C3	GAACAAACCGCA	- TTG CTCTACG ACTTTTAG TTTT IG AG TT-AIG AATTTTTTTG T	TG AAG AAAA TTTTCCTTTATA		- ATGT-TAATTTTTAGCAAAAA-TTTTAAAATGTCAGATCTTGTTGAAAGT	
110 Chi G8 R180289244RC C14	GAACABACCGCA-	- IEG CT CT & CG & CT ITTT AG TITTT IG AG TT - AIG AA TITTT ITTIG T	TE AAG AAAA TTTTCCACTATA	GRART-TGCC-T	- ATGT-TAATTTTTTAGCAAAAA-TTTTAAAAATGTCAGATCTCGTTGAAAGT	
111 Chi G8 R180289247RC C2	GAACAAACGCA	- TEG CTCTACS ACT TTTAG TTTT TG AG TT-ATG AA TTTT TTTT	TG AAG AAAA TTT TCCAC TATA		- ATGT TAATTTTTAGCAAAAA-TTTTAAAATGTCAGATCTTGTTGAAAGT	- TEGT - ATAATACAG AAAATG - AGCCGC TG AAT T CAATG
112 Chi G8 R180289247RC C7	GAACAAACCGCA	- TTG CTCTACG ACT TTTAG TTTT IG AAT T- ANG AAT TTTTTTG T	TAAAGAAAA TTTTCCACTATA		- ATGT - TAATTTTTAG CAAAAAA - TTTTAAAA TGTCAG AT CTCG TTGAAAG T	
113 CH C8 P180289275PC CA	GAACAAACCGCA-	- THE CEPCER & CE & CEPTER DE TREPHENE DE ANTE - A TE AA DEREN DE TE	TY: 33C 33 33 - TTTTTCCACTAT		- APCT-TAATTTTTCCAAAAA TTTTAAAAATCTTAAATCTTCCTTAACACT	
114 Chi G8 P180289275PC C17	GAACABBCOSCA-	- THE CT CT & CC 2.5 T THT BE THEFT IS 3C T T - 2 TE 22 THEFT THE C	TC 33C 3333 TTTTCCACTATA		- ATCT TRATTTTC CREATER TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	
115 Chi G8 P180289275PC C10	GAACABACCSCA	- דדוכ ביד כיד א נזג א ביד ידייד אל דידייד זוג אני יד - איזג אא דידייד ידייזי איז ידייזי איז איז איז איז א איז	TCACTATA		- ATGT TAATTTTTTS CARAAAA - TTTTAAAAATGTCAGATCTCS TTAAGAGT	
118 CH C8 P180289275PC C13	GAATAAACCGCA-	- TTG CT CT A CC A CT TTT AG TTTT TG AG TT - A TG AA TTTT TTTC T	TCARCASA TTTTCCACTATA		- ATGT-TAATTTTTTCCAAAAA-TTTTTAAAAATGTTAAAATCTTCTTAAGACT	TEGT-ATA TATAGAA AATE-AGCCECTE AATTCACTE
117 CH G8 P180289244PC C11	GAACABACCGCA-	- THE CT CT & CE & CT TTT IS TTTT IS 2C TT - ATC 33 TTTTTTTTT	TC 33 TAA33 TTTTCCACTATA	CLARA TOCCT	- ATST-TRATTTTTASCARAAR TTTTARAARTCTCARATCTCCTTCARARST	
119 CH C8 D180287763DC C2	GAACABACCGCA					
110 CH C8 P180287783PC C5	CARCABBCCCCB-		CTARTER TARA	CRATT TO CO	- ATCT TA ATT TO CAN BAR TTT TABAB TO TA A ATCT TO A A ACT	
120 CH C0 D100207703RC C3	BALCA BACCOCA				- APCT TA ATT TO THE CHARMEN THE PARTY AND AT CINE TO A A 20 TH	
121 CH C8 P180287763PC C6	TAACABBCCGCB-				- BTCT-TABTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	
121. CHLOB K100207703KC C0	GAACABACCCA-					
122. CHLOB K100200111 CZ	C 33 TA B 3CCCC3-	- THE CINCENCE ACTION IN THE PARTY ACTION AND A THE PARTY AND A THE PARTY ACTION ATTION AND	TORIANA TIRICOL		- APCT TRAILITICS CONTRACTS AND TRACKING AT TO ALL AND TRACKING	- TOT - TTA THOM AND AND - ACCOUNT ANT CALLS
124 CH C9 D190399111 C3	GAACABACCCCA-					
124. CHLG0_R100200111_C3	GBACKBBCCCCA-		- TO AN I ANAL IT I I COAL DE LA			
128 CHLOB R100200111 C4	CARCARACOURTA-					
127 CH C8 D180287782DC C4	Casca a scructa-				- APCT - DATE TIME CRAMME - III PARAMET INTER A STORE ALC TO A A A A A A A A A A A A A A A A A A	
129 CH C8 P180280247PC C9	GAACABACCCCA-				- breve the second seco	
120. CHLC0_R100209247RC_C9	G SSCS B SCOCO 3.				- APOT TRATING CORASE AND AN ASSOCIATE STORES TO ASSACT	
120 CH C5 D1802827110C C0	CALCABACCCCA.	- THE CONCEPTION OF THE REPORT			- TEATTTER CRAMME TEACHING TO ALL THE	- TECT - TO A TACAS A A TEC - ACTOC TE A ATT CO ATC
131 CH C6 P180284741 C2	GBACBBBCCCCB-					
132 CH C6 D180384741 C5	GBBCBBBCCGCA				- RECT TRAILITING CONSISTENT AND A SAME TO A S	
122 CHLG0 K100204741 CJ	Baaca Baccca				- APCT TRATTITIAC CONTAINS ATTITIAL 23 TO THE ATCT OF A 2 A 2 C	
133. CHLG0 K100204741 C7	Antonnacosca-					
135 CH C6 P180284741 C6	AACABBCOSCA-	-TIG CT CTACS A CT TTT AS TTTT AS A ST A TTTTTTTTT	TTC ANTARAN TITTTCCACTCTA		- APCT TAATTTTTAACAAAAAA TTTTAAAAATGTTG ATCTG TTGAAAGT	TEGT-CTAATACAGAAAATG AGCCCCCTEAATTCAATG
136 Chi G6 R180284741 C10	GAACABACCECA	דייייייייייייייייייייייייייייייייייייי	TTARATAARA TTTTTACACTATA		- ATCT TRATTTTAC ASSARS-TTTTARAS TOTTO STOTOS TOTOS T-GARAGT	TEGT OTA ATA CAG AA A ATE AGCCECTE A ATT CA ATE
137 CH C5 P180282425 C8	AACAAACCSCA-	- TTG (TF CT & CS & CT TTT NG TTTT TG AG T T - A TG AA TTTTT TTTTT	TCAATAAA TTTTTTTTTACTATA		- ACCT - TAATT TTTTATCAAAAA - TTATAAAATC TTAAAACT	TEGT-ATTA ATACAG AA AATG-AGCCECTE AATTCA ATG
138 CH C5 P180282425 C11	BAACABACCCCA-		TC 33 TAA33 TTTTTTCACTATA			
139 CH G1 P180275579 C2	GAACABACCGCA	- TTG (TTCT & CS & CT TTT & S TTTT OS CS TT - A TG & A TTTTT TT	TTG BAT BABA TTTTTCCBTTATA		- STOT TAATTTTTATCASAAAA-CTTTAACATTTTAACTOCCTTAAAAT	- BEGT - ATAG TACAG AA BATG - AGCCCC TG A ATT CA ATG
140 Chi G1 R180275579 C18	GAACAAACOGCA	- TTG (TTCT A CC A CT TTTT AG TTTTT CC AG T T - A TC AA TTTTT TT	TTG AA TAAAA TTTTTCCACTATA		- ATCT TAATTTTTATCAAAAAA CTTTAACATTTTAACTCTCCTCCTTAAATCT	
141 CH G1 R180275579 C6	GAACAAACOGCA-	- TTG OR CTACS ACT TTT AG TTTT OS AG TT-ACT AA TTTTTTT	TTC AAC AAAA TTTTTTCCCTATA		APCT-TABTTTTTATCAAAAA-CTTTAACATTTTAACTCTCC TTAAATTT	
142 Chi G1 R180275579 C12	GAACABACCGCA	- TTG (TTCT & CG & CT TTTT & TTTTT C & C T - 2 TG & A TTTTT TT-	TTC 33C 3333 TTTTTTCCCCTATE		- APCT TAATTTTTACCAAAAAA CTTTAACATTTAACTCTCC TTAAATT	
143 Chi G1 R180275579 C5	GAACABACCGCA	- TTG CTCT & CS & CT TTT & G TTTT 0 3 2G T T - & TG & & TTTT TT	TTG BAG AAAA TTTTTTTCACTATA		- APCT TAATTTTTATCAAAAA - CTTTAACATTTTAACTCTCG TTAAATST	- AGGT - ATA ATA CAG AA AATG - AGCCGCTG A ATT CA ATG
144 Chi G1 R180275579 C11	GAACAAACCGCA-	- TTG CT CT & CC & CT TTT NG TTTT TG AG TT - A TG AA TTTT TT	TTC AA TAAAA _ CTT TCCAC TATA		- ATCT - TACTTTTATCAAAAAA - CTTTAACATTTTAACTCTCG TTAAATCT	
145 Chi G1 R180275588 C2	GAACAAACOSCA-	- CTC CTC CT & CC & TT OPPT NO POPPT TO 2C TT - A TO & A POPPT POP - T	TTC AA TAACA - TTTT PCCAC TATAAC	C TATACCA ACATT - T-	APCT-TAATTTTTATCAAAAA-CTTTAATTATTAACTCTCCTTAAATTT	
146 Chi G1 R180275579 C3	GAACABACCACA	דדו אין אין אין אין אין אין ארא אין אין אין אין אין אין אין אין אין אי	TTG BATABAB TTT TCCAC	GATATTGCA-T	- ATCT TAATTTTTAGCAAAAA CTTTAACATTTTAACTCTCG TTAAATTT	- BGT- MTAG TAGAG AA AATG-AGCCCCTG AATT CAATG
147 CH C9 D190290275DC C19	G 30 B B B B COGC B-		THE ALT ALL THE ALL THE TO COLOR AND		- 2727-72 3077777232 (28 3 3 3 3 - 07777 3 3 - 5 - 7 - 7 - 7 3 - 7 - 7 - 7 - 7 - 7 - 7 -	
148 Chi G2 R180279853 CT	GAACAAACOOCA-	-TIG TCTACS ACT TTTAS TTTT TO AS TT-ATS AA - TT PTTT	TTC ARTAAR TTTTTTTTTT		-ATCT-TAATTTTTTAACAAAAA CTTTTAAACTTTTATATCTTTAAAAAAA	HEGT-TTE ATACAGAAAATG-AGCCCCCCC AATTCAATC
149 Chi G2 R180279653 C11	GAACABACOTCA	-TTG TCT ACCACT TTT AC TTTT AC ACT - ATC AL - TT TTTT		GAAATGC	- ATCT TAATTTTAAC AAAA CTTTAAAC TTTTAAATTTTAAAT	
150 Chi G2 R180279653 C7	GAACABACOECA	-TTG ATCT & CT & CT TTT AG TTTT AG AG TT - A TG & A TT TTTT	TTG ASTASAS TTTTTTTT		- ATCT TAATTTTAACTAAAAAA CTTTAAAA TTTAAAATTTAAAAA	
151 CH C2 P180270852 C42	Cascasacorea-	- THE TAR AND A VERY AND A V	TIL BETSER TILLENGE THE	Casa TCO	- APPT-TESTTTTTESCONTANT OF TESS C TTTTEST CONTANTS AND TESS	
157 CH C2 D180270853 CP	CALCARACCOCK-				- 2000 TALE A LAR AND AND A LAR AND AND AND A LAR AND AND A LAR AND	
153 CH C2 D180279653 C40	GASCABBCCCCA-	- THE BEACH BOX & COMPANY AND				
164 CH C2 D180278659 CE	G 33 CAR SOCCO	- THE COLOR &	TIG AN LOADE TILL COLUMN		- 2007 - 72207 77232 (2823232 - 0777 72233 2007 7723 23 - 0777 723 - 0777 - 0777 - 07777 - 0777	
155 CH C2 D180370652 CO	CARCASSOCCS	- THE OPERATE ACT OPERATING AS A TALE AND A A TALE AND AND A TALE AND A A TALE AND A A TALE AND A A TALE A A TA	TIGALIANA IIIIA COURTE		- APPT TA APPT TER CALLS - OTTAGARA AND TA APPT TA APP	- HOLT-TTA ATACAGA ANALAS AND - ACCOCCTD AND TO AND
156 CH C2 D180270652 C9	GBSCBBBCCC	- THE COLOR AND THE PROPERTY AND A DECEMBER OF A DECEMBER				
150. GILGZ K1002/8003 GZ	GARGARAGUST	- THY ST WARNESS AST TITLES TITLE AND AT TAXA AR - TTTTTT	TTO ARTABAR TITIT COLUMN	Casa Brass	- DIGITIANAL I FERGUNARARA CITTARAR FETARATUMA TARAKAT	- BOOT - I LANDALAN BARAND - BOULDON BART LAADS
157. GILGO K100202724 GZ	CARCARECOSCA-	- TO GLARACO CITITAS TITA BASTI AMAR - TITTTT	TIGATAAAA TIIIGURGAAA		ALGI MASIL MANNAANNO GITTAAAA ITTANATAIGITTAAAA	TOGI TAMATAGANANAN MOCOGUDANTI ANTO
150. CHLG3 K100202724 C0	GRACHARSCOCK-		TIGALIANA TITTTCCCCATA	- Cass - Cass		- WORLDON BROND BARANCE ASCOCISTATINATE
160 CHLG7 R100263/3/ C3	GG MCARACUSCA-	- THE CLARK CONTRACTOR AND THE ARGENT AND A CONTRACT TO THE ACCOUNT AND A CONTRACT AND A CONTRAC	TIMATSAA TITTITTACTATA	- Carson	- ALGI - LANDITTINA CAAAAA CITTAYAA TUTAYAA TUTIG TRAAAAT	- BOGI - CANTAL AN ANALY - ACCUSUTS ANT TAATA
100. GILG/ K100203/3/ C0	COMPARIANCE COLOR	THE GRAD A CONTRACT TO THE TOTAL BAR TO AND ARE TTATT	TIGARIANA TITITI TARA	Cash Bart	ALGI DALLI ITAN GAAAAA UTTAGAATIGTAGAT TIN TAAAATT	MODEL MARATA MARATA MACAN MARATA
101. UILO/ NIOUZO3/3/ UZ		ALCOLOTING TOTAL THE LITT BOAST THE AN-TITIT	I TOWITHRAW DATECTIC	T	MAN MALLILLAR CANADAR CILLAR AND LIG TRAAF T	aves mininent nnenite Heccel Brani Traat

ChLG7 R180285737 C11 ChLC6 P180283586PC C3	CC ABCABBCCCC				A THE THE PERSON AND A REAL PROPERTY AND A REA	
CH C6 D180283588DC C3	001110111000001	TIG UPCTAUS ACT FITTAS TTTTIGAS TT-AIS AATT FFITTA	TIGAATAAAA-TITTT T CAC TATA	GAAAATACC-T	AICI BATTICIACAAAAA CITTACAA TITACAA TIG TICAAAST	ISGT-ATACAS AAARIG-AGCOGCIGAATICAATA
	GAACAAACOGCA	- TIG CICIACG ACTITITAS TITTIGAG IT-AIGAA - TITITIT <mark>IG</mark>	TTG AATAAAA TTTTTTCACCATC		- ATCT-TAATTTTTCGCAAAAAA AATCAAAA	TEGT-CIRATACAG AAAATG-AGCCECIG AATTCAATG
ChLG6 R180283586RC C5	GAACAAACCGCA	TTG CTCTACG ACT TTTAG TTTT 1G A <mark>R</mark> T T- A1G AATT TTTT <mark>TG</mark>	TTG AATAAAA - TTT T T CAC CATC		— – ATCT – TAATT T TT <mark>G</mark> G C A AAAA – AAT C AAAA <mark>T</mark> TTT A A AT CT CA I <mark>G</mark> AAAAG T	T <mark>C</mark> G T - <mark>C TR</mark> A TA C <mark>AG</mark> AA AATG - AGC CGC TG AAT T CAATG
ChLG6_R180283586RC_C8	GAACAAACCGCA	TIG CTCTACG ACT <mark>A</mark> TTAS TTTTIG AG TT ATG AA TT TTTT <mark>TG</mark>	TTG AATAAAA TTT TTCAC CCTA	GAAAATGTC-T	ATCT-TAATTTTTGGCATAAAA-AAFCAAAATTTTAAATCTCATGAAAAGT	- TOGT - ATAAGACAG AAAATG - AGCCGC TG AAT T CAATG
Chi G6 R180283586RC C9	GAACAAACCGCA	TTG CTCTACE ACTACTAC TTTT ICAG TT-AICAATTTTTTT			ATCT-TAATTTTTCCCATABAA-AATCAABATTTTBAATCTCATCAABAAGT	TEGT-ATAGACAG ABARTE-RECORCTE ART T CARTE
CE D100203506DC CE	CALCARACCCC		19172 3 3 10 3 3 3 8	C 33 A DEC TO	- 39/99-9239999900000000000000000000000000000	TOTAL THE ACT ACT AS A STOL MOUTH CONTRACTOR
	C 33/2332CCCC2					
LG0_R100203000RC_C4	GARGARACOGCA			0.0000000000		
nLG6 R180283586RC C7	GAACAAACGCA	- TIG CICIAUS ACTITITAS TITTISAS IT AUGAATITITI	TIGATAAA TTTITCACCATA	GAAAAIG	ATUT TAATTTTING CARAAAA AATUAAAA TTTTAATUTUA IG AAAAS T	TEGT ATATACAS AARATG AGCCGC IS AAT TCAATG
LG6_R180283586RC_C10	GAACAAACCGCA	TTG CTCTACS ACT TTTAS TTTT IS AS TT-AIS AA- TT TTTT <mark>TG</mark>	TTG AATAAAA TTT TTCAC CATA	GAAATG IC - T	— – ATCT – TRATT T TT <mark>C</mark> C C R ARARA – AR T CARARA TTTT A R AT CT CR IC ARANG T	T <mark>o</mark> g T - N T A ATAC AG AAAATE - AGCOEC IG AAT T CAATE
LG6 R180283586RC C2	AACAAACCGCA	TTG CTCTACG ACT TTTAG TTTTTA <mark>A</mark> AG TT-ATG AA-TT TTTTT <mark>TG</mark>	TTG AATAAAA-TTT TTCAC CATA	GAAATGTC-T	— – ATCT – TAATT T TT <mark>G</mark> G C <mark>A</mark> – AAAA – <mark>AA</mark> T <mark>C</mark> AAA <mark>TT</mark> TTT A <mark>A</mark> AT C T <mark>CA</mark> I <mark>G</mark> AAAAG T	T <mark>C</mark> G T - <mark>A TR</mark> A TA C <mark>AG</mark> ARARTG - AGC CGC TG ART T CAATG
LG3 1 R180292591 C2	GAACABACCGCA	TTG CTCTACG ACTTTTAG TTTTTG AG TT ATG AA TTATTTTG	TTG AATAAAA TTT TTCAC TATA		ATCT - TAATT T TTAG CAAAAA - CITIG AAAA TTTTAAAT CITIG TTAAAAAA	TEGT ATA TACAG AA AATG AGCCGC TG AAT T CAATG
1 G3 1 P180202501 C8	GAACABACCCCA		TTC ASTASAS TTTTTTTCACTATC		- ATCT - TRATT TTTAC CRARARS - CTTC AS AN TTTTAN AT CTTC TTAL ARD	TOCT NTA TROAC AS A STC - ACCACCTC A STTCA STC
LO3 1 D100202501 C0	C 33 0 3 3 0 0 0 C 3					
ILG3 KI00282381 C4	GARMARALOGUA	TIGOTOTAGAGITITASTITISASTI AISAA TITITIG	TIGAATAAAA TITTICAL ATA	- GARANTO CIT	AIGI BATTITIA CAAAAA CIIGAAAA	ILST ALBATACAN ARARIA ASCOSTINARI ICARS
hLG3_1_R180292591_C7	GAATAAACCGCA	- TTG CTCTACG ACTTTTAG TTTT IG AG TT-AIG AA-TTTTTTIGG	TTG AATAAAA - TTT TTCAC CATA	GARARTG CT-T	- ATCT - TAATT T TTAG CAARAAA - CTT <mark>G</mark> AAAA <mark>T</mark> TTT A <mark>A</mark> AT CTTG TTAAAA AC	
hLG3 1 R180292591 C3	GAATAAACCGCA	- TTG CTCTACG ACT TTTAG TTTT 115 AG TT - ATG AA TT TTTTT 115	TTG AACAAAA TTT TTCAC TATA	GAAAATG CT-T	— – ATCT – TAATT T TTAG C A RAAAA – CTT <mark>G</mark> AAAA T TTTA A AT CTTG TTAAAA AA	- T <mark>o</mark> g T - a ta a ta c ag aa aatg - agc og c tg aat t caat a
hLG8 R180289244RC C6	GAACAAACCGCA	TTG CTCTACS ACT TTT <i>A</i> S TTTT IS AS TT-ATS AA-TTT TTTT- <mark>G</mark>	TTG AAG AAAA - TTT TCCAC TATA	GAAAATGCC-T	— – ATCT – TAATT T TTAS C <mark>A</mark> AAAAA – CTT TAAAAG TTTA <mark>T</mark> ATCT <mark>C</mark> G TTAAAA <mark>A</mark> T	
G8 R180289247RC C5	GAACABACCGCA	TTG CTCTACG ACT TTTAG TTTT TG AG TT-ATG AA- TTT TTTT- G	TTG AAG AAAA-TTT TCCAC TATA		ATCT-TRATTTTTAG CRAAAAA-CTTTAAAAG TTTATATCTCG TTAAAAAT	- TAGC - ATRACACAG AAAATA - AGC CGC TE AAT T CAATG
H G8 R180289244RC C3	GAACABACCECA		TTG ABC AAAA TTTT TCCTCTATA		- BTGT - TARTTTTAG CABRARA - TTTTTRARG TTTRATET CTGTTARARA	TAGE ATTACACAGASASATA AGCOGOTOSATTCAATG
H CB R180280244PC C12	CALCABACCECA		TTC 35 23 35 TTT TC CSC TETS	C BRANCO - T	- ATCT TA STTTTT ACCORT AND AND CTTTT BEAAC TTTATAT CTTC TTAL ARCT	TAC . BTB & TACAC && A BTB BCCCCCTC & ATT CO ATC
LOU D10020321100 012	C 31 (3 3 3 (0) (0) (0)					
LG0_R100208244RC_C13	GMACAMALOGUM	TIGOTOTAGACITITAS TITTISASTI AISAA ITTITTI G	TIGAAGASAA TITTICCAC	GAMMATGO.	ATCT DAATTTTTAS CAARAAA CITTARAAS TITATATCTUS TRABAAS T	TAGE ATRATACES AAAKIN AGCOGUTGAATTCAATG
LG8_R180289244RC_C10	GAACAAACCGCA	- TTG CTCTACS ACT TTTAS TTTT IS AG TT AIS AA - TTT TTTT 🤤	TTG AAG AAAA TTT TC CAC TATA	GAAATGCC-T	- ATCT - TAATT TTTAS CAAAAA - CTT TAAAAS TTTATAT CTCS TTAAAAS T	TAGC ATAATACAGAAAATA AGCCGC IGAATTCAATG
1LG8 R180289244RC C5	GAACAAACOGCA	TTG CTCTACG ACT TTT <i>A</i> G TTTT IG <i>A</i> G TT-AIG AA- TTT TTTT- <mark>G</mark>	TTG AAG AAAA - TTT TCCAC TATA	GAAAAIG CC T	— – ATCT – TRATT T TTAS C R ARARA – CTT TARAAG TTTA T AT CTCG TTARAAG T	- TAGC ATAATACAG AAAATA AGCCGCTGAATTCAATG
hLG8_R180289247RC_C4	GAACAAACOGCA	TTG CTCTAGG ACTTTTAG TTTTIGAG TT-AIG AA- TTTTTTT <mark>TG</mark>	TTAAAGAAAA - TTT TCCACTATA		— – ATCT – TAATT T TTAG C <mark>B</mark> AAAAA – CTT TAAAAG TTTA <mark>T</mark> AT CT <mark>O</mark> G TTAAAAG T	
LG8 R180289244RC C8	GAACAAACCGCA	TTG CT CT A CG A CT TTT AG TTTT TG A TT A TG A A- TTT TTTT- G	TTAAAGAAAA TTTTCCACTATA			- IGG C ATAATACAG AAAAT <mark>A</mark> - AGC CGC IG AAT I CAAIG
G3 1 R180292591 75	GAATAAACCGCA	TIG CTGTACS ACT TTTAG TTTT IG AG TT ATG ATTTTTTTTTTT	TCSAATAAAA TTTTCCACTATA		GTCT TAATTTTTAGCAAAAA CTTAAAAA	TEGTCTCAAAAGACAAAATG AGCCGCTTAATTCAATG
1 62 1 D190202601 60	Caamaaaccorra	ייייייייייייייייייייייייייייייייייייי		Ganapico		TECT TO A BACK AS A DTC BCCCCCTT A STTTT AND
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1LG0_R180289275RU_C11	GARTAALCOGCA	- TRECTCTAUS ACTITITANTITTUS AS TT AIG AA - TTTTTTTG	TIGAATAAAA TITTUURATATA	-GARATTGCT T	- ATST TAATTTTTAS CAAAAA TTTTAAAATSTUAS ATCIGG TTGAAAS T	- ISST TTTATAUSTAAAATG ASCUSC ISAATTCAATG
nLG8_R180289275RC_C14	GAATAAACOGCA	- TIG CICIAOS ACTITIANTITI OS AS TI-AIS AA-TITITI OS	TTG AATAAAA TTT TCCAATATA	GANATTGOT-T	- AIGH-HARTTTTAG CARARA-TTTTARAATGTCAG AT CIGG TEGARAG T	- ISGT TTATAOS TAAATG AGCOGCTGAATTCAATG
hLG8_R180289275RC_C6	GAACAAACCGCA	TTG CTCTACG ACT TTTA N TTTT <mark>O</mark> G AG TT-ATG AATT TTTT <mark>TG</mark>	TTG AATAAAA - TTT TCCAC TATA		— – AT <mark>S</mark> T – TRATT T TT <i>H</i> S C R AAAAA <mark>– T</mark> TT <mark>S</mark> AAAA TS T CHSAT CT<mark>S</mark>S TTAAA<i>M</i>S T	TEGT TTATAOG <mark>T</mark> AAAATG - AGCCEC TE AATTCAATG
hLG8 R180289275RC C15	GAACAAACCGCA	TTG CTCTACG ACTTTTA <mark>A</mark> TTTT <mark>C</mark> G AG TT-ATG AA TTTTTT <mark>TG</mark>	TTG AATAAAA - TTT TCCAC TATA	GARATTGCT-T	— – AT <mark>G</mark> T – TAATT T TTAG C <mark>B</mark> AAAAA <mark>T</mark> TT <mark>G</mark> AAAA <mark>TG</mark> T <mark>CAG</mark> AT C T <mark>G</mark> G TTAAAAG T	ISGT TTTATAGG <mark>T</mark> AAAATG - AGCCGC IG AAT T CAATG
hLG8 R180289275RC C2	GAACARACCO	- TTG CT CT <mark>G</mark> CG A T T TTT AG TTTT TG A ATT ATG AA - TT TTTTT TG	TTG AATAAAA TTT TC CAC TATA	GANATTG CT-T		TIGGT TTTATAGE TAAAATG AGCOGCTGAATTCAATG
H G6 R180284691RC C2	GAACAAACCCCCA	- TIG CTCTACS ACT TIT AS TITT AS AC TT ATS AN - TT TTTT		GARATTG C	-ATCT-TAATTTTTACCAAAAAA-TTTTAAAATCTCACATCTTCAAAA	- TEGT - GTATAGE CRAARTS - ACCOUNT ANT CANTO
LC5 D10020403110 C5	Baama accura			C 3/2 3 7/2 C		
				a manufactor i		
nLG5_R100202/24_C4	ARCARCOSCA	- TIG CICIAIS ACTITIAS TITTISAS TI AIS AL TITTITIS	TIGAATABAA TITTUCAC IITA		- AFCT-TAATTTTFA; CBATAAA-CTTTAAAAS TTTAAATCTUS TTAAAAS	THE T ATACAAAAATG AGCUSC IS AAT TAATG
nLG7_R180285737_C7	GAAACAAACCGT	TIG CICIAUS ACTITITAS TITTIS STI AUS AA - TITTITIA	TIGAG TAAAA TITITCCATTATA		- ATCT TAATTTTTT STAAAAA CITTAAAAS TITAS ATTIG TTAATAS C	- IGGT - TTAATACAG AAAATG - AGCOGC IG AATT CAAT
hLG7 R180285737 C10	GAACAAACCGTT	- TTG CTCTACS ACT TTTAS TTTT IS TO AIS AA-TTT TTTA	TTG AC TAAAA TTT TCCA TTATA		— – ATCT – TAATT T TT T C TA AAAA – CTT TAAAAG TTTA <mark>G</mark> AT T TCG TTAA T AG C	IEG T T T <mark>A</mark> ATAC <mark>AG</mark> AAAATE - AGCOGC IE AAT T CAAT
hLG5_R180282724_C5	GAA <mark>T</mark> ARACCGCA	. – TT <mark>C</mark> CTCTAC <mark>T</mark> A <mark>G</mark> TTTTAG TTTTIGAG TT-AIG AA <mark>A</mark> TTTTTTT <mark>G</mark>	TTG AATAAAA - TTT TC CAC TATA	GATATTG CC-T	— – ATCT – TAATT T TTAG C <mark>A</mark> AAAAA – CTT TAAAAG TTTA <mark>A</mark> AT CTTG TTAAAAG T	TEGT-TT <mark>A</mark> A <mark>C</mark> AC <mark>AG</mark> AAAATG-AGCCECT <mark>A</mark> AATTCAATG
hLG5_R180282724_C7	GAACAAACCGCA	- TTCTACGATTTTAG TTTT IG AG TT ATG AA TTTT TTTTG	TTG AATAAAA TTT TCTACTATA		ATCT- TAATT I TTAG CAAAAA- CTT I AAAAG TTTAAAT CACG TTAAAAG T	- TEGT-TTAATACAGAAAATG-AGCCECTEAATTCAAGG
L CO R180291860RC C7	AACABACCCC		CTAAATACAA TTTTTCACTATA		ATCT-TAATTTTTTCCTAAAAA-CTTAAAAATTTTAAAACCTCCTCCTCAAAACT	- CGT - TTAATACAC ABARTG - CGTCGCTARATTCARTA
L CO P180201860PC C18	BAACAAACCACA		CTARATOCAL TTTTTCACTATA		- BUCT-TABUTTUTT CRAAAA-CUTTABAAATUTTAAAACUTUCTAAAAACU	COT TTA ATACAC ASA ATC COTCOCTA SATTCA AT
N CO D18020100010 C15	NACABACCCA					
	ARCARACOGUN		GIAAATALAA TITIICACIATA	GATATIG C	ATCT DATT TITLE CARAAA CITLARAAT TTTAAACTUS TTAAAAST	ALL
ILG9 RIBUZ91860RC CZ	GAACAAACOSCA	- TIG CICTAUS ACATITIAS TITTUS AS TI AIG AATITITITI	GTAAATAGAA TTTTTCACTATA	GATATTGCA-C	-ATCT-TAATTTTTT, CAARAAA-CITTGAAATTTTAAATCTUS TTAAAAST	- USG T- ATAATACAS AAAATG - AGCTGC IS AAT TCAATG
hLG9_R180291860RC_C9	GAACAAACOGCA	- TTG CTCTACAACCTTTAG TTTT GAGG T-AIG AATTTT TTTT	GTAATAARC TTTTTCACTATA	GATCTTGCC-T	ATCT-TAATTTTTTCCAAAAAA-CCIGAAAAATTTTAAATCTCGTTAAGAGT	CEGT-ATAATACAC AAAATG-AGCOGCIGAATTCAATG
hLG9 R180291860RC C20	GAACAAACCGCA	. – TTG CTCTACAACCTTTAG TTTT CGAGGT-ATG AATTTTTTTTT	GTAAATAAAC TTTTTCACTATA		— – ATCT– TAATT I TT <mark>T</mark> ; C A AAAA – CCIG AAAA <mark>T</mark> ITT A <mark>A</mark> ATCT C 5 TTAA <mark>G</mark> AG T	CEGT-ATACAGAAAATG-AGCCECTEAATTCAATG
hLG9_R180291860RC_C5	GAACARACCGCA	TTG CTCTACAACCTTTAG TTTT CGAGG T-ATG AATTTT TTTT	GTARATAAAC TTTTTCACTATA	GAT <mark>G</mark> TTGCC-T	— – ATCT – TAATT T TT <mark>T</mark> S C H AAAA – C <mark>C</mark> PG AAAA <mark>T</mark> TTTA <mark>A</mark> AT CT <mark>O</mark> S TTAA <mark>G</mark> AG T	CEGT-ATAATACAGAAAATG-AGCCECTGAATTCAATG
bl G9 R180291860RC C22	GAACAAACOGCA	TTG CTCTACAACT TTTAG TTTT CGAGGT-ATE AATTTT TTTTT	GTABATBARC TTTTTCACTATA		- ATCT - TAATT TTTE CHARARA - CCIG ARAA TTTTAAATCTCG TTAAG AG T	GEGT NTAATACAG AAAATG - AGCCGC TG AAT T CAATG
N CO P180201960PC C14	CARCARBOCCCC			C 3/7 3 (PPC C		
DEG8 R100281000RC C14				GARATIC CO. T		
				- GALAIIGO - I		NOT A TANK ANALIS BOOCA, BARLICARIS
ILG9 R180291860RC C17	AACAAACGCA	TIG CICIAUS ACTITIAS TITTUS AS IT AIG AATITITITIG	GTAATAAAC TTTTTCACTATA	GATATIGO -T	ATUT TAATTTTTTS CAAAAA UTTTAAAA TTTTAAATUTUS TTAASAS T	CSGT ATAATACKS AAAATG AGCCACTAAATTCAATG
nLG9_R180291860RC_C16	AACAAACOGCA	TTG CTCTACG ACTTTTAG TTTT GGAG TT-AIG AATTTTTTTTTT	GTAATAAA TTTTTTCACTATA		ATCT-TAATTTTTT CAARAAA-CTTTAAAATTTTAAATCTCG TTAACAG T	CEGT-NIAATACAGAAAATG-AGCCGCIGAATTCAATG
ChLG1 R180275673RC C3	GAACAAACCGCA	TTG CTCTACG ACT TTTAG TTTT 1G AG TT-A1G AA TTTT TTTT <mark>GG</mark>	TAATAAAA TTTTTTCAC	TACAGATATTGCCT	— – ATCT – TRATT T TTAG C – AAAAAACTT TAAAAG TT TACAT C T <mark>C</mark> G TTAAAAG <mark>A</mark>	TAG T T TTA TAOG CAAAATG - AGC CGC TG AAT T CAATG
hLG4 R180280635RC C5	GAACABACCGCA	TTG CTCTACG ACT TT <mark>C</mark> AG TTTT IG AG TT- AIG AATTTT TTTT <mark>G A</mark>	-TAATAAAA CTTTTCAC	TATAGATATTGC-CT-	— – ATCT – TAATT T TTAG C – AAAAAA CTT TAAAAG TTTACAT CTTG TTAAAAG 🗛	
hl G1_R180275805RC_C6	GAACAAACOGCA	TIG CICINC ACTITING TITTIG AG TI-AIG ANTITTITTTTT			ATTT-TAATTTTTAC C-ARABARCTTTARAAG TTTACATTTCG TTARAAC A	- TEG T - T TCATA C CAARATG - ACCOCCTC AAT T CAATG
6 C1 P180275805PC C18	GAACAAACCGCA			TAT BO AT A TTO C CT	- APPT TA A TO TOTAL C - A A A A A COTTA A A AC TOTAL AT MOUTH A A A C A	- TO GT - TTC & TA BC C & A A BTC - ACCORCTE & ATT TO ATTC
H G1 P180275905PC C12	GARCARACCCC			TATACATATTCC		
LOT D10027300310 012	C 85/25 3///			TATACATATICA CT		
ILG 1 R 1002/3003RC C13	GARCAARCOGCA	- IIG CI CIACS ACTITITAS TITTISAS TT AIS AATITITIT	-TTATAAAA TTTTTCCC	LATASATATIGC CT	ALLI LAALI I TTASU AAAAAAUTTTAAAAS TTTACATTTIG TTAAAASA	ISCO TITATAOSCARARIS ASCOSCISARITCARIG
nLG1_R1802/5805RC_C17	GAACAAACOGCA	- TTG UTCTAUS ACT TTTAG TTTT IG AG TT-AIG AATTTT TTTTTTT		TATAGATATTG C-CT	- ATT - TAATT TTTAG C-AAAAAACTT TAAAAG TTTACAT T TOG TTAAAAG A	IGG <mark>G</mark> -TTTATAGGCAAAATG-AGCOGCTGAATTCAATG
hLG1_R180275805RC_C10	GAACARACCGCA	TTG CTCTACS ACT TTTRS TTTT IS AS TT-ATS AATTTT TFTT <mark>TT</mark>	TTAATAAAA TTTTTTCCC	TATAS ATATTS C CT	— – AT <mark>E</mark> T – TAATT T TTAG C – AAAAACCTT TARAAG TT TACAT <mark>T</mark> TO <mark>S TTAAAAG A</mark>	- TEG <mark>G</mark> - T TTA TA OF CAAAATG - AGC CEC TE AAT T CAATG
hLG1 R180275805RC C15	GAACABACCGCA	TTG CTCTAGS ACT TTTAS TTTT IG AG TT ATG AA TTTT TTTT TT	-TATAAAA TTTT TCG C	TATAGATATTGC CT	– AT <mark>T</mark> T – TAATT T TTAG C – AAAAAA CTT T AAAAG TT TACAT T T <mark>C</mark> G TT AAAAG <mark>A</mark>	TEG G TTTATA OF CAARATE AGC OF CTERATT CAATE
hLG1_R180275805RC_C11	GAACAAACOGCA	TTG CTCTACG ACT TTTAS TTTT IG AG TT-ATG AATTTT TTTT TT	T-AATAAAA-TTTTT			IGG <mark>G</mark> - T TTA TA OG CAARATG - AGC OGC IG AAT T CAATG
hLG1_R180275805RC_C14	GAACAAACCGCA	TTG CTCTACG ACT TTTAG TTTTTG AG TT-ATG AATTTTTTTTTTTT		TATAGATATTGC-CT-	- ATT - TARTT I TING C - AAAAAACTT TAAAAG TT TACAT TTS: TT AA ABC	- IGGT-TTTATAGCCAAAATG-AGCCGCTGAATTCAATC
N C1 P180275905PC C14	GASCARACCOCK			TATECATATEC		
	CARCEARCOCC	NAMES AND ADDRESS OF A DESCRIPTION OF A	TITIC CONTRACTOR	INTRODUCTION CONTRACTOR	AND REAL TIMES AND ADDRESS TO ADDRESS AND ADDRE	ACCOUNTS AND A CONTRACT OF A C
ALG1_K1802/5805KU_C2/	GARCARACOGCA	TIG CTCTA OF ACTITITAS TITTIS AS TT AIS A TITTITTT	-TAATAAA TTTTTCAC	TATASATATISC CT	AFCT TAATTTTTATC ARAAACTTTAAAGS TTTACATTTCS TTAAAASA	ISGT TITATARSCAART ASCOSCISARTICAATG
nLG1_R180275805RC_C33	GAACAAACOGCA	- TIG CICITAGE CTITITAS TITITISAS TI-AIS A TITITITITI	TAATAAAA-TTTTTTCAC	TATAGATATTG C-CT	ATCT- LAATT TTTATC-ARARAACTT TARAAG TTTACAT CTTG TTARAAG	IGG T - T TTA TAGG CAAAATG - AGCOGC IG AAT T CAATG
hLG8_R180288746_C5	GAACAAACCGCA	TTG CTCGACG ACT TTTAG TTTTTG AG TT-ATG AATTTTTTTTTTT	GTAATAAAA TTTTT T CAC		ATCT-TAATTTTTAG C-AAAAAACTTTAAAAG TTTACATCTTG TTAAAAG	TEGT TTTATAGE CAAAATG - AGCCECTE AATT CAATG
hLG8 R180288746 C2	GAACARACCGCA	TTG TTCTACS ACT TTTAS TTTT IS AS TT-ATS AAT TTT TTTTC	GTARATARA ATTTTCAC	TGTAGATATTGC T	— – AFCT – FAATT T TFAG C – AA T AAA CTT F <mark>G</mark> AAAG TFTACAT CTTG TFAAARG <mark>A</mark>	TEGT TTTATAOS CAARATE - <mark>G</mark> GCOSC TERATT CRATE
hLG8 R180288746 C8	GAACAAACCGCA	- TIG CTCTACS ACT TITAS TITT IS AS TT - ADS AAT TIT ITTT	GTAATAAA ATTTCAC	TATAGATATTGC CT		- IGGT - TTTATAGCCARAATG - AGCCGCTG AATTCTATG
H G8 R180288610RC C10	GAACAAACCGCA	- TIG CTCTACE ACT TITIE TITTIE ACT T- ATE AATTTT FFTT-	AFAATAAA TTTTTTTTAC	TATAGATATTGCCT	-ATCT-TAATTTTESC-AAAAACTTTAAAASTTTACATCTTGTTGAARG	TEGT-TTTATAOGCARAATG-AGCCECTERAATTCANTG
H G8 P180280457PC C4	GABCARACCCCA		ATTALLY ALLA TOTAL	TATECATATEC		
	C 33 CE 3 3 CCCC C			mamac amage of the		MOLE STATISTIC CONTRACTOR STATISTICS
	GARGAARCOGCA	- INCLOSED AND AUTITING TITING AS TT AND A TITITIT -	ATAAATAAAA TITTITAC	LATASATATIGC CT	- ALCI-LAATITTEASC-ABAAAACTITABABSTTTACATCTTGTTABAAASA	- ISG 1 - 1 11ATA OF CARARIS - ASCOSC IS ART TCARTG
1LG0 K18028915/KU C6	GAACAAACCGCA	- TIG GIGTRUS ACTITITAS TITTISAS TI-AIG AATITTTTTT-	ATAATAAA TTTTTAC	TATAGATATIG C-CT-	- ATUT - TAATT TTTAS C - AAAAAACTT TAAAAS TI TACATCIIG TTAAAAG	- B.G.T.T.TTATAUS CAAAATG - AGCOGC IS AATT CAATG
nLG8_R180288610RC_C15	GAACAAACCGCA	. – TTG CTCTA T S ACT TTTAS TTTTTG AG TT-ATG AA TTTTTTTT- <mark>6</mark> – – – – –			— – ATCT – TAATT T TTAG C – AAAAAA <mark>P</mark> TT TAAAAG TTT ACAT C TTG TT <mark>G</mark> AAAG <mark>A</mark>	- TEGT - TTTATAGCAAAATG - AGCCECTGAATTCAATG
hLG8 R180289157RC C9	GAACARACCGCA	. – TTG CTCTA <mark>T</mark> S ACT TTTAS TTTT IG AS TT-ATG AATTTT TTTT - C		TATAGATATTGCCT	— – ATCT – TAATT T TTAG C – AAAAAA <mark>T</mark> TT TAAAAG TTTACAT CTTG TE <mark>G</mark> AAAG <mark>A</mark>	TEGT TTTATAOGCAAAATG - AGCOGCTGAATTCAATG
hLG8 R180289157RC C3	GAACAAACCGCA	- TTG CTCTATE ACT TTT AS TTTT IS AG TT - ATG AATTTT TTTT -	AFAATAAAA TTTTT	TATASATATTGC CT	- ATCT - TAATT T TTAG C - AAAAAA CTT TAAAAG TTTACAT CTTG TT <mark>G</mark> AAAG A	BGT TTATAGS CAARATG AGC SAAT TCAATG
H CA P180288748 CT	GAACAAACCAC		CTARTARA A TARRA	TATAGATATTGC-CT-		- TEGT-TTTATATECANANTE-AGCORCTENATICS ANY
LOG D100200748 00	C 33 C3 3 3 C C C C C			EXTRACTOR AND AND COMPANY		
1LG0_R10U200/40_C0	GARGAAACUSCA	- INCLURADAUTTITAS TITT DE ASTT ATS ARTITITTT	CRAATABAA TTTTTCAL	LATASATATTS C-CT-	ALCI LAATT TITAS CAAS AUTTTARSES TITAS ATUTTS TRAKES	- ING I - TITATA - CARARIG - MSCUSCES ARTTCARTG
nLG8_R180288610RC_C20	GAACAAACOGCA	- TTG CTCTACS ACT TTTAS TTTT IS AS TT ATS AATTTTTTT -	GTAATAAA TTTTTCAC	TATAGATATIGC CT	AFCT - TAATT T TTAG C - ARAG AACTT TAAAAG TTTAG AT CTTG TTAAA GA	- ISGT TTATATE CARACTE AGCOSC TO ANT TCAATE
hLG8 R180288610RC C21	GAATAAACCGCA	TTG CTCT T CE A T T TTT <i>A</i> S TTTTT A AG TT-ATE AATTTTTTTT TC	GTAATAAAA TTTTTTCAC		— – ATCT – TAATT T TEAS C – ARA <mark>S</mark> AACTT TAAAAS TTT A <mark>S</mark> AT CTTS TEARA <mark>T</mark> S A	TEG T T TTA TAC <mark>T</mark> CAAAATG - AGCCGC TG AAT T CAATG
hLG8 R180288746 C7	GAATAAACCGCA	TTG CT CT TCG A TTTTAG TTTT TAG A TT- A TG A A TTTT TTTT	GTAAATAAAA TTTTT	TATAGATATTGC-CT-	— – ATCT – TAATT T TTAG C – AAA <mark>G</mark> AA CTT TAAAAG TTTA <mark>G</mark> AT CTTG TTAAA T S <mark>A</mark>	TEGT TTTATAC <mark>T</mark> CAAAATG - AGCCEC TG AATT CAATG
	GAACABACCGCA	TIG CTCCTCS AT TTT AG TTTT IG AG T T ATG AA TTTT TTTT	GTABATAAAA AFTTTCAC	TCTAGATATTGA CT	ATCT TAATTTTTAGC AAAAATCTTTAAAAGTTTA	TEGT TTTATAGCAARATG AGCOGCTGAATTCAATG
hi G8 R180288746 C9				TATAC 3TA TTC C. CT	ATOT TRATTTACC BEARS COTTARASC TTTRATCOTC	TO AT TTTATACCCAR CARCE ACCOCCTS A ATTO AT
hLG8_R180288746_C9	CARCABACCCCA			the second se		

244 CH C9 0190299960 C6	ር 38 ር 8 8 ዓር/ርር ር 8 ዋብረ (ምር ርዋ 8 ርር 8 ርዋ ጥጥ 80 ጥጥም መር ወር ዋ በ8 ብር 8 8 🗗 ጥጥዋ ምር ም 🗖		
245 CH C0 D100200000 C0		TRANSAR AND THE TRANSAR	
245. CHLGO R 100200000 C4			EXTERISTIC C. ALL GRANTITIES CRAMMER TIMENED TIMENED TO AND A CONTRACT
246. ChLG6_R100206000_C0	GARCAARCUSCA TIGCTCTAGACTITTASTITTIGASTI AIGAA-TITTITT	GTAATASAA TTTTTCAC	TATASATATISC CT - ATCT TATTITIAS ARAAACTITAAAS TITACATING TATAAAS ING T TITATAG CAARAG AGCOC BATTICACT
247. ChLG8_R18028915/RC_C11	GARCARACOSCA - TTACTCTACS ACTTTTAS TTTTIS AS TT-AIG ARATTTTFTT	GTAATAAAA TTTTTCAC	TATASATATIGC CT AFCT TRATTTIFASG RAAAACCTTTAKAASCTTTAKAASCTTTAKAASA - ISGT-TTTATAGCAARAFG RSCOCCISAATTCAARS
248. ChLG8_R180288860_C2	GACCARACOGCA - TIG CTCTR C ACTITITAE TITTIE ACTI-AIG AR TITTITT	GTARATARAA TTTTTARC	TATAGATATIGC-CTATCT-TRATTTTRGC-ARABACITTARAAGITTRCATCTIGITAATAGAIGGT-TTTATAGCARAATG-AGCOGCIGAATTCAATG
249. ChLG10_R180276688_C4	GAA T AAACCGCA - TTG CTCTACG ACT TTTAG TTTTTG AG T T-ATG AA TTTT TTTTG	GTAAATATAAA TTTTTCAC	TATAS ATATIS C-CTATCT-TAATTTTAS C-AAAAAACTTTAAAAS TTTACATCTIS TTAAAAS <mark>A</mark> BSST-TTTA <mark>G</mark> AOS CAAAAT <mark>A</mark> -AGCOSCIS AATTCAATS
250. ChLG8_R180288610RC_C22	GAACAAACCGCATTG CTCTACG ACT TTTAG TTTTTGAG T T-ATG AA TTTT TTTT <mark>TT</mark>	GTARATARAR-AFTT T CAC	TATAGATATIGC-CTATCT-TAATTTTIAGC-AAAAAACTTTAAAAGTTTACATCTIGTTAAAAG <mark>A</mark> IGGT-TTTA <mark>G</mark> AOGCAAAAT <mark>A</mark> -AGCOGCIGAATTCAATG
251. ChLG1 R180275554 C2	GAACAAACCGCA TTG CTCTATE ACT TTTAG TTTT TEAG TT ATG AATTTTTTT	GGTG AATAAAA TTT TTCAC	TATASATATIST TT ATCT TAATTTTTASCAAAAAAC-TTTAAAASTTTACATCTAS CTAAAAS AIGST TTCATAOSCAAAACG-AGCOGCTAAATTCAATG
252. ChLG1 R180275588 C7	g aacaaaccgca – ttg ctctacg act a ttag tttt ig ag tt – aig aa tttt ittt	<mark>GG</mark> TG AR TARAR TTT T <mark>T</mark> CAC	tatag atatic c- <mark>t</mark> tatct-tratt titre c r araana-it trarage titracat cite crararg <mark>r</mark> ieg t-cttatace carareg - access to carare
253. ChLG1 R180275554 C5	GAACAAACCGCA - TTG CTCTACG ACT TTTAG TTTT 15 C TT-ATG AATTTT TTTT	GGTAAAAAAAA TTTTT	TATAG ACATIG T-CTATCT-TAATTTTTAG CAAAAAACTTTAAAAG TTTACATCTIG CFAAAAG AIGG T-T CCATAOG CAAAATG-AGCOGC IG AATTCAAIG
254 Chi G1 R180275673RC C5	GARCAR-COGCA-TIG COCTARS ACTITIAS TITTIS AS TI-AIG ARTITITIT	TGAA TAAAA TTTTACAC	
255 Chi G4 R180280835RC C7	GAACAAACOGCA-TIG CTCTACCACTITTAG TITTIG ANT T-AIG AATTTT TTT	GGAAAATAAAA TTTTTTTAC	TAT CATATIC C-CTATCT-TAATT TTES CAAAAGC-TT TAAAG TTTACATCTTC CAAAAAA AUG T-TTATAC CAAAATA-AGCCCCTGAATT CAATG
256 Chi G1 B180275673BC C6	GAACAAACCGCA-TTGCTCTACSACTTTTAGTTTCSACTT-ATGAATTTTTTTTT	GGTAAATAAAA TTTTTTCAC	
257 Chi G1 B180275673BC C7		CCTARSTANAS - TTTTTCAC	
258 CH G1 D180275570 CA		COTO DE TES DE TETETO COC	
250. 01101 1002/30/5 04			
239. CHLGT R 10027 3300 CO		GOIGANIANA IIIICUNC	
200. CRLG1_R100273379_C/	GARCARACUSCA TIG CTCCACG ACTITITAS TITTIGAS TT ALGARTICITITIT		TATASATATISC AT - ATCT TATITITASC AAAAA CITTAAAAS TITACATCIUS TAAAAS - AISGT TITATAUS CAAAAAS - AGCUSC ISA TITAAAB
261. ChLG1_R180275579_C10	GARCARACOSCA TTG CTOCAUS ACT TTT AS TTTT IS AS TT AIG ARTTOTTFT	GGTGAATAAAA TTTTCCGC	TATABATATIGC AT - ATT TAATTTIPASC AAAAAACTTTAAAAS TTOACATCIOS TTAAAAS - ABSGT TTTATAGCAAAASG ASCOCCISAATTCAACG
262. ChLG1_R180275579_C13	GAACAAACOGCATTGCTCTACGACTTTTAGTTTTTGAGTT-ATGAATTTTTTTTT	GGTGAATAAAA TTTTCCAC	TATACATATIGC ATATCT-TRATTTITACC-RAAAAACTTTAAAAGTTCACATCICGTTAAAAC-AUGCT-TTTATAUGCAAARIG-RGCCGCUCAATTCRATG
263. ChLG1_R180275579_C15	GAACAAACCGCA - TTG CTCTACG ACT TTTAG TTTT-GAG TT-ATG AA TTTT TTT-	GGTG AATAAATTTCCAC	TATAGATAT-GC ATT-GCATTT-AGCAAAAAACTTTAAAAGTTCACATCTOSTTAAAAG-AGGT-TTTATAGGCAAAAG-AGCCGCTGAATTCAAAG
264. ChLG1_R180275947_C4	GAACAAACCGCA TIG CICIACGACITITAG TITITAGAG I - AI A AATITITITI	GGTGAATAAAA TTTTCTAC	– – – TATAGATATIGC 👖 – – ATCT TAATTTTIAGC AA <mark>G</mark> AAACITTIAAAAG II <mark>G</mark> ACATCIIG IIAAAAG – 👗 IIGGT TITAAA 🛱 CAAAAIA AGCOGCIGAATICAGIA
265. ChLG10 R180277075 C18	GARCARRCOGCA TTG CTCTROG ACT TTTRATTTT 16 AG T T- ATG AR TTTT TFTT	<mark>GG</mark> TG AA TAAAA TTT TCCAC	TARAS ATATIS C-CTATCT-TARTT TIMS C-RAMARACIT TARAS TITACAI CITS TIARAS - AIGS T-TITATAGS CAMARIA. ASCOSCIS RATICAATS
266. ChLG10 R180277076 C19	G AACAAACOGCA TTG CTCTAO3 ACT <mark>G</mark> TTAS TTTT TEAG TT-ATS AATTTT TTTT	GGTG AR TARAR - TTT TCCAC	tatre atatic c-ctatct-ic attt tire c-araaractt trarae tttacat ctce trarare Aigs t-tttatace caarat <mark>a</mark> -agcoscie artt crats
267. ChLG10 R180277076 C8	GAACAAACCGCA - TTG CTCTACG ACT TTTG; TTTT 15 AG TT-ATG AATTTT TTTT	TGTG AATAAAA- TTT TCCAC	TATAG ATA ITAC-CTATCT-TAATT I TTAG C-AAACAA CTT TAAAAG TTTACAT CTTG TTAAATG
268. ChLG10 R180277076 C16	GAACAAACCGCA - TTG CTCTACJ ACT TTT <mark>G</mark> G TTTT IG AG TT - ATG AATTTT TTTT	TGTGAATAAAA TTTTCCAC	TATASATATISC CA ATCT TAATTTTTASC AAACAACTTTAAAASTTTACAICTTG TTAAATS 🚾 ST TTTAIACSC AAATG ASCCCCTG AATTCAATG
269 ChLG1 R180275588 C9	GARCAARCOGCA - TTG CTCTACE ACTTTTAS TTTT IS AS TT-AIS AA TTTT TTT	GGTG AATAAAA - TTT TCCAC	TATNE ATATIG C-CTTCT-TAATTTTTING C-ARARACCTTTARARG TTTACC COARAAT NIGG T-TTAATAG CARARTE-ACCOCCIE AATTCH
270. ChLG1 R180275588 C10	G AACA AACCGCA - TTG CTCTACCACATTT AS FITTE AS FIT AS A FITTE TO AS TA THE FITT	GOTE AATAAAA TTTTTCCAC	
271. Chi G1 R180275588 C11	GARCARACCECA - THE CTCTREE ACATTINE TITLE AS TT-ATCARTTTTTTTTTTTTES IS NO	TARGTG ANTANAN - TTTTCCAC	
272 Chi G1 R180275588 C5	GAACAAACCGCA TTG CTCTACS ACT TO AG TITT TA AG TT ATG AA TITT TITT	GGTGAATAAAA TTTTTCCAC	AT AGATATIGC CT ATCT TAATTTTTAGC ARABACCTTARAAGTTTACATATGCTARAAA TTACATATGCTARAAA
272 CH C1 D100275500 CO		TO THE REAL AND THE POINT	
273. CHLOT R100275500 C0		COC 22 US2 22 US2 22	
274. GILGI RIOUZ/3000 GIZ		GREAT AND THE CAL	
275. ChLG10 R180277075 C2	GARCARACCECA - TIG CACTACIS ACTITITAS TITTI IS AS TT ALIS A TITTITT	GOIGAATAAAA TTTTCCAC	TATASATATISC CT ATCT TAATTTITASC AAAAAACTTTAAAASTTTACATCTUSTTAAAAS- AIGST TTATAGCAAAATS CGCCGC IGAATTCAAAS
278. ChLG10_R180277076_C4	GAACAAACCGCA-TIG CTCTACS ACTITITAS TITTISAS TI-AIGA	GGTG AA TAAAA - TTT TCCAC	TATAGATATIGC-CTATCT-TRATTTINGC-ARARA-CITTARAAGTTTACATCTCSTTARAAGAIG-T-TTATAGCARAATG-CGCCCCGCAATTCRATG
277. ChLG10_R180277076_C11	GAACAAACCECATTG CTCTACGACTTTCAG TTTTIGAG TT-ATGATTTTTTTT	GGTG AATAAAA TTTTTCCAC	TATAGATATIGC-CTACCT-TAATTTTIAGC-AAAATACTTTAAAAGTTTACATTTCSTTAAAAG-ATTAGAGGC-AAAATG-AGCCGCIGAATTCAATG
278. ChLG10_R180277076_C3	GARCARACOGCA - TTG CTCTACG A CTTTTAG TTTTTG AG TT-ATG AR TTTTTTTT	GGTG AATAAAA - TTT TC CAC	TAT TS ATATIG C-CTACT-TAATT TIAG C-AAACAAATT TAAAAG TITACAT CTOG TIAAAAG
279. ChLG10 R180277076 C5	GAACAAACOSCA TTG CTCTACG ACT TTTAS TTTT IS AG TT AIG AATTTT TTTT	GGTG AATAAAA TTTTCCAC	TATES ATATIGC CT ACCT TAATTTTING C AAACAAATTTAAAAG TITACATCTOS TTAAAAG - AISGT TITATAG CAAAATG AGCOGCIS AATTCAATG
280. ChLG1 R180275588 C3	GAACAAACOGCA TTG CTCTA <mark>T</mark> : ACT TTTAG TTTT IG <mark>C</mark> C TT-AIG AATT <mark>A</mark> T TTTT		tatae ata tig c-ctatct-taatt titae c-aaaaa actit taaaag titacat ct cac taaaag a igg t- tita tage caaaatg - agcogc is aa <mark>c</mark> t caatg
281. ChLG1 R180275652RC C13	GAACAAACCGCA - TTG CTCTACG ACT TTTAS TTTATACS TT-ATG AATTTT TTT	<mark>G</mark> TTE AATAAAA TTT TC <mark>T</mark> AC	TATAG ATA TIG C- T TATCT-TAATT TI <mark>G T</mark> ; C-AAAAAA CTT TAAAAS TTTA TT I CTTG TTAAAAG A TG A T-T TTATA T G <mark>G</mark> AAAATG -A C CCCC TG AATT CAATG
282 Chl G1 R180275652RC C25	GAACAAACCGCA TTG CTCTACG ACT TTTAG TTTATAAG TA ATG AA TTTT TTT-	GTTG AATAAAA TTTTCCAC	
283 Chi G1 R180275829RC C3	G AACAAAC GCA- TTG CTCTACG ACT TTTAG TTTATAG TT-AIG AATTTT TTT	GTTG AATAAAA TTT TCCAC	TATAC ATATIC C-CTATCT-TRATT TITE C-RABARACTT TARAGE TTTATE CTTC TEARAC ATC AT-T TATATC ARACC-ACCCCC TC AAT T CRATC
284 Chi G1 R180275629RC C11	GAACABACCICCA - TTG CTCTACS ACT TTTC: TTTTTAC TT-ATS BATTTTTT	GTTCAATAAAA TTTTTCCAC	
285 CH G1 P180275620PC C13			
205. CH C1 D190275620DC C0		C 100 3 3 7 3 3 3 3 100 10 C C C C	
200. CHLGT R 10027 0029RC C9		CONCASTS SS	TARGETATION OF A THE TRANSPORTED A ASAA AND TARGETATION OF A ANY - AN ANY - AND AN ITERATION AND A ANY - AND ANY - A
207. CHLG1 R1002/3029RC C21		GITGAATAAA TITTCCAC	INTERNITING CT - ATCI MATTITISC ANAMARTITIAN ITTA I CTG ICAAAS - AIGAT TAATA BOARAAS AGOOC BAATTOAKG
288. CILG1_R180275629RC_C19	GARCARALLIGCE - TIGUTCTALS ACTITITAS TITTIAS TTALGARTITITT	TIGATAAAA TTTTCLAC	ATTALATATIST CT - ATTT THESE AAAAAACTT TARAAS TITALATCING MAAAAA ATTG TITATA SCAAAATS - KGCAA ATTS - KGCAA ATTS
289. ChLG1_R180275629RC_C36	GARCARACCICCA - TTG CTCTRCS ACT TTTAS TTTT TAG TT - ATG ARTTTTTTT-	GTIGAATAAAA TTTTCCAC	ARTRGATATIGE CT ATCT TARTTTITE C - ARARACTT - ARAG TTTACATCTTG TGARARG BIGGT - TTATATE CARAGE - AGCCGCIGAATTCRATG
290. ChLG1_R180275629RC_C28	GAACAAACOGCATTG CTCTACG ACT TTTAG TTTT TAGG T T-ATG AA TTTT TTT	G TTG AA TAAAA TTT T <mark>T</mark> CAC	TATASATACISC-CIATATATCI-TARTITITEC-ARABACITIARAAGITITARAAGITITARAAA
291. ChLG1_R180275629RC_C37	GAATAAACCECA TTE CTCTACE ACT TTTAE TTTATAG TT-ATE AA TTTTTTT	GTTG AATAAAA- TTT TCCAC	TATA-ATACIGC-CT RTAT ATCT-TARTTTTTCC-AAAAAA T TTTBAAAG TTTACATCTTG TTAAAA <mark>A</mark> - AIGGT-CTTATATCCAAAAIG-AGCOGCIGAATTCAATG
292. ChLG1_R180275629RC_C17	GAACAAACCECATTE CTCTACE ACTTTTAE TTTTTEAS TT-ATE AATTTTTTT	G TTG AA TAAAA - TTT TCCAC	TATAS ATA CIG C-CI TTAT ATCT-TAATTTTTAG C-AAAAAA ATTTAAAAS TTTACATCITIS ITAAAAA <mark>A -</mark> AISG T-CITATATS CAAAATS-AGCOGCIG AATTCAATS
293. ChLG1 R180275629RC C24	GAACAAACCGCA - TTG CCCTACS ACT TTTAG TTTT CS AG TT - ATG AA TTTT TTT	G TTG AA TAAAA TTT TCCAC	
294. ChLG1 R180275629RC C29	GAACAAACOGCA TTG CTCTACS ACT TTCAS TTTTTAG TT-ATAATTTT TTT	<mark>G</mark> TTG AATA <mark>C</mark> AA-TTT TCCAC	TTIRE REALTING C-TTATCT-TARTTITING C-ARAGAACTITIAGAATTITACATCITU TEAGAAAATTCC-TTIATATCCAAATC-AGCCGCUG AATTCRATG
295. ChLG1 R180275629RC C38	GAACAAACCGCA TTG <mark>AC</mark> CTACGA <mark>T</mark> T TTCAG TTTTT A AG TT-AT A AATTTT TTT	GTTG AATAAAA- TTT TCCAC	TATAGATATIGC-CTATCT-TAATTTTTT;C-AAAAAACTTTAAAATTTTACATCTTGTTAAAAA
296 ChLG1 R180275652RC C29	GARCARACCECA TIG CTCTRCS CTTTAS TITATAS TTATAS AT TTTTTTTTTTTTTTTT	G TTG AA TAAAA TTT TCCAC	TATAGATATIGC CT ATCT TAATTITTEC AAAAAACTTTAAAATTTTACATCTIG TTAAAAA- AIGGC TTATATCCAAAATG AGCCGCIGAATTCAATA
297 Chi G1 R180275829RC C20	GARCARACOGCA - TTG CTCTRCS ACT TTTAG TTTATASC TT - ATG ARTTTT TTT	GTTGGATAAAA-TTTTTCAC	
298 ChLG1 B180275629BC C18	GACCAACCGCA - TIG CTCTACGACT TECH TTTTAG TT-ATAMPTTTTTT	GTTGAATACAA TTTTCCAC	
299 ChLG1 R180275673RC C2	GARCARACCECA TTG CTCTRCS ACT TTT 76 TTTT 16 26 TT-ATG ARTTTTTTT	GGTG ANCARAN TTT TCCAC	TATEGATATIGC-CTATCT-TRATTTTEGC-AAAAACTTTAAAAGTTTACATCTCATTAAAAA
300 Chi G1 R180275673RC C4	GAACAAACCACA TTG CTCTACAACTTTT AG TTT CTAAG TT ATG AA TTTT TTTT	GGTARATACAR TTTTTCC	TATAGATATIGC. TT. ATCT. TAATTTTTAGC. AAAAGACTTTAAAAG TTTACATATCATTAAAAA. ATGCC. TTTATATA AAAGA ATG. AGCCGC TAAAATCAATTCATTG
301 CH G1 R180275629RC C2	CAACAAACCONTA - TTC CTCTACS ACT TTT ACTTTT CAC TT - ATC AA FTTTTTT		
302 CH C1 D190275620DC C22			
302. CHLGT_R100275028RC_C33			TATALANDER AND
204 CH C1 D120273028RC C10			SALESCALAVE AL ALE MAILING ARABINATION AND AND AND AND AND AND AND AND AND AN
305 CH C4 D1002750000 C4		TIGHT NAME TITICAL	
305. UNLG1_R180275629RC_C4	GARCHARDOGLA - TIGUNCTAUS ACTITITAS TITTUS ASTT-RIGARTITITT		IN INFALL IN CONTRACTOR AND A ANALY
306. ChLG1_R180275629RC_C31	GARCARACCECA - TIG OCCTAGACTTTTAS TTTTESAGTT - ATG ARTTTTTT	GTIGAATASAA TITTTCCAC	TATHSATATISC CT - ATCT TAATTITTAGC AAAAAACTITAAAAS TTTACATUSTS TAAAAC A BIGGT TTTATASCAAAATS - AGCGSTIGAAT CAANS
307. ChLG1_R180275629RC_C6	GAATAAACCACA - TIG CCCTACG ACT TITAG TITTE AG T T-AIG AATTITTIT-	G TTG AA TAAAA - TTT TT CAC	TATASATATIGC-CTATCT-TARTTTTAGC-ARAAAACTTTAAAAGTTTACTITTITTITTITTIGTTAAAAS-ANGGT-TTAAAAGCAAAATG-AGCCGCIGAATTCAAAG
308. ChLG1_R180275652RC_C9	GAATAAACCACATIG COCTACE ACTITINE TITT GAG TT-AIG AATITITT	GTTE AATAAAA-TTT TCCAC	TATAGATATIG C-ITATCT-TAATT TITE C-ABABAACTT TABAAG TITAII CITG TEABAAG - BIGG T-TIAATAG CABAATG - AGCOGC IG AAT T GAATG
309. ChLG1_R180275629RC_C5	GAACAAACCGCATTG CTCTACG ACTTTT <mark>G</mark> S TTTTT T AG TT-ATG AATTTTTTT	<mark>G</mark> TTG AATAAAA TTT T <mark>T</mark> CAC	TATAG ATATTG C-CTATCT-TAATTTTTAG C-AAAAAACTTTAAAAG TTTAC <mark>H</mark> PTTAG TFAAAAG A IG G T-TTTATAGG <mark>A</mark> AAAACG-AGCOGC IG AATTCAATG
310. ChLG1 R180275629RC C8	GAACAAACCGCA TTG CTCTACG ACT TTTG: TTTTT TAG TT-ATG AATTTT TTT	<mark>G</mark> TTG AA TAAAA - TTT T <mark>T</mark> CAC	TATAG ATATIG C-TTATCA TAATT TITAG C-AAAAAA CITI TAAAAG TITAC TITAT TIATAAAG - 🖬 IG G T- TITATAOG 🕻 AAAATG - AGCOGC IG AATI CAATG
311. ChLG1 R180275629RC C22	GAACAAACCGCA - TTG CTCTAC5 ACTTTT <mark>6</mark> 6 TTTTT <mark>A</mark> AG TT ATG AATTTTTTT-	GTTG AATAAAA TTT TTCAC	TATAS ATATIG C CT — ATCT TAATTTITING C ARAAAACTTIAAAAS TITAC TIT TIG TIAAAAS – A ISG T TITATAOS CAAAATS ASCOGCTS AATTCAATS
312. ChLG1 R180275629RC C23	GAACARACOGCA TTG CTCTA <mark>T</mark> ; ACT TTTAG TTTTT <mark>R</mark> AG TT- ATG AA TTTT TTT	<mark>G</mark> TTG AATAAAA- TTT TCCAC	TATAS ATATTS C-CTATCT-TAATTT TINS C-ARABAACTT TARAAS TIT AC <mark>H</mark> ITTTS THABAAS A IIS S T-T TTATAOS <mark>C</mark> ABARATS - ASCOSC IIS AAT TCRATS
313. ChLG1 R180275629RC C40	GAACAAACCGCAAIG CTCTA <mark>T</mark> ; ACTTTING TTTTI <mark>A</mark> AG TT-AIG AATTTTTTT	GTTE AATAAAA- TTT TCCAC	TATNG ATATTS C-CTATCT-TAATTTTTNS C-ARARARCCTTARARS TTTAC TITT TTTS TITTATAGE ATCG T-TTATAGE - ASCCGT GAATTCAATS
314. ChLG1_R180275629RC_C30	GARCAARCOGCA - TTG CTCTACS ACTTCTAG TTTTTAG TT- ATG AATTTTTTT-	GTTG AATAAAA TTT TTCAC	TAT MG AT AT TIG C CT ATCT TAATT TIT THAC A AAAAACCTT TAAAAG TIT AC TIT TTAAAAG - NIGGT TIT ATAGG AAAATG AGCCGC IG AAT T CAATG
315 Chi G1 R180275852RC C7	GAACAAACOGCA - TTG CTCTACE ACTTTTAG TTTTTAG TT- ATG AATTTTTTT-	GTTG AATAAAA TATTCAC	TATN'S ATATIG C. CT
318 CH C1 P180275852PC C40	GAACAAACCISCA - THE CREATAGE ACTIVITY OF PURPHICAL PURPHICAL PURPHICAL		
317 CH C1 D1902756520C C18			THE REPORT OF TH
310 CH C1 D100273032R0 014		CONCERNENCE LITERAL	TARGET AND TRANSPORTATION AND TRANSPORTATION AND TRANSPORTATION TO A TRANSPORTATION AND T
310. CHLOT K1002/3002KG C20		CINCARTARAA TITI	LALASALALISE CI ALCI IAMITILIASE AAAMAGUINAMASI INAMISI INAMISI INAMISI DINAASE DISELE INAMAGU AAAAN AAAAA
318. CILGI R 1002/3629RC C26	CARCARAGE CONTRACTOR CONTRACT IN A CONTRACT OF	CONTRACTOR AND A DE CONTRACTOR	BALESCHARTS ST. ALL IN THE RECENT ANALYSI IN THE THE THE THE THE THE THE ALL ST. ALL S
320. UNLG1_K180275652RC_C3	GARCAARCUSCA TITS CTCTATS ACTITITAS TITTTAS TTTTAS TTTAIS AA TITTTTT	TIGATASAA TITTCCAC	LATHAATATISCHIT ALUT TAATTITESC AAAAAACTITEAAASTITTATATUTISCIAAAAS TITATAGCAAAAS ASCOCCTGACTTAATS
321. CnLG1_R180275652RC_C10	GARCAARCOGCA TTG CTCTATG ACT TTTAG TTTTTAG TT AIG AA TTTTTTT	GTTG AATAAAA TTT TCCAC	TATHGATATIGG TT AUT TAATTTTTAGC ARAMACTTTAAAGTTTAGAAGTTTAGATGTAGGT TTTATAGCAAAAG AGCGCTGAATTCAATG
322. ChLG1_R180275629RC_C34	GAACAAACOGCATTG CTCTAT; ACTTTTAG TTTTTAG TT-AIG AATTTTTTT-	GTTG AATAAAA TTT TACAC	TATAGATATIG C-CTATCT-TAATTTTTTE C-ARAAAACTTTAARAG TTTATATATTTG CTARAAG - AIGG T-TTTATAGG CAARATG-AGCOGC TG ARTT GAAGG
323. ChLG1_R180275629RC_C7	GAACARALOGCA TTG CTCTACG ACTTTTATTTATTAG TT-ATG AATTTTTTT	GTTG AATAAAA-TTT TCCAC	TAT BUATA TIG C -CT ATCT- TRATT TING C - ABAARA CTT TABAAS TITA TATAT CARAGE - ATE CA TA AGE CARARIE - AGC CC CI G ANT C CARAGE
324. ChLG1_R180275629RC_C27	GAACAAACCGCA - TIG CTCTA CACTITIAG TITTIAG TITTIAG TIT AIG AA TITTITT	GTTG AATAAAA TTT TC CAC	– – – TATASATATUS C - CT – – ATCT - TAATTTTTAS C - AAAAAACTTTAAAAS TTTACATCTUS TEAAAAS – 🛛 👖 IIG ST - TTTATAUS CAAAAUS – ASCOSCUS AATTCAAUS
325. ChLG1 R180275652RC C16	G ARCARACOGCATYC CTCTR <mark>IC</mark> ACT TTTRC TTTTT <mark>R</mark> AG T <mark>C</mark> -ATG ARTTTTTTT	<mark>C</mark> TCS ARTARAR - TTT TCCAC	Tatas atatis C-Ctatct-taatt tites C-abaaas ctt tabbas tites cats tites tabbas a iss t ittatass cabrats -as cos cos t <mark>a</mark> bat cabis

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320	. CREGT_R180275652RG_C21	GAACAAACOGCA	-TIGEFETAT ACTITTAS TITTTAAS TE	AIGAATTTTTTT-	TUS AATAAAA	TTTTCCAC	-TATASATATIGC-CT-	-ATCT TAATTTTTASC	-ARAARACIT TARRAG TITACATCITG TIRARAS-	AIGGT-TTTATAUSCAAAATG-AGCOGCESAATTCAATG
321	. ChLG1_R180275629RC_C15	AACAAACGCA	-TTTTTCTATS ACTITTAS TITTTAAS T	AIGAATTTTTTT-	GTUGAATAAAA	TTTTCCAC	-TATAGATATIGC-CT-	ATCT TAATTTTTAGC	-AAAAAACTTTAAAAGTTTACATCTTGTTAAAAG-	AIGGT-TTTATAUSCAAAATG-AGCCBCTGAATTCAATG
328	. ChLG1_R180275652RC_C28	GAACAAACCGCA	- TTG CTCTA CACTTTTAG TTTT TAG T	AIGAATTTTTTT-	- <mark>G</mark> T <mark>C</mark> GRATAAAA	TTTTTTCAC	TATAGATATTG C-CT	-ATCT-TAATTTTTAGC	-ARARACTT TARRAG TTTACAT TTG TTARAAG -	- ATEGT - TTTATAOSCACAATE - AGCOECTEAATTCAATE
329	. ChLG1 R180275652RC C8	GAATAAACCGCA	- TTG CTCTACG ACT TTTAG TTTT TAGT	ATG AATTTTTTTT-	- <mark>G</mark> T <mark>C</mark> G AA TAAAA -	TTTTCCAC	TATAGATATTGC CT	-ATCT TAATTTTAGC	-AAAAA-CTTTAAAAG TTTAC-T <mark>T</mark> TTG TTAAAAG-	- AIGGT - TTTATAOG <mark>G</mark> AAAATG - AGCCGCTGAATTCAATG
330	. ChLG1 R180275652RC C4	GAACAAACOGCA	-NIG CTCTACS ACT TTTAS TTTT TAAG TT-	ATG AATTTTTTT-	- GTCG AATAAAA-	TTTTCCAC		-ATCT-TAATTTTTAGC	-AAGAAACTT TAAAAG TTTACAT CTTG TTAAAAG-	- ATEG C - TTAATAGE CAAAATE - AGCOGC TE AAT T CAATE
331	ChLG1_R180275652RC_C12	GAACAAACCGCA	-RIG CTCTACS ACT TTTAS TTTTTAS TTTTTAS	ATGAATTTTTTT	-GTCGAATAAAA-	TTTTCCAC	TG TAG ATA TTG C-RT	-ATCT-TAATTTTTAG C	-AAGAAACTTTAAAAG TTTACATCTTG TTAAAAG-	- AIGGC TTAATAOSCAAAATG - AGCOGCTGAATTCAATG
332	ChI G1_R180275652RC_C24	GAACAAACCGCA	- TTG CTCTATG ACT TTTAG TTTT TAG T T	ATGAATTTTTTT	-GTCGAATAAAA-	TTTTCCAC	- TGTAGATATTGC - TG	-ATCT-TAATTTTTAGO	-AAGAAACTT TAAAAG TTTACAT CTTG TTAAAAG-	- NIGGC TTAATAOGCAARATG - AGCOGCTGAATTCAATG
333	Chi G1 R180275829RC C25	GAACAAACCGCA	- TTG CTCT AT A CT TTT AG TTTT TAAG T	8 TG 88 TOTT TTTT-	GTOR BATAABA-	TTTTTTCCTC	TATAGATATTGC CT	ATCT TAATTTTAGC	- BAAAAA CITT TAAAAG TITT ACAT CITTG TTAAAAG -	AGGC TTAATAGCAABATG AGCCGCTGAATTCAATG
334	CH C1 D1902756520C C2	CALCABACCCCA	ייים ער מער מייר אייר מער מיירים אייר מיירים אייר מיירים אייר מיירים אייר מיירים איירים איירים איירים איירים אי	S dis 3 9 designed data	07073373333	THE POINT OF CALC	TATACATATTCC	- ATCT TRATTTOTAC	AZARAR TTTTAR SAC TTTTAC AT COTTC TTAR A BC	
334	CILGI R100275052RC CZ	GARCRARCGCA	- HOCICIAL ACTIVITATION IN THE ACTIV	AIGAA1111111	TOD AN I ANAM	TITICARC	INTRANIATIOC CI	ALCI DARITITIASC	ARARAGIIIARAASIIIACRICIIGIIIARAAS	ALSO I - I TIRIROS CAS RAIG - ASCOSC DE ARI I CARIG
222	. CILG I_R 1002/3032RC_C23	GARCAARCOGCA	TIGCTCTAN ACTITTAS TITTINAS TI	AIGAATTTTTTT	TUS ANTABAR	TTTTCCAC	- INTAGATATIGC CT	AFCT BATTTTTASC	-ARAAACTITARAAS TITALATUTIS TIARAAS-	ABSGT-TTTRIAUSCALARIG-ASCOSCISARTICARIG
336	. ChLG1_R180275629RC_C35	GAACAAACOGCA	ATG CTCTACG ACTTTTAG TTTTTAG TTTTT	ATG AATTTTTTT-	GTCG AATAAAA-	TTTTCCAC	TATAGATATTGC CT	-ATCT-AAATTTTTAGC	-AAAAAACTT TAAAAG TTTACAT CTTG T <mark>C</mark> AAAAG -	MIGGT-TTTATAGGCAAAACG-AGCCGCTGAATTCATTG
337.	. ChLG1_R180275652RC_C11	GAACAAACOGCA	- AIG CTCTACS ACT TTTAS TTTT TAAG TT-	ATG AATTTTTTTT	- <mark>G</mark> TCGRATAAAA-	TTTTCCAC	TATAGATATTGC-CT	ATCT-TAATTTTAGC	-ARAARACTT TARRAG TTTACATCTTG TTARAAG-	ACSGT-TTTATAGCCARAATG-AGCOGCTGAGTTCAATG
338	. ChLG1 R180275629RC C16	GAATAAACOGCA	- TTG CTCTACG ACT TTTAG TTTT TAG TT	ATGAATTTTTTT	- <mark>G</mark> TCGAATAAAA-	TTTTTTCAC	TATAGATATTG C-CT	ATCT-TAATTTTTAG C	-AAAAAACTT TAAAAG TT TACAT CTTG TTA <mark>G</mark> AAG -	- ACSGT - TT <mark>AG</mark> TAOSCAAAATG - AGCCSCTGAATTCAATG
339	. ChLG1 R180275652RC C17	GAATAAACCGCA	- TTG CTCTACG ACT TTTAG TTTT TAGT T	ATG AATTTTTTT-	- <mark>G</mark> T <mark>C</mark> G RA TAAAA -	TTTTTTTCAC	- TATAGATATTGC - CT	-ATCT-TAATTTTTAG C	-ARARA CTT TARRAG TTTACAT CTTG TTARANG-	ACCOUNT AND CARAGE ACCOUNT AND A CARE
340	Chi G1_R180275652RC_C5	GAACAAACCGCA	- TTG CTCTACG ACT TTTAG TTT ATAG TT-	ATGAATTTTTTT	GTTG AATAAAA	TTTTTTCAC	TATAGATATTGCCT	ATCT TAATTTTTAGC	ARARRACTT TARAAG TTTACAT CTTG TTARAAG -	ACSGT-TTAG TAGS CARAATG-AGCCGCTS AATTCAATG
341	Chi G1 P180275852PC C8	GAACAAACCECA	- THE COLOR & CE & CT THE RE POPPT TO AC THE	ATT AT TTTTTTTTT	CTTC ARTAARA -	TTTCAC	TATAGATATTCCCT		CAAAAACTTTAAAACTTTACATCTTC TTAAAC	TEGT-TTATACCCAABATC-ACCCCCTCAATCCATC
375	CH C1 D10027505210 00	C 33 C3 3 3 C C C 2			C 0007 33 033 33					
342	OLLO4 D480075050D0 000	CARGARACOGCA			CITCARIAAAA		INTROATS INC. CI	-ALCI DATITITIAS		BIG T TITATAG CHARATO BCCCC BARTICARIO
343	. CILG1_R1802/3032RC_CZZ	GAATAAACOSCA	TIGCTCTAGACTTTTAS TTTTTAAS TT	AIGAATTTTTTT	TTO AATAAAA	TTTTTCAC	TATASATATIGG GT	AFCT TARITTTRAC	ARAAAACIT TAAAAG TITATATUTIG TIARAUS-	AIGGT-TTTATAGGCAAAAIG-AGCTGCIGAATTCAAIG
344	. ChLG6_R180284741_C9	GAACAAACOGCA	-TTG CTCTARS ACTTTTRS TTTTIG AG TT-	AIGAATTTTTTT-	-GTTG AATAAAA-	TTATCAC	- TOTAGATATTG C-CT-	-ATCT-TAATTTTTAGC	-ARAARACTT TAARAG TI <mark>G</mark> ACAT <mark>T</mark> ITG TTAAAAG-	- MIGGT-TTTATAGCAAAATG-AGCCGCTGAATTCAATG
345	. ChLG6_R180284741_C12	GAACAAACCGCA	TTG CTCTA N S ACT TTTRE TTTT IG AG TT	ATGAATTTTTTT-	- <mark>G</mark> TTG RATAARA -	TTATCAC	- TCTAGATATTGC-CT-	-ATCT-TAATTTTAGC	-AAAAAACTT TAAAAG TT <mark>G</mark> ACAT <mark>T</mark> TTG TTAAAAG -	ATEGT-TTTATAOGCAARATG-AGCCECTGAATTCAATG
346	. Chlg3 2 R180296143RC C8	GAACAAACCGCA	- TTG CTCTACG ACT TCTAG TTTT TG AAT T-	ATG AATTTT TTT-	- <mark>G</mark> TTG BA TAAAA -	TTTTTT	TATAGATATTG T CT	-ATCT TAATTTTAGO	- ARAARACTT TARAAG TT TACATATTG TTARAAG -	AIGGT-TTTATACGCAAAATG-AGCCGCTAAATTCAATG
347	. ChLG1 R180275805RC C7	GAATAAACOGCA	- TTG CTCTACGGCTTTTAG TTTTTG AG TT-	AIGAATTTTTTTT	-GGTAAAAAAA-	TTTTCCAC		-ATCT-TAATTTTAGC	-ARARACTT TARAR TTTTCATCTTC CTARAC-	A IGG T-TTTATAGC CAARATG-AGCOGC TRAAT TCAATG
348	ChLG1_R180275805RC_C19	GAATAAACOGCA	- TTG CTCTACGC CTTTTAG TTTTTE AG TT-	ATGAATTTTTTTTT	-GGTAAATAAAA-	TTTTCCAC	TATAG ATATTG C-AA	-ATCT-TAATTTTTAGC	-AAAAAACTT TAAAATTTTTCAT CTTG CTAAAAG-	AIGGT-TTTATAOGCAAAATG-AGCCGCTAAATTCAATG
346	Chi G1 P180275905PC C23	GAACAAACCCCA	- דיזיב בייר א רכב בייר אביים אב ייזיים אר אייזיים אביים אביים אביים אייזיים אר אייזיים אר אייזיים אביים אר איי	7 415 FF distant data data	COTARA TARAS-	TTP TT TTC [TB ("	TATAC ATATTCC	-BTCT-TBBTTTTTBCC	- 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	TCGT-TTTATATACCARBATT ACCOCCTERATTCARC
350	Chi G1 D180275805DC C20	GANCABBCCGCB	ייים באב ביותי מייים אב כינים מיייים אב הייים אב הייים אב הייים אב ייים אב הייים אב הייים אב הייים אב הייים אב מייים אב הייים אב היי	2 413 2 2 destate date date	CCT BBATBABA	TET TO CO		ATCT TAATTTTAGC	- 8 5 3 5 TTT T 3 8 3 5 TTTT AC BT CTTTC TT 3 5 3 3 -	TTCGT TTTATATACCAABATT ACCOCCTCAATCAATC
264	CH C47 D490077078 C10	BAACA BACCCCA			CC. BRURARR			NOT TRACTICE	B 3 3 3 5 COURS 3 3 3 COURS OF COURS A S AC	
301		ANGARAGOGCA			CO-RAAINAAAA	TTTTCCAC	IN MARKING CI		AAAAAAGIIIAAAAGIIIACAIGIIGIIGIIAAAA	BIG T TITRING CHARACE ASCOC BARTICARIS
322	. CILGO_R100200010RC_C2	GAAGAALCGCA	TIS CICIALS ACTITIAS TITTIS AS TI-	ALL AND TTTTTTT	- AATAAAA	TTTTGGAC	- TATASATATTGC CT	-ALCT TARTTTTTAGC	-AAAAAACTTTARAASTTTACATCTTSTTAAAAS-	THE ST TTTATAUS CARATE ACCUSCIES ANTTCARTA
203	. ChLG4_R180280270RC_C3	GAACAAACCGCA	- TTACTCTACS ACTTTTAS TTTT	AIG AATTTTTTTTT	-CGTAAATAAAA-	TTTTCCAC	- TATAGATATTGC-CT-	-ATCC TAATTTTAGC	-AAAAAACTT TAAAAG TTTACAT CTTG TTAAAAG-	AIGGT-TTTATAGGCAAAATG-AGCCTCIGAATTCAATA
354	. ChLG4_R180280270RC_C4	AACAAACOGCA	TTG CTCTACG ACTTTTAG TTTT CG AG TT	AIGAATTTTTTTT	CGTARATAAAA -	TTTTCCAC	TATAGATATTGC CT	-ATCCATAATTTTTAG C	-AAAAAACTT TAAAAG TTTACAT CTTG TTAAAAGG	A IGGT - TTTATAOS CAARATG - AGCOGCTGAATT CAATG
355	. ChLG1 R180275554 C4	GAACAAACOGCA	- TT C CTCTACG A <mark>T</mark> TTTAG TTTT A G AG TT-	ATG AATTTTTTTTTT	-GTTAAAAA-	TTTTTTTAC	TATAG <mark>G</mark> TA <mark>C</mark> IG <mark>G</mark> -CT	-ATCT-TAATTTTAGC	-AAAAAACTTTAAAAATTTACATCTTGCTAAAAGA	IGG T-T TTATAOG CAAAATG-AGCOGC IG AAT T CAATG
356	. ChLG1 R180275554 C7	GAACAAACOGCA	- TTCCTCTACGATTTTAG TTTTAG AG TT-	AIGAATTTTTTTT	-GTTAAAAA-	TTTTTTTAC	TATAGGTACTG C-CT	ATCT-TAAT <mark>G</mark> TTTAG (-ARARARCTT <mark>CG</mark> ARA <mark>R</mark> TTTACATCTTG TT <mark>C</mark> ARAG <mark>R</mark>	
357	Chi G4 R180280489RC C2	GAACAAACCGCA	TTG CTCTACGCTTTTAG TTTTTG AG TT	ATGAATTTTTTTT	GGTAAAAAAA	TTTTTTTAC	TATAGATATTGC	-ATCT TAATTTTTAGO	- AAAAAA CTT TAAAAG TT TACAT CTTG TT <mark>G</mark> AAAG T	
358	Chi G4 R180280489RC C6	GAACAAAC	- TTG CTCT ACC ACT T AG TTTT IG AG TT-	AUGAATTTTTTTT	CGTAAATAAAA-	TTTTTTTAC	TATAAATATTGC	ATCT TAATTTTTAC	ARABARCTT TARRAG TTTACAT CTTG TTCARAC	- TEGT-TTTATAGE CARAATE-ACCOUNTERATTCAATE
350	Chi CA P180280480PC C0	CANTANAGORCA	- THAS CARCENES AS A CARDINAL SIZE HARDING THE SIZE OF TH	S dia FF datated debutat	COTARA TOCAR	THE PROPERTY COMPANY	- TAT 3C 3T 3		- 3 3 3 3 3 2 COMPT 3 3 3 3 C THE A C 3 C COMPT 2 C 3 3 3 C 3	TECT TTTATACCAABARC ACCRETATTCAAVE
360	CH C4 D400200405RC C9	C 33C 3 3 COCC2								
200	. CILG1_R1002/3003RC_C22	GARGAARCOGCA	TTTCTCTAGACTTTTAGTTTTGAATT	AIGATTTTTTTT	Tornaarassa-	TTTT TTT ,	TRAGATATIGC CT	AFCT CARITTITA;	ABABACIA TABBAS TITALATUTAS TIBBABAB	- ISST TTTATASSCAAASIG ASCUSCISAAIGCAAIG
301	. CREGT_R180275805RC_C28	GAAGAAACOSCA	TTTCFCTASSACTTFTAS TTTTUSAS TT	AIGANTTTTTTTT	TOTAAATAASA	TTTTTTGC	TARASATATIGC CT	AFCT CAATTTTRAC	ARAAAACTATAAAAG TITACATCITG TIAAAAA	- ISGT TTTATAGSCAAAATG AGCOSCIISAATGCAATG
362	. ChLG1_R180275805RC_C25	GAAGAAACOGCA	- TTTCTCTAGG ACTTTTAG TTTTGG AG TT-	AIGATTTTTTTT	TGTAAATAAGA-	TTTTTTGC	TAAGATATTG C-CT	-ATCT-TAATTTTAGC	-AAAAAACTATAAAAG TTTACATCTTG TTAAAAA	IEG T-T TTATA <mark>G</mark> CAAAATG-AGCOGC IG AAT <mark>G</mark> CAATG
363	. ChLG1 R180275805RC C31	GAA <mark>G</mark> AAACCGCA	- TT <mark>T</mark> CTCTA <mark>G</mark> G ACT TTTAS TTTT <mark>G</mark> S AG TT-	AIGATTTTTTTT	- <mark>TGTA</mark> AATAA <mark>G</mark> A -	TTTT <mark>TTG</mark> C	TARGATATTG C-CT	-ATCT TAATTTTAG C	-AAAAAACT <mark>A</mark> TAAAAG TTTACAT CTTG TTAAAA AA	TEGT-TTTATA <mark>G</mark> CAAAATG-AGCCECTEAAT <mark>G</mark> CAATG
364	. ChLG3 2 R180296143RC C4	GAACAAACCGCG	- TTG CTCT A TG A CT TTT AG TTTT IG AG T T-	ATGATTTTT	GTA AATAAAA	TTTTTTTCAC	TAT GATATTG C AT	-ATCT-TAATTTTAGO	-RAARACTTTARAA TTTACATCTT TTAAA AG	
365	ChLG3 2 R180296143RC CE	GAACAAACCACA	- TTG CTCTAR ACT TTTAG TTTT TG AG TT-	ATGAATTTTTTTTT	GTAAAAAAA-	TTTTTTAC	TATAGATATTG C-AT	ATCT-TACTTTTAGG	-ARARAR TTTTARAR TTTACATCTTG TTARAR	TEG T T TTA TAOS CAARATG-AGCOGC TG AAT T CATTG
386	Chi G1 R180275579 C14	GAACAAACCGCA	- TTG CTCTACS ACT TTTAS TTTT	ATGAATTTTTTTTT	-GGTAAATAAAA-	TTTTCCAC	- TATAGATATTGC - TT	-ATCT-TAATTTTTAG	-AAAAAACTTTAAAAGTTTACATCTCGTTAAAAG	IGG T-TTTATAGC CAARATG-AGCCGC IG A-TTCAATG
367	Chi G1 P180275579 C18	GAACAABCCCCC	- דיזעב ביייר א ביב א ביי יידייי אב יידי א ביב א א יידי א בייי א	7 412 77 destate date date	COTARA TARAS-	TERM THE COLO		-BTCT-TABTTTTAGC	- 8 3 3 3 5 6 7 7 7 5 5 3 3 6 7 7 7 3 7 5 7 7 7 7 3 3 5 5 7	
320	Chi G1 D100275500 C4	GAACABAC				THE RECORD		ATCH TA ATT THE AC	BAAABBCTTTTTAABACTTTTTACBTCTTTTAABAC	
300	OHLO4 D48007580500 04	C MONTANCA				1111100 <mark>0</mark> 0		ALCI DANITITIAN	AAAAAACII IAAAAS II IACAI CIUS IIAAAAS	BOI TITATAGO CANANIG AGCOSC ISANI I CANIG
208	. CHLG1_R1802/3803RC_C0	GAACAAABOGCA	- TIG CTOCAUS ACT TITAS TITTUS AS TI-	AIGAATTTTTTTT	GINAA TAAAA	TTTTTAC	ATASAFATIGC CT	ATTITATI	ARAAACTT TAAAAS TI TACAT TUS TIAAAAS	- IGG TTTATAUS CARAATG - AGCOGC IS AATT CARTG
370	. ChLG1_R180275947_C5	GAATAACCGCA	- TIG CTCTAUG ACT TTTAT PTTT GG AG TT-	AIGAATTTTTTTTTT	GAATAAAA-	TTTTCTAC	- TATAGATATIG C TT-	-APCT-TAATTTTTAGC	-AAAAAACTTTAAAAGTTTACATTTGTTAAAAGA	ISGT-TTTATAGCAAAATG-AGCCECTAAATTCAATG
371	. ChlG1_R180275805RC_C2	GAACAAACOGCA-	- TTG CTCTACG ACTTTTAG TTTT G AG TT-	AIGAATTTTTTTC	-GGTAAAAAA-	TTTTTTCAC	TATAGATATTGC-CT	-ATCT-TAATTTTTTG	ARARA CTT TARAAG TTTACAT TTG TTARAAG	IGGT-TTTATAOGCAARAT <mark>T</mark> -AGCOGCIGAATTCAATG
372	. ChLG1 R180275805RC C9	GAACAAACOGCA	- TTG CTCTACG ACTTTTAG TTT - CAG T	ATS AATTTT TTT	-GGTAAAAAAA-	TTTTTTCAC	TATAGATATTG CT	ATCT-TAATTTT AT	- <mark>G</mark> AAAAACTT TAAAAG TTTACAT <mark>T</mark> TTG TTAAAAG <mark>A</mark>	IGG T-T TTATAGE CAARATG-AGCCGC IG AAT T CAATG
373	. ChLG1 R180275805RC C24	GA <mark>CG</mark> AAACCGCA	- TTG CTCTACS ACTTTTAG TTTT	AIGAATTTTTTTT	-GATAAATAAAA-	TTTTTTCAC	- TATAGATATTG C - CT	ATCT-TAATTTTTA <mark>TG</mark>	- AAAAAACTT TAAAAG TTTACAT TTG TTAAAAG	
374	ChI G1_R180275805RC_C30	GACCARACCECA-	- TTG CTCTACG ACT TTTAG TTTT	ATGAATTTTTTTT	GATASATAAAA-	TTTTTTCAC	- TATAGATATTGC - CT	-ATCT-TAATTTTTATG	ARARRACTT TRARAG TTTACAT	IGGT-TTTATACGCAAAATT-AGCCGCTGAATTCAATG
375	Chi G1 R180275805RC C3	GACGABACCECA	TTYS CTCT & CS & CT TTT AS THTT OS AG T T	איזיגי אא דייזייי דייזייי	GGTABATAABA	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TATAGATATTGC CT	ATCT TAATTTTTA	BAAAAACTTTAAAAG TOTACAT TTG TTAAAAG	TEGT TTTATACS CARBATS AGCOSCTS AATTCAATS
376	CH C1 D180375905DC C31	CALCABACCCCA		Y dia F Y distants data and	CATABB TABBA	THE PACE		ATCT TRATTTAT		
349	CHLOI R100275005DC C21	CALCADADOGCA					DATASALATIOC CI	ALCI DALIIIIAI		
311	. CILG I_R 100273003RC_C0	GARCAARLOGCA	TIGUTUTAUS ACTITITAS TITTUS AS TI-	AIGAATITITIT	WULBOATSSAA	TTTTCAC	TRIASALATICC C	ATCT TAATTTTTAT	ABABACTITABBAS TITACATITIS TIBBABS	- BOT TTRATAUSCARASIG AGCUSCIGARTICARIS
3/8	. ChLG1_R180275805RC_C20	GAACAAACCGCA	TTG CTCTAUS ACTTTTAS TTTTUS AS TT	AIGAATTTTTTTT	GGTAAATAAAA	TTTTTCAC	TATAGATATTGC CA	ATCT TAATTTTTATC	AAAAAACTTTAAAAGTTTACATTTGTTAAAAG	- ISGT - TTTATAUS CAAAATG - AGCUSC IS AATT CAATG
379	. ChLG1_R180275805RC_C26	GAACAAACOGCA	- TTG CTCTACG ACTATTAG CTTT GAG TT-	AIG AATTTT TTTT	-GGTAAATAAAA-	TTTTTTCAC	-GATAGATATTG CT-	ATCC-TAATTTTTATC	-ARARAACTT TARRAG TTTACAT	ISG T-T TTATAGS CAARATG-CCCCCC IS AAT T CAGTG
380	. ChLG1_R180275805RC_C32	GAACAAACOGCA	- TTG CTCTACG ACTAPTRE CTTT CG AG TT-	AIGAATTTTTTTT	-GGTAAATAAAA-	TTTTTTCAC	- GATAGATATTG CT-	-ATCC-TAATTTTTATC	-AAAAAACTTTAAAAGTTTACATTTGT AAAAG	IGGT-TTTATAOGCAAAATG-OGCOGCIGAATTCAGTG
381.	. ChLG3_2_R180296143RC_C	GAACAAACCGCA	- TTG CTCTACG ACT TTTAG TTTT CATG TT	AIG AATTTT TTTT	- <mark>G-</mark> TAAAAAA-	TTTTTTCAC	T <mark>G</mark> TAGATA TTG C-CT	ATCT - TAATT T TTA <mark>T</mark> C	-AAAAAACTT TAAAA <mark>T</mark> TT TACAT CITG TTAAAA <mark>AA</mark>	ISG T TTAATAGC CAARATG-AGCCGC IS AAT I CAATG
382	. ChLG3 2 R180296143RC C7	GAACAAAG CGCA	- TTG CTCTACG ACTTTTAG TTTT CATS TT-	ATAATTTTTTTT	- <mark>G</mark> -T A AATA <mark>C</mark> AA-	TTTTTTCAC	TG TAGATATTG C CT	-ATCT TAATTTTTATC	-AAAAAACTT TAAAAG TTTACAT <mark>T</mark> TTG <mark>C</mark> TAAAAG <mark>A</mark>	- IGG T - T TTA TA OG CAARATG - AG <mark>T</mark> OGC IG AAT T CAATG
383	. ChLG3 2 R180296143RC C2	GAACAAACCACA	- TTG CTO <mark>CG</mark> CG ACT TT <mark>CC</mark> S TTTT <mark>C</mark> G AG T T-	ATAAATTTTTTTT	-G-TAAAAAA-	TTTTCCAC	TATA <mark>AG</mark> TATTGC-CT	ATCT-TAATTTTTA <mark>A</mark> C	-AAAAAACTT TAAAAG TT <mark>C</mark> ACAT <mark>T</mark> TTG TTAAAAG <mark>A</mark>	IGG T-T TTATAGE CAAAATG - AG <mark>T</mark> CGC IG AAT T CAATG
384	Chi G10 R180276688 C5	GAACAAACCGTA	- TTG CTCTACG ACT TTTANTTTT G AG T	ATGATTTTTTTTT	-GGTAAAAAA-	TTTTTTTAC	- TATAG ATATTG C - CT	-ATCT TAATTTTTAG C	-AAAAAACTT TAAAAG TTTACAT CTTG TTAAAAG	
385	Chi Ga R180288610RC C23	GAACAAACCG	TTG CTCTACS ACT TTTANTTTT OF ACT	ATGATTTTTTTTT	GGTABATAAAA	TTTTTTAC	TATAGATATTGC CT	ATCT TAATTTTAG	AAAAACTTTAAAAGTTTACATCTTGTTAAAAG	TTAT TTTE TAGE CAARATE AGCCECTE AATTCAATE
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390	. ChLG9 R180291860RC C4	GAACAAACOGCA	- TTG CTCTAC <mark>A</mark> ACT TTTAG TTTT <mark>G</mark> G AG <mark>G</mark> T-	ATS AATTTT TTTTT	<mark>GTA</mark> AATAAAA-	TTTTTTCAC	TATAA ATATTG C-CT	-ATCT-TAATTTTAG C	-ARARA CTT TARAAG TT TACAT CTTG TTA <mark>G</mark> AR <mark>AR</mark>	Igg A-T TCATAGE CAAAATG - AGCOGC IG AAT T CAATG
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398	. ChLG4_R180280933_C5	GATCAAACOGCA	- TTG CTCTACG ACT TTTAG TTTT G AG TT-	AIGAATITTTT	- <mark>G</mark> TT <mark>A</mark> AATAAAA -	TTTTTTTAC	TATAGATATTGC-CT	-ATCT-TAATTTTTAG C	-AAAAAACTT TAAAAG TT TACAT CTTG TTAAAA <mark>AA</mark>	- TEG G G TTATACE CAARAT<mark>A</mark> G GCCEC TE AAT T CAATE
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407	. ChLG4 R180280798 C10	GAACAAACOGCA	- TTG CTCTACS ACT TTTAS TTTT CAG ACT T	ATGAATTTT TTTTT	-GGTAAAAAA-	TTTT TCGC		-ATCT-TAATTTTAGC	-AAAAAACTT TAAAAG TTTA <mark>T</mark> AT CTTG <mark>G</mark> TAAAAG <mark>A</mark>	IGG T-T TTATACG CAARAT <mark>T</mark> -AGC CGC T R AAT T CAATG
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AAATAAAA-	TTTTTCAC	ATRATISC	C.T.
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-- TAT NG AT ATTG C - CT - --- - ATCT - TAATT T TTA<mark>A</mark>C - ARAANAC<mark>O</mark>CT AAAAG TTTA<mark>T</mark>AT CTTG <mark>C</mark> TAAAAC <mark>A</mark> -- IGG T - TTTA TAOG CAAAAT<mark>T</mark> - AGCOGO T<mark>A</mark>AAT T CAATG - ATCT - TAATTTTTTAKC - AAAAACCTTAAAAACTTTAKAAAACA - TSCT - TTTATACCCAAAATT - ACCCSCTAAATTCAATS - ATCT - TAATT I TTA<mark>A</mark>C - AAAAAAC<mark>G</mark>I I AAAAG ITTA<mark>T</mark>AI CITIG<mark>G</mark> TAAAAG <mark>A</mark> - - IGG I - I TTA IAOG CAAAAI <mark>T</mark>AGCOGCI **A**AAI T CAAIG ATCT TAATTITTINGC ARAAAASTITARAASTITACATCITS TAARAASA ISGT ITTATAGCAARATS ACCECTGAATTCAATS - ATCT - TRAIT IT THE C - ARABAR<mark>C</mark> IT I ARABE IT TRCAT CITY IT ARABC<mark>R</mark> -- BEG I -- I THA TROC CARARIE - AGCOGOUR ART I CANTG - apcy - raamperpanet - a a a aa<mark>c</mark> the raa aac the rac ar control the a a ac <mark>a</mark> - the control ta a act - acceler to a app ca and ATCT TAATT IT - ACC - AAAAA- - CI IAAAAG ITTACAT CITG ITAAAAGA - IGG I - ITTAIAOG CAAAAIG - AGCCGC IGAAIT CAAIG ATCT TRATTTTTANC RAMARACCTTARAMS TTTACATCTTG TTARAMS A BSGT TTTATAGE CHARACE AGCCGCTERATTCANTG - ATCT - TAATT T TEA<mark>R</mark>C - AAAAAAC<mark>O</mark>T TARAAG TTT ACAT CTTG TTAAAAG<mark>A</mark> -- ISG T - T TTATA OG CAAAATG - AGCOGC IIS AAT I CAATG - ATCT - TAATT T TTA<mark>A</mark>C - AAAAAAC<mark>C</mark>T TAAAAG TT TACATCTTG TTAAAAG<mark>A</mark> -- TGG T -- T TTATAGG CAAAATG - AGCCGC TG AATT **T**AATG ATCT TAATTITTAAC AAAAAACCITAAAAG TITACATCITG TAAAAGA 15 AT TITATAGS CAAACTS AGCCGCTSAATTCAATG - ATCT - TRAIT I TIME C - ARAAAA<mark>G</mark> II I AAAAG II TACAI CIIG II AAAA**AA**A -- IEG I -- I II A IACC CAAAAIG - AGCCGCIG AAI I CAAIG - ATCT - TAATT T TTAG C - AAAAAACTT TAAAAG TT TACAT CITG TTAAA**TTA** -- ISG T -- T TTA TAGE CAAAATG - AGCCECIG AAT T CA<mark>B</mark>IG - ATCT - TAATTTTTTAG C - AAAAAACTTTAAAAG TTTACAT CTTG TTAAA**TTA** -- TGG T -- TTTATAGE CAAAATG - AGCOGC TG AATT CA<mark>G</mark> TG ATCT TAATT TING C AAAAAACTT TAAAAG TITACATCITG TIAAATA BEGT TITATACS CAAAATE AGCCGC BAATTCAGIG ATCT - TAATT I TIME C - AAAAAACTT TAAAAG ITTACAI CIIG ITAAAITA - IGG I - I TIAIAOG CAAAAIG - AGCOGCIG AAI I CA<mark>g</mark>ig ATCT - TAATT I TIKE C - AAAAAA<mark>T</mark>TI I AAAAG ITTIACAT CITE ITAAA**TTA** -- ISG I -- I TITA I AGE CAAAATS - AGE CGE I AAT I CA<mark>B</mark>IG ATCT TAATTTTTAGC AAAAAAGTTTAAAAGTTGACATCTTGTTAAAAGA OGT TTTATAGCAAAAGG AGCOGCTGAATTCAATG - ATCT - TAATT TTTM: C - ARAAAACTT CAARAG TT<mark>RE</mark>CAT TTG TT<mark>C</mark> AAAC A -- TGG T - T TTATACC<mark>C</mark> AAAATG - A<mark>A</mark>CCGC TC AAT T CAATG ATCT TRATTT TING C. A CAARACTT TRAAMS TO TACHTCTTS THE AMERA. TEG T. TITATAGE CAARATS - A COSCI TRAAT CAARS ATCT TAATTTTTCAC AAAAACCTTTAAAAGTTTACATCTTGTTGAAAGA TEGT TTTAAACCCAAAATG ACCCCCTAAATTGAATG - ATCT - TAATT T TTA<mark>A</mark>C - AAAA<mark>TC</mark>CTT T<mark>T</mark>AAAG TTTACAT CTTG TI<mark>G</mark>AAAG <mark>A</mark> -- IGG T - T TTA TA (G CAAAAT<mark>A</mark> - AGC<mark>TT</mark>C T<mark>A</mark>AAT I CAATG - ATCT - TAATT TITKE C - ARARACTT TARAGE TITACAT CITE TICAARE A - TEE T - TITAAGE CAARATE - ACACECE AATT CAATE ATCT - TAATTTTTTAG C - AAAAAACTTTAATAG TTTACATCTTG TCGAAAGA -- TGG T -- TTTAAACG CAAAATA AGACGCTG AATTCAATG ATCT TAATTTTTTAGC AAAAAACTTTAAAAAGTTTACATCOR TTAAAACA BGT TTAATACGCAAAATG AGCCGCTGAATTCAATG ATCT - TRATT TETATC - ARABARCTT TEARAGETTTACATCTTG TTARARCE - TGG T - TTATAGE CARARTE - AGCCGC TERAT TCAATG - ATCT - TAATTTITES C - AAAAAACTTTEAAAAGTTTACATCTTG TEAAAG<mark>A</mark> -- TGG T -- TTFATACCCAAAATG - AGCCCCTE AATTCAATG ATCT TAATTTTTAGC AAAAAACTTTAAAAGTTTACATCTTG TTAAAAGA TIGGT TTTATAGGCAAAATG AGCOGCTGAATTCAATG ATTT - TAATT TTTAG C - AAAAAACTT TAAAAG TTTACAT CTTG TTAAAA-A - BG T - TTTATAG CAAAATG - AGCCGC BG AATT CAAT - ATTT - TAATT TITKS C - AAAAAACTT TAAAA TTTACAT CITY, TITAAAA - A. - ING T - TITA TAGE CAAAATE - ACCORC TE AATT CAATG RTCT TAATT T TTAG C AAAAAACTT TAAAAG TTTACAT CITS TTAAAAGA GSGT T TTATAG CAAAAG - AGCCCC IG AAT T CAATG ATCT TAATT I TING C AAAAAACTT I AAAAG ITTACAT CITIG ITAAAAGA CIGI T I TITATACI CAAAATS AGCCGC II AAAT CAATG - ATCT - TRATT TITHE C - ARAMACCT TARARS TETACAT CITE ITARARC A -- IS G T - T TTATAOS CARARIS -- ASCOSC IS ART I CART ─ APCT─ F& A TT FT FAC C ─ A A AA AA CTT F AA AAG TT TA AAC CTTC TT AA A AG A── TC C T ─ TT FA AG C AA A ATC ─ ACCCCC TC A AT F CA AT ATCT - TAATT I TING C - AAAAAACTT I AAAAG ITTIACAT CITG IT<mark>G</mark>AANG<mark>A</mark> -- ISG I -- I TITA IAOS CAAAAIG - NGC<mark>I</mark>GC IG AAT I CAAIG ATCT TAATTTTTAGC ARAAAACTTTAAAAG TTTACATCTTG TTAAAAGA BEGT TTTATACGCAAAATG AGCCGCTGAATTCAACT - NTCT - TRAIT IT THE C - ARABARCIT I FRAME IT TRCAICITG IT FRAME<mark>R</mark> -- BEG T - I THA TROC CARARE - AGCOGO B- A<mark>G</mark>I I <mark>B</mark>AN<mark>O</mark>G - X P P 7 - F X X T P P 2 C - X X X X X P T T X X X X P T T A P P T Y X P Y C T Y X P X P X P Y X P X A X X Y X ATCT TAATTITTAGC AAAAAACTTIAAAAGTTIACATCITG CIGAAAGA ISGT ITTAIACGCAAAATS AGCCGCIGAATTCAATG - ATCT - TRAIT IT THE C - ARMANN CIT I ANNAS IT THCAIL CITG CITC AND CALL AND CANNERS - AGC COSC 10 ANT I CANTG - ATCT - TAATT T TTAG C - AAAAAACTT TAAAAG TTTACAT CTYS TI<mark>G</mark> AAAG<mark>A</mark> -- IGG T - T TTA TA OG CAAAATG - AGCOGC IG AAT T CAATG – B.T.C.T. – TB.B. TTTT TO B.B.B.B. C.T.T.T.B.B.B.B.C.T.T.T.B.C.T.T.T.C.T. – TC.C.T. – TC.C.T.C.B.B.B.T.C. – B.C.C.C.C.C.T.B.B.B.T.T.B.B.T.C. ATCT TAATT TTAATC ARAAAACTT TAAAAG TTTACATCTTG TIGAAAGA ISGT TTCATAGE CARAATE AGCCGCIE AATT CAATG - ATCT - TAATT T TTA<mark>T</mark>C - AAAAAACTT TAAAAG TT TACAT CTTG TT<mark>G</mark>A AAG<mark>A</mark> - - UGG T - T T<mark>C</mark>A TAOG CAAAATG - AGCOGC UG AAT T CAATG ATCT - TAATT IT THE C - AAAAAACTT I AAAAS IT TACAT CITS IT AAAAS A - ISG I - ICTATAGE CAAAATS - AGCOSCIE AAT I CAATS - ATCT - TAATT T TTAG C - AAAAAACTT T AAAAG TTTACAT C TTG TTAAAAG A - TGG T - T TTA TAGG CAAAAG - AGCOGC TG AATT C AATG - ATCT - TAATT T TTAE C - RARARACTT TAAAAG TT TACAT CITE TTARAMGA - TEE T - T TTATAGE CARAATE - AGCCGC TE AAT I CAACA - ATCT - TAATT I TIME C - AAAAAACTT I AAAAG ITT MCATCING ITAAAAG 🗛 - IIG I - TITA TAGE CAAAANG - AGCCECIG AAT I CAACA ATCT - TAATT I TING C - ARAAAACTT I ARAAG ITTACAT CITIS I TAAA TIA - IIGG I - I TIATACS CAARATG - AGCCGC IIG AAT I CAAG - ATCT - TAATT T TTAG C - AAAAAACTT TAAAAG TTTACAT CTTG TTAAA TTA - TGG T - T TTATACG CAAAATG - AGCCGC TG AATT CAAG - ATCT - TRAIT I TIME C - ARAAAACTT I ARAAG TI TACATCITE TIARA **TIA** - IEG T - I T<mark>C</mark>ATAGE CAAAATE - ACCCECTE AATTCAA<mark>E</mark> ATCT - TRATT I TING C - ARARARCTT I ARARG ITT ACAT CITIG ITARA TIA - ING I - I CITA I A OG CARARIG - NGCCGCIG AAT I CAAIG ATCT TAATTTTTING C AAAAAACTTTAAAAG TTTAT-TCTTG TTAAACA TGGT CTTATACGCAAAATG AGCOGCTGAATTCAATG - ATCT - TAATT T TTAG C - ARAAAACTT TARAAG TTTACAT CTTG TTAAAAG 🗛 -- 15G T - T TTATACC CAARATG - AGCOGC 16 AAT 1 CAATG - ATCT - TAATTTTTTAC C - AAAAAACTTTAAAAG TTTACATCTTS TTAAAACA - ISG T - TTTATAOG CAAAATG - AGCOGCIG AATTCAATG ATCT TAATTT TTACC - AAAAAACTT TAAAAG TTTACATCTTS TTAAAAGA -- TSG T-T TTATACG CAAAATG-AGCCCCC GAAT CAATS ATCT TRATT I TENS C CANARACTT FARMS ITTACHT CTTS ITCAMS A BEST I TTATACS CANARA - ASCCSC BANT ICANTS ATCT TAATT TITAS C AAAAAACTT TAAAAS TITACATCT TAAAAAAA TIGGT TITATAGE CAAAATS ACCOSC TEAATT CAAGS ATCT TAATTTTTAGC AAAAAACTTTAAAAG ITTACATCTOG ITAAAAAA IGGT ITTATACG CAAAAIG AGCOGCIGAATTCAAG ATCT TRATT TIME C - RAMARACTT FARMS TTTACHTCTC TFRAMAR - BSG T - TTTATAGE CRAMATS - RECOOCTE ANT CARTS - ATCT - TAATT I TIME C - AAAAAACTI TARAAS ITTACAT CTOS TIAAAAAAA -- USG T - I TIATAOS CAAAATS - AGCOSCUS AATT CAATS - ATCT - TAATT I TIME C - AAAAAACTI TARAAS ITTA<mark>R</mark>AT CTOS TIAAAA**AA** -- USG T - I TIATAOS CAAAATS - AGCOSCUS AATT CAATS ATT TAATTTTTMC AGAAAACTTAAAAGTTTACATCTTGTTAAAAGA BGT TTTATACGCAAAAG AGCCGCBAATTCAATG ATCT - TAATTT TTACC - AAAAAC CTT TAAAAC TTTACATCTIS TTAAAAAA - ISG T - TTTACAGE CAAAATE - AGCOCCIE AATT CAADA ATCT - TAATTTTTAG C - AAAAAACTTTAAAAG TFTACAT CITIG TFAAAAAA - TGG T - TTTATAG CAAAATG - AGCCGTTG AATT CAATG ATCT TRATTTTINGC RAMARACTTIANAS TITACAICITS TRANAMA BEST TITATAGE CARACTS ACCESCERANTICANTS ATCT - TAATTTTTAGT - AAAAAACTTTAAAAG TTTACATCTCT TTAAAATA atct - Taatt Titag C - Bababactt Tab<mark>c</mark>ag Titacat CT<mark>CA</mark>TTABABG T -- TIG T - TITATAG<mark>G</mark>ABBARG - AgC CGC TG BATT CAAT**A** - AFCT - TAA TT T TT AS C - A A AA AA CTT T AA CAG TT T AC AT CT<mark>CA</mark>TT AA A AG T - - TGG T - TTT A TA GA<mark>G</mark> AA A ATG - AGCCGC TG A ATT GA AT **A** ATCT-TAATTTTTACC-AAAAAACTTTAACAG TTTACATCTCATATAAAGT- IGGT-TTTATAGG AAAATG-AGCCGCIGAATTCAATA ATCT TRATTTITING C - AAAAAACTTTAAAAS TTTACATCT S TTAAAAS T -- TSG T - TTTATAOS GAAAANS - AGCOSC 15 AATTCAATS ATCT - TAATT T TTAG C - ARAAAACTT T ARAAG TT TACAT CTOS TTAAAAG T -- TGG T -- TTA TA CG<mark>G</mark>AAAATG - MGCCGC 15 AAT T CAATG ATCT TAATTTTTAGC AAAAAACTTTAAAAGTTTACATCTOGTTAAAAGT ISGT TTTATACGOAAAATG AGCCGCEGAATTCAATG - ATCT - TAA TT T TTAC C - AAAA AA CTT T AAAAC TT TAC AT CT OF TTAA A AC T - TGC T - TTA TACC<mark>C</mark>AA AATC - ACCCCC TG AATT CAATG - ATCT - TAATT I TIKG C - AAAAAA<mark>T</mark>TI TAAAA**XII TIAG AGTI G**I TIKAAAA**XI** - - IGG T - T**X**TA TA GG<mark>G</mark>AAAATG - AGCCGC 16 AAT I CAATG ATCT TAATTTTTAG C AAMAANTTTAAAMS TTTAAAMS TTTAAAMT - 196T TATATATSGAAAATG - AGCOGCTAAMTTCAATG - ATCT - TRAIT IT THE C - ARAAAACTT I CAARS IT TACAT CIC: THAAAC I -- IEG I -- ITTA TAGE AAAATG - AGCOGOU AAT I CAATG - ATCT - TRATT T TTAG C - AAAAAACTT T <mark>C</mark>AAAG TT TACAT C T<mark>O</mark>G TTAAAAG T - - TGG T - T TTA T<mark>T</mark>OG<mark>G</mark> AAAATG - AGCOGC TG AAT T CAATG ATCT TRATTITING C RAMAMACTITRAA-G TITCCALCUS TRAAMST ISST TITATAGS AAAATS MCCCSC BAAT CAATS - ATCT - TRAIT I TIME C - ARABAR CITI TARA-G TITI CATCI CI TIARAS T -- IEG T -- TITATACC CARACTC - ACCOCCI CATT CANTO

490	. ChLG5 R180282864 C2	GAACAAACOGCA	TTG CTCTACG ACT TTTAG TTTT TG AG TT-	ACGAATTTTTTT	<mark>G</mark> TTG AA TAAAA	TTTTCCAC	TATAGAAATTG C-CT	-ATCT-TAATTTTAG C	-AAAAAACTT TAAAAG TTI	- TCATCTCC TTAAAAG T	-TGG T-1	T TTATACG <mark>G</mark> AAAATG	-AG <mark>T</mark> CGC IG AAT I CAAIG
491.	. ChLG5 R180282864 C6	GAACAAACCACA	TTG CTCTACG ACT TTTAG TTTT IG AG TT-	AIGAATTTTTT	<mark>G</mark> TTG AA TAAAA	- TTT T <mark>T</mark> CAC	TATAGANATTG C-CT	-ATCT-TAATTTTTAGC	-AAAAAACTTTAA-GTTT	CATCTC TTAAAAGT-	– IG <mark>T</mark> T– I	T TTATAOG <mark>G</mark> AAAATG	- AGCCGC IG AAT T CAATG
492.	. ChLG5_R180282864_C9	GAACAAACCGCA	TTG CTCTACG ATTTTAG TTTT IG AG TT-	ATGAATTTTTTT	<mark>G</mark> TTG AA TAAAA	TTTTTCAC	TATAGANATTG C-CT	-ATCT-TAATTTTTAGC	-AAAAAACTT TAA-G TTT	CATCTOG TTAAAAG T-	– IG <mark>T</mark> T– 1	TTTATAOG <mark>G</mark> AAAATG	- AGC CGC TG AAT T CAATG
493.	. ChLG5 R180282864 C4	GAACAAACCGCA	TTG CTCTA CGGCT TTTAG TTTT TG AG TT-	ATGAATTTTTTT-	G TTG AA TAAAA	-TTTTCCTC	TATAGANATTGC-CT	-ATCT-TAATTTTTAGC	- AAAAAACTT TAAAAG TT 1	CATCTCG TTAAAAG T	IG T 1	T TTATA OG <mark>G</mark> AAAATG	-AGCCGCTGAATTC <mark>T</mark> ATG
494	. ChLG5_R180282864_C7	GAACAAACOGCA	TTG TCTACS ACT TTTAS TTTT IS AS TT-	AIGAATTTTTTT-	<mark>G</mark> TTG AA TAAAA	TTTTCBAC	TAT C-CT	-ATCT-ICATTTTAGC	-a <mark>g</mark> ararctt taraag tti	CATCTCG TTAAAAG T-	-IGGT-1	T TTATACE <mark>C</mark> ARAATC	-AGCCGC IG AAT T CAATG
495.	. ChLG5_R180282864_C10	GAACAAACCGCA	TTG TTCTACG ACT TTTAG TTTT TG AG TT-	ATGAATTTTTT	<mark>G</mark> TTG AA TAAAA	TTTTCAAC		-ATCT-TCATTTTAG C	- a <mark>g</mark> aaaactt taaaag ttt	CATCTCS TTAAAAGT -	-IGGT-1	T TTA TA OG <mark>G</mark> AA AATG	-AGCCGCTGAATTCAATG
496.	. ChLG5_R180282864_C5	GAACAAACCGCA	TTG CTCTACG ACT TTTAG TTTT IG AG TT-	ATGAATTTTTTT	<mark>G</mark> TTG AA TAAAA	TTTTCARC		- ATCT - T <mark>G</mark> A <mark>C</mark> TTTTAG C	- a <mark>g</mark> aaaa ctt taaaag ttt	CATCTOS TTAAAAS T-	- IG T- 1	t ttat <mark>t</mark> og <mark>g</mark> aa aatg	-AGCCGCTGAATT <mark>G</mark> AATG
497.	. ChLG5_R180282864_C3	GAACAAACCGCA	TTG CTCTACS ACT TTTAS TTTT TTAAT T	ADGAATTTTTTT-	G TTG AA TAAAA	TTTTCCAC	TATAGAAATTGC CT	-ATCT-TAATTTTAGC	- AAAA <mark>T</mark> ACTT TAAAAG <mark>G</mark> TT	CATCTC TTAAAAGT	-IGGT-1	TT <mark>C</mark> ATAOG <mark>G</mark> AAAATG	-AGCCGCTGAATTCAATG
498.	. ChLG5_R180282864_C13	GAACAAACCGCA	TTG CTCTACS ACT TTTAS TTTT IS AS TT-	ATS AATTTT TTC-	<mark>G</mark> TTG AA TAAAA	-TTTTCCAC		-ATCT-TAATTTTTAGC	- AAAAAACTT TAAAAG TTT	CATCT <mark>C</mark> G TTAAAAG T -	-IGGT-1	TTTATAOS TAAAATG	-AGCCGCTG AATTCAATG
499.	. ChLG5_R180282864_C12	GAACAAACOGCA	TTG CTCTACG A <mark>T</mark> T TTTAG TTTT IG AG T T-	AIGAATITTTTT	<mark>G</mark> TTG AATAAAA	-TTTT T CAC		-ATCT-TAATTTTTAGC	-AAAAAACTT TAAAAG TTT	CATCTCG TTAAAAGT -	-IGGT-1	T TTA TA OS <mark>G</mark> AA AATG	-AGCCGCTCAATTCAATG
500.	. ChLG1_R180275579_C17	GAACARACCGCA	TTG CTCTACG ACT TTTAG TTTT TG AG TT-	ATGAATTTTTTC	G TTG BATAAAA	TITTCCAC	TATAGATATTGC AT	-ATCT-TAATTTTTAGC	-AAAAAACTT TAAAAG TTT	ACAT CTOG TTAAAAG A	-IGGT-1	TTTATACCT AAAATG	-AGCOGGTGAACTCAATG
501.	. ChLG4_R180280635RC_C9	GAATAAACOGTA	TTG CTCTACG ACT TTTAS TTTT TG AG TT-	ATGAATTTTTTCCT	- AGTA AATAAAA	-TTTTCCAC	ARTAARTC TTGC-CT	-ATCT-TAATTTTTAAC	-AATAAACTT TAAAAG TTT	ACAT CTTG TTAAAAG T-	-IGG <mark>G</mark> -1	T T <mark>C</mark> ATAÓG <mark>G</mark> AAAATG	-AGCEGCTG AAT T CAATG
502.	. ChLG10_R180277076_C7	AACAAACOGCA	TTG CTG TACG ACT TTTG G TTTT TG AG TT-	AIGAATITTTTAA	TAAATAA	- TT CGG CG C AT CC		-AT <mark>TAA</mark> TAA <mark>A</mark> TTTT <mark>TAA</mark>	CTAAGT CIT CGAGTAAGC	TAGTG TTG TAAAAGG	GCSGT-C	S TAATACAG AAAATG	-AGCCGCTAAATTCAATG
503.	. ChLG10_R180277076_C15	AACARACCGCA	TTG CTGTACG ACT TTTGG TTTT IG AG T T-	AIGAATTTTTTTAA		-TTCGGCGCATCC-		- AT <mark>TAA</mark> TAA <mark>A</mark> T T TT <mark>TAA</mark>	CTAAGT CIT CGAGTARGG	TAGTATTG TAAAAGG	GCGGT-G	G CAATACAG AAAATG	-AGCCGCTAAATTCAATG
504	. ChLG10_R180277076_C13	AACAAACOGCA	TTG CTGTATS ACT TTTGG TTTT IG AG TT-	AIGAATTTTTTAA		TTCGG CG CATCC	-ACCATT TT CAACTTA	ATTAATAAATTTTTAA	CTAAGTCATCGAGTAAGG	TAGTG TTG TAAAAAGG	GCSGT G	G TAATA TAG AAAATG	-AGCCGCTGAATTCAATG
505.	. ChLG10_R180277965_C4	GAACAAACCGCA	TTG CCAACG ACT TTTAG TTTT TAGG TA	AIGAATTTTTTAA	TGAATAA	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		AAATAT TTTTTAA	-AAATTAT - CGAGTAAG	TAGTG TTG I <mark>G</mark> AAA T G C	CIGG T-	ATTCTARS CAATTIC	-AGCAGCAGAATTCACTG
506.	. ChLG10_R180277965_C6	GAACAAACCGCA	TTG CCCTACS ACT TTTAS TTTT TAG TT-	ATGAATTTTTTTAA	TGAATAA	CCCCC CC CATCC		AAATAT TT TT TT	-AAATTTTT-CGAGTARG	TAGTG CIG IG AAA TGG	CIIGG T-	ATTCTARG CAATTTG	-AGCAGCAGAATTCACTG
507.	. ChLG10_R180277965_C2	GAACARACOGCACT	TTG CTCTACG ACT TTTAS TTTT IG AG TT	ATGAATTTTT-AA	-TGAATAA	CCCGG CG CAT CC		AAATAT TTTTTTAA	AAATTTTTCGAGTARG	TAGTG CIG IG AAA TIG	CIGGT	ATTCTARS CARTTG	AGCAGCAS AAT T CACTG
508.	. ChLG5_R180282711RC_C4	GAACAAA <mark>T</mark> OGCA	TTG CTCTACS ACT TTTASC TTT IS ANAT-	ATGATTTTTTAAA		-TTT <mark>CC CC CATCC</mark> -		TAAAAATRA <mark>GCC</mark> TT <mark>T</mark> AA	ATAAGTTCICAAGTCAA	TATIG TIG TAAAAATG	GC AC	ATAACACE TAAAATA	- A AT CG AGA AAT T TG C FG
509	. ChLG5_R180282724_C3	GAACARACCGCA	TTG CT <mark>S</mark> TACS ACT TTTAS TTTT IS AS TT-	ATGATTTTTTAAA		-TTTGG CG C AT CC		<mark>T</mark> ARAAA TAA <mark>KE C</mark> TT <mark>T</mark> AA	- A <mark>T</mark> AA <mark>GTTC</mark> TTAA <mark>GTCAA</mark>	TATIG TIG T <mark>A</mark> AAAA <mark>TG</mark>	GC AC	ataaca t e taaaata	- A at cg aga aat <mark>C tg C</mark> tg
510	. ChLG7_R180285737_C9	GAACAA <mark>G</mark> CCGCA	TTG CTCTACG ACT TTTAG TTTT IG AG CT-	AIGAATTTTTTAA	-TAATAG	CCCGG CG CATCC	-ACCATT TTATAA TTTT	AAATAT TTTTAGAA	ATATGTTCTCAATTCAAC	TGGTG TTG T <mark>G</mark> AAAA AA	TTAGT	AAAACACACAAAATA	AGCCGC AAAATTCACT
511.	. ChLG7_R180285737_C6	GAACAAGCOGCA	TTG CTCTACG ACT TTTAG TTTT IG AG CT-	ATG AATTTT TT AA		CCCCC CC CATCC		AAA TA <mark>T</mark> TT T T <mark>AGAA</mark>	ATATCT TCT CAA TTCAA	TGGTGTTGTGAAAAAA	TTAG T-	AAAACACACAAAAATA	-AGCCGC AR AATTCA <mark>C</mark> F
512	. ChLG7_R180285737_C3	GAACAAACOGCA	T C C TCTACS ACT TTTAS TT C T IS AS C T-	ATAAATTTTT-GA		CCCCCCCCCCATCC		AAA TA <mark>T</mark> TT T T <mark>AGAA</mark>	ATATGTTCICAA TTCAGG	TE TIG TIG I <mark>G</mark> AAAA <mark>AA</mark>	ATAG T	ATAATACACAAAATG	-AGCOGC AA AATTCA <mark>C</mark> T

c) alignment of cluster 3

Consensus	1 10 20 30		77	100 110 120	100 140 150 110 AAACTAGAACGAAAAA	171 111 110 200 	210 210 210 210 210	260 290 270 290 •• TTA TREE CLARKET TTO TIANA 225 1945 CLARK 444	20 30 30 30 20 - WACAGAATTA 10 10 10 10 10
1. ChLG4_R180250662_C2	COTTO BAGAITTA	-LACAL GIGTTT	AGRECAL BAAT TAGT	TTR-IT-CT TGITTT ATT	AAACTA GAACGAAARRAA TCACARRA TITCH 7	CGAARA TRAC CAARRA ITTACCTT TOCTA	AGCONTTA TELAG CARADACACA	A TTA TROCACARABITIC TIAN BAG TRACOCRAMARA	TRACARA TT TA THE RAA ANA TOCC TIT TA THE
2. ChLO4_R190290962_C6	TUT ROTICORAGENTA	-ACA OTATT	AGACIAL LAA TILIT	TIP-II-IE INITIII ATI I	ABACTA GRACHAARAAR TURURAR TITOUT	CGAARANAG CAARA TTREETT TO TA	ANGUTTA TRUN CA-ARGIN	A THE TROTAL ASAGET TIC TRADE AND TRADUCE AND A THE TROTAL ASAGET AND A TRADE AND A THE TRADE AND A THE TRADE AND A THE AND A	- REALING AND IN THE A - AND THE CATTA TITT
4. ChLG1 R180275693 C1 5. ChLG1 R180275693 C2	TOC ALGETC TRAGGARERA TOC ALGETC TRAGGARERA	-ARCAN GETTTT -ARCAC GETTTT	AGATCAR BAAR ACREST	772-110CL SUITET AFE J	ABECTA GARCGRARARO -CACGARA TAYOG 7 ABECTA GARCGRARARA	CGAAR BAC CAARA STRACT7 STCTA 	AGCORTTA TELAG CABARACITA	A FER TENC CARAGETEC TECRARAM - INASCCAREARA A FER TENCCARRAGETEC TEARRAR - INASCCAREARA	— STACADAAT IN SANCAA — AAN FUR CA TTA TFIFF — SCACADAAT IN SACCAA — AAN FUR CA AFA TFIFF
8. ChLG1 R180275593 C4 7. ChLG6 R180283811 C3	TOC ARGINE TERGER TOR	-ARCAC GTTTTT -ARCAC ATTTTA	AGCCAL AAA CCART	TINGER GITTA ATT	AAACTA GAACGAAAAAAC - CAOCAGA TITOG 7 AAACTA GAACABAAAAAA CCAACAA TITOG 7	CGAAARTAC CAAAAR ITTACCIT IICA CAAARTAC CAAARR ITTACCIT IICTR	AGCETTA TELAG CHARACTON	A TTA TIGGE BARANITIC TIABARAG TARCOCANIARA A TTA TICTOCARANITIC TIABARAG TAGORCANIARA	– TAACADAAT 78 TEAA – AND TGACA TTA TITT – TAACADAAT 72 TE RCAA – AND TAACA TTA TITT
8. CHLOG R150283811 C6	THE ALGETTE THANKS TTL	-LACAC ATTTA	AGACCAA AAA- CCAAGT	TITICTITE TOITIT ATL	RARCTA GARCELAARRA CCATCARA TITOT 7	CAASAR TRAC CAASAR ITTACCTT THE TA	ASCOTTA TRUNG COLARS TRUN	A TRATECTOCARA STRUCT TARRAR - TRADUCER ISS.	TURCAGEATTR TO CAL - ARE TOR CATTA TTPT
10. ChLG8 R18028391T C2	TOC ABOTIC TRADUATTE	-ARCAC GATTIN	MACCAR ACA- CARST	TTRETTER CANTER OT	AAACTA MACGAAAAAA C-ACAAAA TTT00 7	CGAAR BRAC CAARA STREETT TTETA	ASCOTTA TECAS CABARACIÓN	A FER TERCOCAAAR STEC TEN BAARD- TRADECAR FARR	SCACAGAAT IN SUICAL -AND PACATTA TITT
12 Ch. G10 R180277974 Cd	TGC AASTIC TEARSTTA	A ACAC ACATTT	AGC DA AAA 7 CAAST	GTITETTIC TOITIT ATT	AAACTA GAACGAAAAAA TCAOCAAA 756067	CARAR TO CARARA CTIACCT? TICTA	ANTITAN ING CAAAAACICA	A TTA TREE CCARALITIC TTARAAA TTAACCCARTAAA	REACADAATTA TA REAA -AAA REACTITA TIN
13. ChL04_R160250548_C6 14. ChL08_R160256567RC_C6	THE ABOVIE TO A MAINTA	A ACAC GTICTT	ABRECKA BAAT CARST	TTICTIC RETTY AF	AAACTA GRACALAAAAA TOAGCAAA TITOO 7	CGLAR HAC CARAGE TIMECTT THE TA	AGCOTTTAT TEAG CARARACTER AGCOTTTAT TEAG CARARACTER	A TTA TROCOCRARA I TEC TTARARA - D TRADUCACTARA	- REACASSAT IN IS IN A A A REACTING THAT IT IT IT IN THE CASE AND A CASE AND
16. ChLG8_R160286567RC_C8 16. ChLG8_R160286567RC_C1	THE ARGINE THANKASTER	A ACAC OTICIT A ACAC OTICIT	AGACCAR BART CRACK	TINGTIC IGITIT OF	AAACTA GAATAAAAAA -CAUCGAA TTT99 7	CGAAR BRC CARAR STREET TICTA	ASSITTAT TAS CALARATIA ASSITTAT SCAS CALARCINA	a fer trougcarar effic tearra - 5 teagocar tear A fer tegegeraar effic tearra - 5 teagocar far	- Reaganan in ny koar -araanar ca tta ttett - Reacanaat in ny koar -araan-aca tta ttett
17. Chi Ga R180288587RC C4 2	TOC ALST TO AGAITTA	A ACAC DISCIT	AGACCAA AAA 7 CAACA		AAACTA CAACAAAAAAA - CACCCAA TITOS 7 AAACTA CAA-AAAAAA	CGAAA ELC CAAAA TTACCIT THE TA	AGECTIAN SCAL CAAAACCECA	A FER THE CORRAR STREET TARARA STRACCCAR SARA	- XIACAGAAT IN NU NUA ANNY CACA THA TANY - NUACAGAAT IN NU NUA ANNY CACA THA TANY
19. Ch. 65 R160296567RC C3		- A ACRC GTTTTT - A ACRC GTTTTT	AGRECAL BAAT CART		AAACTA GAATAAAAAAA - CACCAAA TTTGG 7	CORAR TRAC CARRAR STRUCT TT TA	AGEOTITAT TRAG CABARA TITA	A TTA TTO DCARABITIC TTARRAB OT ACCESSIBLE.	- TOACAGAG TTA TO TOAL - AAAAA- CATTA TIT
21. Chi G5 R1602965778C C4	The arguig ter ter ter	A ACAC QITTIT	AGACIGAN BART CRAST	TITICTIC TOITIT ANT A	AARCTA GRATERARAR -CAUCARE TITEST	COARAN TERC CANARA STRUCT TICKS	AS STITAT TESS CARAARTTA	A TTR TROPOCRARE TTC TTRARR. 9 T MOCCAR TARK	TORCADART'S BY TAR ARRANGE TRATTY
23 Chi G8 R180288587RC C8 2	TEC ALCENE TRAGGARTER	A ACAC GETTTT	AGAC CAL AAA 7 BAS T		AAACTA CAACAAAAAA	EGE CAAR PERCETT TIT	AGECTIVAT REAC CARCAN FER	A FER TREE CCARABITTE TTARAR STRATECRARAS	BCACAGAAT 25 SE SCAA- AAA AA A CA TTA TFFF
25. ChLG6_R160286567RC_C3_2	THE ARGUT IS INCLUDED THAT	A ACRC GTTTTT	AGREGAL AGAT CARST	TITET ATT	AGACTA GAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	-CGAAR BAC C-ARR ITECTI TIC IS	AGOTTAT TUAL CABARCINA	A TRA TISCOCRARA ITTO TIARAGE DI TENCOCRA IARA	- TRACAGAAT TA TE ECAS - AXAAGACA TTA TTTT
27. CHLG5 R18028667RC C7	TEC ALOTIC TOROGATITA	A ACAC OTTTT	AGACCAL AAAT MAGT	TTERTER POINT AT	ABACTA GRACELARRAN - RACCARA TITON T	Charlenge C-area street 77 - 710 a	AGENCITAT SCAL CARAGE TO	A TRA THU OCAMUM THE TRANSPORT TO OCCUPANT A	- REACASAAT IN NO REAL - AARASA CA TTA TITIT - SCACASAAT IN NO SCAL - AARASA CA TTA TITIT
28. Chi G3 2 N 18029886296C C4 29. Chi G3 2 R 18029886529C C5	TGC ALCTIC TEAGGAITTA	A ANC DITTT	TRACCAR ARA T CARS T	CTITUTIC IGITIT AND	AAATTA GAATAAAAAAA TYACCAAA TYYOO 7	CGARAGEC CARAGE STREECE 7 - TING	ANGESTITET SCAG CAAAAACECA	A TTA TROCK CARAGETEC TTARAGE 5 TRACCCRETAGE	- SCACAGART'S SU SCAL - ARCTULCA TTA TFS - SCACAGART'S SC SCAL - ARTULA CA TTA TFST
30. ChLG5 R160282057RC C2 31. ChLG8 R180289838 C2	TURALITZA	ACAC DITTTT A ACAC DITTTT	TRACCAL AND T CARD T	TTICIL GITTT -II I	ALLCTA GALLAARRA CACCAR TTTOUT	CGSAR HAC CARRENT TIMECTT THE TR CGSAR HAC CARRENT TIMECTT TO TR	AGCOTTAT ELAG ABARA CELA AGCOTTAT ELAG GABARA TEA	A TRATIC CARALITIC TTARE O TRADCCALCARA.	- KCACADAAC 78 KS KCAA - AXA KKACA TOA TTY - KCALALAAT 10 KS KCAA - AXO KOA CA TTA TTYY
32 CHL05 R16029636 C5	THE ARGENE THE THE	A ACAC GITTTT A ACAC GITTTT	AND COAR AAAC CRAST	TINGING TRITIT AT	TAL-TA GRACGAAAAAA	CAARA MAC CAARA ITTACKIT TICTA	ARESTING TRAS CARARCTER	CITE TECHCARA INTENTAREA - 5 TRASUCER INF 3 FER TECHCARA INTENT TO RAN - 8 9 CRASUCER INF.	- HIAGANATING HIAA - AND THA ITA TINT - MIAGANATIN NI KIAA - AND NACATIN TINT
34 Chi G1 R180276605 C7	THE ARCTIC DE COMPTEMENT	A ACAC GETTTT	AGCIAL BART CART	77220021- 2017201 A21 3	ABACCA CRAN-AAA AAA TAACCACACATTICAT	CGAAR GAL CAAR STRECT	AGCOPTTA TECAS CABARACTER	A TTR TROCOCRAR STERIT TTARE A CARCOR STAR	SCACALART'S SC SCAL - ARE TORCA TR TTPP
36. Ch. G1 R160273605 C1	TE TE CALL TTA	-A-ACAC		TITIOIT RETTO ATT	ALLCAN CARLANA AND TROCACA TTOOT	CGAAAA MAC CAAAAA ITIACCII IIII		A TTA TRECOCARABITIC TTARA - AGAAGCARATAAA	XIACARAAT TO THE RAA - AND TAACA TOA TTET
38. CHLG6 R160294461 C4	TTA AN TIT TO AN ATTA	A ACAC GITTTT	AGACCAR BART CRAST	TINGTOC SATIS	ABBCTR BRACEBAA-ASA TTACSARATATTO-T	CGAAR-GAC CAARA ITINCCTT TICT-	ANGETITA TICAS CABARACIAN	A TTA TRECOCARABITIC TIARAR - A TRACCARIAR	REAGAGAAT IS IN ICAL - ASA ITA CATTO TIT
40 CH G3 2 R180207259RC C2	TOC ARGUITER	A ACAT GTTTT	AGATCAR ASA T RAST	TITICTIC GITTLE ATT	ABACTY CARDEAR AND TRACCARE CTTCC 7	CARAN SEC CAMER IIIICCT IICT	AGCOTTATION ANALASCET	A TTE THE COMMENT OF THE ACTION AND A DESCRIPTION AS THE THE ACCARTER AND A DESCRIPTION AS THE THE ACCARTER AND A DESCRIPTION AS THE ACCARTER AND AS THE ACCARTER AND A DESCRIPTION AS THE ACCARTER AND A DESCRIPTION AS THE ACCARTER AND A DESCRIPTION AS THE ACCARTER AND A DESCRIPTION AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER AND AS THE ACCARTER	SCALARA ACCASS SCAL - ARE TRACK TO THE
41 Chi G3 2 H1602972538C C3 42 Chi G3 2 H1602872538C C4	THE ABOTTE TEACHTA	A ACAT ATTOTT ACAT DITTIT	AGRECIAL ASA T TAST	TTTT TIL TUITIT AT	AAACTA GAALABAA AA	CARAR HAC CARACE ITIACCIT TIT	ARCOTATA TING ARAAACTI	A TTETTEC CCAARE TTC TTAN IN - RO TRADOCRETARIO	TUARAAATCA TU TUAR - AAG TUALA TUA TTATT TUARAAATTA TI TUAR - AAG COLCA TA TTAT
43. ChL03_2_R180287253RC_D5 44. ChL03_2_R180297253RC_D5	THE ALTIC TACHATTA	A ADT GITTT	ADRECK BAAT BABT	TTICINC INTIT AND	ARACTA GREC-LAA-RAA TYACCRAR GTTTTT ARACTA GRECGRAR-RAA TYACCRAR GTTGG 7	CGRARERAD CARDLE TTECCTT TITLE CGRARERAD CARDLE TTECCTT TITLE	ANGESTITA TICKS CLARKERY	A TTETTO CCARLETTC TTALE - A GTLAGOCRETAR -	- ICARABATCH TETERG - AND THE CATTA TTHE - ICARABATTA IS ICAR - AND CATTA TTHE
46. ChLG7 (180288115 C9 46. ChLG6 (180283544RC C3	TGC AAGTIMUAGUATTY TGC AAGTIMUAGUATTY	A ACAR OTTTT A ACAR OTTTT	AGACCAL LAAT CLAST	TITCIC CONTENT AND J	AMACTA GRACINAATAAN CACCAAR TITERT AMARTA GRACINAA AAN TAACCAAR TITERT	CGARAR SEAC CARRA STERCTT TICT CCARRA MAC CARRA STERCTT TICT	CASCARTA FECAS CARAACCER CASCARTA FECAS CARAACCER	A FER TENCOCRA THE TECRETARIAN - A TERAS COAR FARA	- SCACABAAT IA SI SCAL - AAA KIR CA TTACTIF - SCACABAAT IA SI SCAL - AAA KIR CA TA TTACTIF
47. Chi 06 R160283544RC C5 48. Chi 05 R160283544RC C11	THE ALT THE ALL TTA	A ANC DITTT	AGACCAA AAA.T CAAS.T AGACCAA BAA.T CAAS.T	TITCIC SUTTER AT	AAAATT GAACAAAA AAA TCACCAAA TTCAT AAAATA GAACAAAA AAA TCACCAAA TTCAT	CGAAAN TAC CAAAAA ITTACCII IICI- CGAAAN MAC CAAAAA ITTACCII IICI-	CAGCARTTA TELA CAGARACICA	A TTA TTO CCARAGE TTC TAARABA TAACCCAR TAAA	– KEAGARAAT 78 KE KEAA – AARKAALA TTA 77 KK – CEAGARAAT 78 KE KEAA – AARKAALA TTA 77 KK
49. Chi Ge R180283544RC C2	THE ASSISTED AND THE	A ATAC GITTTT	AGRECAL LAAT CARST	TITICIC PRITIT AT I	REFET ORECELAR-RE TOACHARE TITOP7	COBARS HIRC CARSES ITTACCTT TTCT-	GANCOTTA TELC CAGARACIÓN	A TTA TROCOCARA I ITA TTARA - A TRADUCAR I ARA	TRACK BATTS IN ICAL - AXX TOR CATTA TTIT
51. Chi Ge R180283544RC C8	THE ARE THE RANGE THE	A STAC GETTTT	ASACCAR AAAT MAAST	77272021C 2017217 AG 3	ABBRITA GRACEBAR-ARE TRACCARE 27799 7	CGAAR MAC CAARA STRACCT? TTCT-	CACCULTA TECAC CACARACTER	A TER TENCOCRARATE TOTAL A TRANSCORD AND A TRA	SCACABART'IS SUBCAL - AND THE CATTA FFIT
53. ChLOG R160283544RC C9	THE AAATTEINAGATTEA	A CTAC STITTT	AGARCAA AAA7 AAAST	TITLING STITT AT	AAAATA GAALGAAA AAA TTAOCAA TTITOG ?	CGARAN TAC CARANA ITIACCTT THE T	CASCETTA TELA CASAAACTA	A TTA TREE GEARART TTE TTARA A TARE CERTIAN	CLACADATTS TO ICAA - AAA TORCA TAA TFIT
56. CHLG6 R160283544RC C10	THE ALL TIMOLANA TTE	A GTAC OTTTTT	AGACCAL LAAN MAGT	TTITICITCE TOITTT ATT	ALLET GALCONA-ARE TCACCARE TITOS 7	COLARS BIAC CARARS OTILCCTT TTCT-	RAICIGTTA TRUS CABASACION	A TTA TROCOCARABITIC TRABA-22 TRACCCRATARA	VERSEARCE IN ICLE - ARE THE CATTA TITE
57. ChLG4 R180280882 C5	TOC AND TO TRADUCE	A AGAC GTICIT	AGRCCAR ART CRAFT	TITICTEL TOTAL AND	ALACT- XMACALARAX TCACCARATOT-ANT	CARAR BRAC CARARA STERCATT THE TA	AGCETTA ZON CALARCEN	A SAR TESC OC CCAR STEC TRABARS - TRACKCAR SARA	SCACABATTS SATAA AAA TORCATTA FFF
59. ChL05_R1602837578C_C4	TEC AND TE TEACANTTA	A ACAC DITTT	TRACCAL AAAT CAST	TTTTTTCC TOTTT AT I	ACAT - ACAACCAAAAAA - TCACCAAATT CAT-	CALAR SIA CCARR STERCET THE TA	AG CARARCTER	A TER TREE OCARAGE TEC TRABALE TRAECCRACALA	- SCACARARTIN SCHLARART SCACE TA FIN
50. ChL96_R160283767RC_C2 51. ChL96_R160283767RC_C3	TOC ARGITE TURGERITTE	A ACAC OTTTT	TRECAL BART CLAST	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	ALLCT CARGARCHAARAR TCACCAR TT-00 7	CALL OF THE COMPARE ITERCITY THE TA	AG CALAAA CIAA	A TTA TTA COCARA A I TTC TTARARA - TRADOCRA CARA	- TUAC GAAAT 78 HI KIALAAA TUR COTTA TTIT - RCACATAR HI KI KI KI KI LAAA TUR CA TT T TT
82. ChLOS R1602837678C C5 83. ChLOS R1602833678C C4	TCC AAATTTIGAGAATTA TCC AAATTC THAAATTTA	A ACAC ATTTT A AC- OTTTT	AGACCAL LART CLART AGACCAL LART CLART	TITITIC C CLINIC CI I	ABACT- AMALGAARAR TCADCARATT-007 ABACT- AMACGAARAR TTACC RATT-007	CRAR BAC CARAR STREET TICT	AG CARTTATICAG CARAGACAM	A TTO TTO I TO ART TTO TTARAAR TARGECAR TARA	— KCACADAAT 78 KO KCAA - AAA - KOACA TTA TTAT — KCACADAAT 78 KO KCAA - AAA - KOOCA TTA TTAT
84. Chi G5 R180282204 C5 65. Chi G8 R160289836 C4	TGC ALCONE TEAGLACTEL TGA GAATITIAGAATETA	ACAC CETTT	AGACCAL BART CARST	TITETE CONTENT AND I	AAACT AGACCARARAA TCACCARART GG 7 AAACT AGECARARAA TCACCARARTITEG 7	CARAR SEAR CARARA SCREET? SECT.	A 50 AAAAACTCA	A FER THE COCACARITY CITARRAN TRACCCARIAN	— SCAR GAAT IN SU SCAA- AAA- NACA TTA TINI — SCACAGAAT IN SUCCAA- AAA- NACA TTA TINI
55. ChL06 R160283357RC C3 67. ChL08 R160283567RC C5	TOC ARTITURARTYA	A ACAC OTTTTT	AND CAR BART CARST	TTTTITC TOITIC ATL	ALLCT - AGAOCOLARRA TTACCARETT- 00 7	CLARS DAC CONSERVED THE TO THE	AGCOTTATION ALLARACION	A TTA THE OBARANT TIC TTAR DAG. TRANSCRADARA	– YEA-AAAAT 78 HEAAAA AAA - YAAA TTA TTIF – HIABAGAAT 78 HI HIAA - AAA - YAACA TTA TTIF
88. ChLG6 R180283357RC C2 89. ChLG6 R180289648 C2	TOT AN TITGE AGAINTA TOC AN TITCH THAT A TITL	A ACAC GITTIT	ANTARA AAAT CAASA	TITITCC TOITIC AT A	ABACT- AND COMMANNA TOADONA TT-96 T ABANT- ACAACCAARANA TOACCARATT- AN T	CAARA BOC CAARA TIMCCTT TICT	AGCSTITATICCOC ARAAA-CITA AGCSTITATICAGC ARAAACICA	A TTA TTOCOC TOART TTO TTARARAD TRACCAREARA	- XCACAGAAT TOTO TCAA-AAA - TGACOTTA TTYT - MGAC GGAAT IN III III III III III
70. Chi Ga R180289648 C3	THE ALTER DEACHARTE	A ACCA GTTTT	AGACCAL AAA 7 CAAC	TITUTE AT A AND A	AAAR - MEARCAAAAAA	CAAAA MAX CAAAAA III CII III III	ACCENTATIONS ANAAACTO	A TRATECICARABITEC TIARRABI TRAECCARTERA	- ACACAGAAT 28 SCAA-AAA- 2 COATA TA TTE - ACAGAGAAT 28 TO TO A-AAA- 2 CAATA TTA TTE
72 CH 08 R160269645 C4	THE ALL TO THACKAT TTA	A ACC OTTTT	AURCEAL BAAR CARG	TTTTTTTT	ABART ROARCORARRA TOROURART TO TO	CEARS HEAC CEARS ITTACTT THAT	ARCONTTATION - ARAAR CIGA	A TTA THE CARABITE TTARRAD TOM MARKAN	- TUACHGAUT TANK KCAR-AAA - TAACA TTA TTF - NCACHGAAT TA TT TCAR - AAA - TAACA TTA TTF
74. Ch. 01 R180276503 Ca	THE AN OTIC TRANSATTER	A ACAC GITTIT	AGACCAR BART CRARG	TTITITIT TIGITATT ATT	AMACTA GRACGAAAAAAC -CADCAAA TITOG 7	CRARATERC CARRA TTERCTT CONTR	ASCOTTA TINAS CARAARC- TO	A TTA TRECOCANG-ATT TO TANAAA STANSTONA TAAS	TREADANT IN TON AND AND TON CATTATION
76 ChLG1 R1802/5583 C8	TOC ACCTIC TEARACTIC	ATACAC GITTTT		TITLE GITTL AT	AAACTA GAACAAAAAA - TACAAA TITGG 7	CGARAN REAC CARARA ITTACK 7	ACCENTIA TICCE CAAAAAC	CTR THECECCEA - ATT ICI PARARE IS ACCCRATARA	KACAGAA 73 K KAA AAA KARA TA TIT
78. CHL09 R180282001 C1	TC TUR BATTL	A ACRO OTTTTT	MIRCOR BART CREST	GTOTITIC CAGITITT ATT	ALL TR OL C-BARREN TOAGGRAD TTOAT	CGRARR HEAC CARREN ITTAC TT TTTT	AGCOTTA TELAG CABARRO TT	A TTA TRICOC CCI - ATT TCT PARALA TRANC-ALTERA	TALASSAT 78 HI SCAL ARA TOACA
60. Chucs R160292001 CE	TOC ANGOIN THE	A ACAC QTTTT	AGREAL AART CRAST	TTTTTC CASITIC AT	ABACTA CARCANA TOACTAR TITOT	CGAAR SAE CAARA ITECCTT IICTA	AGCOUTT TECAS CABARACE-	A THE THE GOLDAN - ATT TTALALLE TRADUCER THE	CACAGEATE IS INCLES AND THE CACE TATIF
82. Childs R100292001 CS	THE BOTTLE TRACETTER	A ACAC GETTTT	AGACCAL AAAT CAAST	TITITE SGITIT AT	ABBOTA GARGE RARE TOACTAL TITLE T	CGAAD SAC CAARA TESCTT TICCA	ACCUTT TEAC CALARC	A TTR THE GEAR AT TALAAAACA TAACCCA GTARA	- KACAGAATIN XANAA AAA TIRCA TATITI KACAGAATIN XANAA AAA TIRCA TATITI
83. ChL09_R160282001_C4 84. ChL09_R180282001_C6	TOC ALOTIC TORGENTITA TOC ALOTIC TORGENTITA	A AC- DITTTT A AC- DITTTT	AGRECAL LART	TITT ATL	BARCTA GARCHAARRA -CASCRRA TITOS T BARCTA GARCHAARRA -CASCRRA TITOS T	CGRARA BILC CARRAR ITILCCTS TTC TA CGRARA BILC CARRAR ITILCCTS TTC TA	AGCOTTT TICAG CALARAC	A TTA TROCOCARA CA TTACT CARAGAS TRACCERATARA	- TOACHDAAT 78 III ICAA - AAA - TOACHDAAT 77 II - TOACHDAAT 78 III ICAA - AAA - TOACHDAAT 77 III
86. ChLGS_R160292001_C7 86. ChLG1_R160275605_C2	TOC ALGETIC TOLOGALITIA TOC ALGETIC TOLOGALITIA	A ACAC OUTTT	AGACCAR RAAT CRAST AGACCAR RAAT CR-T	TITITO CAUTTY AT A	AAACTA GRACEAAAAAA CAACAAA TITUG 7 AAACTA GEACGAAAAA TCACCAAR TITUKA	CGAARA ERAC CAARAA TTEACUTT TIUTA CGAARA ERAC CAARAA ETEACTT TIUTA	ASCENTE TICAS CARAACC 70 ASCENTES TECES CARAAC	a fer teo ocaz – ite ett de barre e tragucar fra -	- KLACADAAT 78 KERA-AAA - KACA FA TTIT - KLADAAT 78 KEKAA-AAA - KACA TTA TTIT
87. Chi G1 R180276605 C4 88. Chi G1 R180276606 C6	TGC - AACTIC TCARCATTEA GCC - AACTIC TCARCATTEA	A ACAC CETTT?	AGCCAL ART CL. T		AMECTA C-ACCARARA TCACCARA TITCAA	CCARAR SCAC CARARA STRATCT? STC TA CCARAR SCAC CARARA STRATCT? STC TA	ACCOUNCE THE CAASAR	TTER TTE COCAR - ITTE IT BARARE TARE CARDINA -	— EC CAGAATTR EC CAA-AAA - FACA TTA TTEF — EC CAGAATTR EC CAA-AAA - FACA TTA TTEF
89. ChLG5 R160282864RC C3 80. ChLG8 R180282884RC C6	TOC ALGUE TOLGAITTA	A ACAC ATTTT A ACAC ATTTT	AGRECAL BAAT CARST AGRECAL BAAT CARST	TTITICIT COITTL ATL	ALLCTA GATGLAARARA TCACTARA TITOS 7	CLARR BLAC ARAR ITTOCTT TECTA	AGCOTTA TRIAG CALARAC	a fta tto decara - a c t toc t araa f t taa to cra d aa A fta tto cara - a c t toc t araa f t taa t cradaaa	– YEACAGAAT 78 WICCAA-AAA-YEACOTTA TTYY – YEACAGAAT 78 WICCAA-AAA-YEACOTTA TTYY
91. ChL 65 R160292964RC C4 92. ChL 65 R160282864RC C2	TOC ARGITC TOROUR TTE	A ACAC ATTTT	AGRECAL BART CRAST	TITITI - TOITI AT A	ALCON CALENCER STORAGE STORE	CGAAR MAC CARRA ITERCTT TICTA CGAAR MAC CARRA ITERCTT TICTA	AGCONTTA TECAS CABARAC CO	n yyr yyg yrgerar - ac y ycc y rrar y y chrona ar	- Yaqaqaat 78 Toolaa - Aar - Taqotta TTTT - Yaqaqaat 78 Toolaa - Aar - Yaqotta TTTT
93. Chi G5 R180282884RC C8	TOC ARCEL DEACCASTER	A ACAC ATTTT	ACACCAL LART CLAST	TITIATIC CITILS AND	ALCONTA GARGAAAAA TURCCAAC TITEC 7	CARAR SEAC - DARAR STRACT TO TO TA	ACCUTTA TECAS CAASACC	A THE THE DECAME AND A THE THE AREA OF A DECAME AND A THE THE COMPANY AND A THE THE AREA AND A T	- SCACAGAAT IS SCEAL AAA - SCCA TTA FFIT
85. ChLG5 R160282057RC C3	THE ALOT TO TRANSPORT	A ACCT ATTTT	AGC DAR TABBAR T CARD T	TTTTCTC- CTGITTTT ATT	ALACTA GASC - LAGRAR TCLINGAL TITOS 7	CRAAR MAC CAASAR STRATT TO TA	AGCOTTON TELAS CABARAG	A TTA TTOC & A G	TIACAGAAT TA TATATA AGA TAACA TTATTIT
17. CL 810 B180278201 C4		A ACAC OTTTT	DACCAR ARAT CRAPT	TREATE CONTRACT	ARE TR DRACORARRA TROUCARE TITIO 7	CRARK WAR CARREN - TACCTT TTUTA	ACOUTTA TIMAS BARARGEN-	A TTA TTOTAL ANA - ATT TOT PARAGE TRACTING TAR TARA	TURURAN TAXATURA AR- TERCATTATTAT
99. Chi G10 R180278291 C5	TCC ALL TIC TCACCATTAL	A ACAC GTTTTT	TRACCAL BART TRACT	TICTITE CIGITETT APP	ARE TA CRECCERRER TO TOACCARE TITOS 7	CAAAA SCAC CAAAAA - SACC77 - 250 78	ACCRITA TERG BAAAACE	A FER TROPACARA - A TE DE PARAGA PILA CCAR SALA	SCACAG ATTS SANCAA - AAA - SACA TTA TTEF
101. ChLG10 R160276281 C2	TOC ALGUIC TOLOGA ITTA	- A ACRC OTTTTT	AGAEGAA AAA 7 AAG T	TITITICE CIGITITE ATT	AAA TR GAACGAAARR TTA CRAS TTTOE 7	CGAAR BAC CAARR ANTATIT TIC TR		A TTA TTO ACARA - OTT OT - ARAAA TRAECCRA FARA	REACASSANTER TREAS AND THE CATTA TITE
108. ChL07. R180296193_C4	THE ARTIC HARDEN THE	A ACAC CITTT	AGREGAN ANAT CRAST	TTHETTE BIGITIT AT	ALOTIA GALCALARA TOAUCARE TITOUT	CGAAR THAL CARRA TITLOGT TICTA	AGEDTITA THEAD CA-ARACC	A THE THE CLARE - ATT IS TRANSPORT AND THE THE	REALEDRAT IS IN REAL ARE THELE THE
106. Chi G7 R180286193 C3	TOC ALGENE TEAGLETTEL	A ACAC CITTTT A ASAC 2TTTT	AGACCAL BART CRAST	TITETTE CIGITATE AND	ABOTTA GLACGARADA TCACCARA TITAN T ABOTTA CARCERRAR TCACCARA TITAN T	CGARAR MAC CARARA TIME TT TICTA	AGEGETTA TECAG CA-AAAAC	IN THE TRUE CARD - ATT TO PARABAS CONCERNMENT	- SCACADAR THE STREET AND THE CARE A THE CARE A THE - SCACE GAR THE STREET AND A THE SCALAR A TH
106. ChLG7_R180296193_C8 107. ChLG9_2_R180296652RC_C2	THE ALL TO THE AGE IT THE	A ACAC CITTIT A CCAC GITTIT	BACCAL AAAT CAASA BACCAL BAAT CAAST	CTITITIC CIGITIT ATL	AAGTTA GAACGAAAAAA TCATCARA TITGGC	COLAR DEC CARRE ITESC IT TECT	AGCATITA THAS CARAAAAC IC	A TTA TRECOCAAL ATT TO TAALAAS TAACOCAA TAALAA	TCACAGAGAAT TATG ICAA AAA TABCAAT ITTT TCACAGAGAAT TA TI ICAA AAA CGACAATA TTIT
108. ChL04_R150280548_C3 109. ChL04_R150280549RC_C7	THE ADDIE TRANSFITTE	A ACAC OTTTT A ACAC OTTTT	ARCCAR BART CRO-	TTITIC CALIFIT AF	CARCTA GRECHAARA TCACCRR TITLIT CARCTA GRECHAARA TCACCARE TITLY 7	CGRARE THAT CARRE ITING TT TICTA CGRARE THAT - ARRES ITINCCIT TICTA	ANCATTA THEAS CALARAC 70	a ita teococada – Aiti ni kaaaas ta ni caa iaa a tia nococcaa – Aiti Titaaaas ta Asucaa iaa	- TCCCLOLAGYR THCCLL ARR TO CL TT TT - TCLCLAGART IN TO LL ARR TGLCL TT TT
110. ChLG4_R180280549RC_C3 111. ChLG3_2_R180296852RC_C3		CCC CLERTY	AGACCAL LART CLL	CITERIAL CREATER APR 3	ALLCTA GLACGLARACE TURCCARA TITU 7 ALLCTA GLACARARAC TURCCARA TITUC 7	CALAR SA AAAA STRACT7 STC TA CALCAS SEAC CASAAA SCCC: 777 750 TA	AGCONTA TECAS CARAGO	A THE THEORY CARE - I THEORY CARE AND TRADE CONCERNED.	- SCACAGAAT IN SU SCAA-AAA - FOR CAT - SCACAGAAT IN SU SCAA-AA <mark>A</mark> - FOR CA THA THIS
112. ChLG4_R180280549RC_C5 113. ChLG4_R180280548_C4	16 - Argy 10 16A gg 1 17A 1 0 - Ar 67 10 Tex 66 1 17A	A ACAC GTITTT A ACAT GTITTT	ARCCAL ART CAL ARTICAL BRAT CAL	GTT SITUT AT	CAACTA GAACAAAAA TTACCAAA TITUS 7	CARAAR IGAC CARARAR I TITAACT7 TIC IC CORAAR IGAC CARARAR I TITACCT7 TIC IX	ACCETTA TECAS CAASAAC	a tea tege acaaa are tee taaa gaa taar cora taaa	– ICAC BAAT 28 IG ICAA - AAS - IGACA ITA TI IT – ICACA BAT 28 III ICAA - AAS - IGACA ITA TI IT
114. ChLG6 R180283911 C4 115. ChLG6 R180284491 C3	THE ARGY TO A GO THE	A ACAL GITTI	ANACCAL LAAT CLL	-TITITICTT CIGITITT AFT	CARCTA CARCARARA THACARAR TITUAT	CGLAR MAC CANAR ITECCT TICT	AGESTITA TELAS CALARAG IN ASCETITA TELAS CALARAG IN	r ter tege zerr - ett stitter i skrivere ser	- Yealay batts in feat. Are - if catta tter - Nealay batts in flat. Are - Neala tte Tter
118. Chice R180284461 C5	THE AREA TO DEADER THE	A ACAA GROTT	AGACCAL LAAT CLO-	-TERETT CREETE ARE A	ALLCTA BRACGLARANG TULCANA TITOS 7	CORRANNAL CAADAA FURCHIT TU TU CAADA MAC CAADAA FURCHIT TU TA	AUCOUTA TECAS CARAAC UC	A FER THE COAR - THE COMPARES THAT CAR FEE -	- SCACAGAATEA SCALAAA - NACATA TINT - NACAGAATEA XACAA - AAA - NGCA TA TINT
118. ChLG8 R180268747RC C3	TOC AASTIC TARGEAT TTA	A ACAN GGTTTT A ACAN GGTTTT	AGACCAL AAAT CAAST	-TATCOTTY CTGITTIT GTT /	AAACTA BAACGAAAAA TITGG CCAAA TITGG 7	CGAAAA MAC CAAAAA TTATCTT TICT	AGCETITA TELAG CABARAC	A TTA THE CARA STATE TO ARABA CASE COAR TANA	TRACAGAAT TA TRACGA AAA TRACATTATTAT
120. ChLGe R190288747RC C2	THE ALL TO TARGET THE	ACAR DOTTT	AGACCAR BART CREST		ALLCTA RECHARRA COCCAR TITCAT	CGRARE MAC CARRES TTERCIT THE T	ANCOTTA TRIAS CALARAC TO	A TTR TROCKIARA - TTY TTY ARRANGE TRANSPORT	TRACASSAT 78 TRACAS AND TRACATTATIT
122. CLC8 R180288747RC C4	THE ARCHIGANARTH	A ADA GOTTT	AGACCAR AAA7 COMMCTOTIC	TOTALCONTE CROINETT ONE	ALLCTA PARCELARAR TOCCCARE TITIG 7	CGAARA MAC CAARAA PERATCIT IN TO	ASCOUTA TECAS CARAAAC DC	A PER TROC L'AND - NOV DICTIONNAND TRANSCOM TANK	CACAGAATTA NALCA AAA WALCA TTA TTAT
124. ChLG8 R180268774RC C6	XICA TTOC ALGINE TO ALTRA	A ACAN GOTTTT	AFACCAL AAAT CAAST	TRICCITT CIGINGIT ATT	AAACTA AAACGAAAAAA TCACAAAA TTTOGT	CARAN MAC CARANA ITTACCTT TTCT	AGCETTA TECAS CALARAC	TES TROC CARS - TO TRADA SA TA ACCESS TANA	EXACAGARATES CARA AND AND A TARTAT
126. ChLG6 R150265774RC C2	THE ARDITE TRANSFITTE	A ACAG ATTTT	AUAUGAR BART TREDT	-TITIONC CONTRACT AND	REALTA DE LARRA TURURAR TITO 7	CGARRENAL CARRE TIMETT TO TO TR	ARCOTTA TREA CARARG 70	A TIN TING A DAR - ATT DU TARABATI DAI CORÈ TÈÈ È. A TIN TING A DAR - ATT DU TARABATI DAI CORÈ TÈÈ È.	TINGALANT IS IN THE ARE TRUE TRATIT
128. CHLG8 R180288774RC C4	CC-ARCENC TEACCA FTEA	A ACAC ATTTT	ACACULA AAAT CAMAT	-TITICAL CREATER AFF	ALLCTA CARCEARAA TULCUAAA TITOG 7	CARAGERAC CARAGE STECCT TO TH	ARCOTTA TELAS CABARAC TO	N THE TROCK CAR - AND TO THE REAL OF THE REAL OF THE PARTY OF THE PART	- Real and the second and the statement of the second seco
128. ChLGIO_R180288774RC_C3 130. ChLGIO_R1802277087/RC_C7	TOC ASSTITUCE CLAITER	A ACAC ATITIT AACAC ATITIT	ALCONSCION AND TO CARET	TITICIT - IICT ATT	ABACTA BAAGAAAAAA TICACCAAA TITOG 7	CERAM DAG CANANA ITIACHIT TICIC COLANA HAC CANANA ITIATIA TINGT	ARCOTTA TEAS CARARO	ALL THE CONTRACT TO TAMAGE THE CONTRACT OF	Disustanta TRACAS ASA INSCATTA TIT
131. ChLG6_R180283968_C6 132. ChLG6_R180282087RC_C7	THE ALGET THE MALE TH	ALACAC GITTTT ALACAC GITTTT	ANGCOR BART CREST ANGCORE BART BRANT	-TITIOT- CONTINT ARI	RABUTA MARCHAARAR TEAGERRA TITONT RABUNA BRANAARAR TUAULARA TITONT	COMARK MAD CARREN IT- CAT TITC	AMUSTITA TICAS CABARA - ICAL AMUSTITA TITAS CABARA - ICAL	- TRADITICUS ARABITIC TIAGA COTARA C. CANTARA	- RUBLED BATTR IN RUBL ARR - T RUBLED BATTR IN RUBL ARR - RUBLED IT A 75 FF
138. ChLG5 R190292097RC C8	THE ARGENE THAN AND	ARRIN GETTT	AGACCAL CAAT CLAST	-TEFECET- CERCETETT AFE J	ABECON GRAEGAAAAAA TURCCAAR TITOOT	CGARAR BRAC CARRAR STE-SCOT TINCE	ARGCARTTA TERS CARARA	- EAR TEGC OCARABLETEC TITARAR EU LA CO -CAR EAR	- SCACABAT IN SUBCAB. AAA. SIRCA TTA TITE

134 CH C4 P189290301PC C3		TOTI NAME	0	Maccaa	BANT-CAR	-78111	T- 70 7977777	ATT MACTA	SOCCOLANSES	TT02223 TT027		777.72	ALIGTITA TIMO CHARACTING	- TTO TTO PRABA TITO TRABA CONTRACTA	
135. ChLG4_R180260201RC_C6	THE PAGTIC TORNER TT.	ABACAC	ATTTT	AUX TOAL	AAAT MCAGE	TITIC	T- CONGENEET	ATT ABACTA	GRAC GRAANNA	TCACCARA TITOST	CGAAR MRC CAARA TTELCTT	TTCTA	ANTOTITA TITAS CARARAG- ITAS	- TTUTTOC ACAAAATTIC TTAAAAAQCAAQC -CAATAAA	TRADAGAAT 78 19 1788 - 888 - 178 CA TTA TTY
138. ChLG9 R180291764RC C2 137. ChLG9 R180291784RC C3	THE ARGENE TRANSACTOR	MACAC AC	111177 111177	A26-38A	AAA7 BAAT			ATT ALCON	BACGAAAA	TCA CAAR TITOS 7	CARAR SEAC CARARA STRACTT	25C 72	CCCCTTL TILL CALARC ILA	- FER TEQCOCARAR FITC TORARAGO TARGO CAR HAR	- TAC BAAT 25 STAL AAA TO CACTA TFT - TACACAAT 25 STAL AAA TO CACTA TFT
138. ChLG8_R180291764RC_C7	TGC AASTIC TEANAITZ-	ALATAT	GTTTTT	CTA- BA	AAAT BAAGT	-77770	T- CCRGITITI	ATT AATCT	ARCEARAG	TCATCARA TITLE ?		TICT	GECETTA TYPAT CAASAAC- YAA	- ITA TRECECARAATTIC TEAARAAGTAAG	- PRACASAAT IN IS ICAA - AAA - IS CAATA TITT
138. ChLG8_R180291764RC_C4 140. ChLG8_R180291764RC_C5	THE ABOTT TEAMATT	ALACAC	GITTTT	ATR-CRA	AAAT BAGG			CTC AACCTC	AACGAAAAGA	TCATCARA TITOST		TICT	BICGTTTA TYPAT CARARAC TARA	TTA TROCOCARABITIC TAARA GIA GE CRAINAA	TRACAGAAT TA TE ICAA AAA TO TATATT
141. ChLG9_R190291794RC_C8	THE ARGITE THRASANT-	ALACAC	WAITIT	ATA-CAA	BAAT BAGT		T- CONGENEET	ATT ASTCT	TRACQUARKAR	TCACCARA TITOS	CAARA TRAC CAARA TTENCOTT	TTUT	AUCOTTA TATA CABARAC- YAR	- TTR TIGC OCRARA TTIC TORRARA TAN OC-CAR TARA	TRACEBRATTA IN ICAR ARE TO CREAT ATT IT
142. ChLC10 R190277097RC C8	OC ALGUNC DERARD TE	MARAC	CHITT?	LGACARA	AAAT CAAGT	-72220		ATT ALLETS	TRACOL PLACE	TCACTARA TCINE 7	CGA TAA SEAC CAAAAA STEA		ACCUTTA TURAS CARARA SCAC	- TEA TROBECAARA STREE TRABARAS TOLOG- CAR BARA	- SCACAGARTON SOUCAL ARR
144. ChLG4 R180260058RC C7	TEL AAGTIC TEAACAITT	ALCONC	GATTT	AGCORA	AAAT CASS	-77770	T TGITTIT	ATT ASACTA	GAACGAAAAAA	TCACCARA TITGE 7		TTT	ARGCATITA TICAS CARARAC ICAR	TTA TIC TCARA TITIC TTARARACCA CC CRATARA	TEACAGAAT TA RECTAA - AAA ACCEATTA TTR
145. ChLG4_R180280055RC_C10 148. ChLG4_R180280055RC_C17	THE ALGENE THAN ATT	ALC: AC	GUITIT	ABCCRA	LANT CAGE	-77770		ATT ASSCTS	GAACGAAAAAAA	TACCARA TITOST	CGAAAR WAC CAARR TOTIC TT	7777	BRICHTTTA TREA CALARAC TEAL	TTA TTO POCARA TI TTC TTARRACCE OC CRATARA	WINCHSART TO WINCHA AND AND CATTA TT IN
147. ChLG4_R180260056RC_C6	THE ARGITE THAN ATT-	ALACAC	GATTTT	AGCCAA	AAAT CADAG	TITIC	T- TOXUITIT	ATT ABBCTA	GRACGAAAAAA	TAXAR TITOST	CGAARA TRAC CAARAA TOTACTT	TTT-	ANGERTTA THERE CARARAGE THE	- TTR THOTOCRAR TITTC TTRARRAGE - CRATARA	TRADAGAATTA TRADA AAA AQUCATTATTI
148. Chilo4 R180280058RC C8	TOC AA GESC DEARARS	MACAC		AGCCAA	AAA7 CROAC	-7992203		ATT ALLCTA	TRACCALLARA	TCACCARA 277007	CGARAR SRAC CARARA SCHOOL TT	21212	ASCANTA TECAS CALARC SCAL	- THE TROPOGRAME STRUCT TRADAL CHE OF CARELLE	SCACASARTON SOCIAL ARA AGO CATTA TTSC WEATAGARTON SOCIAL ARA AGO CATTA TTSC
150. ChLG4_R180260058RC_C15	TOS AAGTIC TEANAITI-	ACAC	GATTT?	AGCCRA	AAAT CACAG	-71710	T- TGIGITITI	ATT ASACTA	GLACGAAAAAA	TCACCARA TITLE ?		77277	ARGCATTTA TECAS CAAAAAC-ICAA	- ITA TIG CARAATTIC TIAAAAACTA- CC- CRAIAAA	TEACAGAATTA EGCCAA AAA AGCCA TTA TTE
151. ChLG4_R180290056RC_C11	TOO AAGTIC TOARAITT	AACXC	GATTTT	ABCCRA	LAAT CAGAO	-77770		ATT ASSCTS	02.ACGLAARRA	TCACCARA TITOS 7	CGAARS WEC CAARR TOTIC TT	TITT	BRICHTTTA TICAS CALARAS TOAL	TTA TTO DCARALTTIC TTARRACTA - OC - CRATAAA	WINCHSART TO WINCHA AND AND CATTA TTYL
163. ChLO4_R180290068RC_C16	TON ANGINC TOR AN ANTI-	ALACAC	GOTTTT	ATCCCAR	ALLT CADES	TITIC	T- TONGETHE	ATT ABBCTA	GRACGAAAAAA	TCACCARE TTTOST	CGRANN TERC CACANA TOTACTT	TIT	ARCANTA TING CARAARC- ICAR	- TTR TROCOCRARA TITIC TTARARA COMPACING CARDAR	TCACAGAAT TA TO CAL ARA
164. Child4 R180280068RC C9	TOC ALGEST TEARATTE	MACAC	C. C. C. C. C. C. C. C. C. C. C. C. C. C	AGCCCAA	AAA7 CROAG	-77720		ATT ALLCTA	CALLARA	TCACCARA 211007	CGARAR SERC CARRAR SCIENCE TT	21212	AGCANTA TECAS CARAGAC SCAR	- FEA TROBIC AAAA ETEC TIMAAAAC TA-OC-CAA BAAA	- SCACASAS T28 25 SCAR ARA - NOR CANAR 7750
158. ChLG4_R180260056RC_C18	TOS AAGTIC TEANAITT	ACAC	GATTT?	AGCCRA	AAAT CACAG	-77770	T TGITITI	ATT ASACTA	GAACGAAAAAA	TCACCARA TITLE ?		TTTT	ARGCATTTA TECAS CARARAC ICAR	TTA THE TOTAL AND THE TRADAL CTA- OC CRAINAA	- REACAGAST IN IS ICAA - AAA - REACA TAA TTIC
157. ChLG4 R180290056RC C5	THE AGENE THAN ITS	ALC:NC	GATTTT	ABCCAA	LAAT CAGO	-77770	T- TORGETEIT	ATT ALLOCA	08.8C08.8A3.8A	TCACCARA TTTOS 7		77777	ARCATITA TICAS CABARAC ICAL	- ITA TIGTOCARASI TIC TIARRACIA- GC-CRAIRAA	- TEACAGAGT 73 TH TCAA - AAR - TCA CA TAA 77 TO - TCACAGAAT 78 TH TCAA - AAR - TCA CA TAA 77 TO
169. ChL04_R180290066RC_C2	TCC AAGTTC TOR BATT	ALOCAC	GATTTT	AGCCAA	AAAT CAALG	TITIC	T- TOXOXXXII	ATT ABBCTA	GRACHARAA	TCACCARA TTTOST	CARARA TRAC CARARA TOTACTT	X1 T	ANGCARTTA TERAS CARAARC- ICAR	- TTR TROCOCRAR TITIC TORRARA COM OC-CAR TALL	P-ARAGAATTA NI NGAA ARA NGA TATTATTIN
160. ChLG4 R180280201RC C5	THE ARGENE TEARSTY	MACAA	111177 111177	AGACCAA	AAAT AAAT	-722220		ATT ALLCTA	TACGARRAR	TCACCARA TITUS 7		21212	ARCANTE TERS CALARAC- ICAL	- FEA TROCOCARAA STIC TIAAAA - CAARAA - CAARAAA	- BCACAGAAT 25 BU AA AAA - RAA - RAA TA TA TA TA TA TA TA TA TA TA TA TA T
162. ChLG4_R180260548_C2	TOC AN CITC TOR GOAT TT-	ALACAC	BETTTT -	ACR TCRA	AAAT CAAD	-71117	T- CCRGITATT	ATT ASACTA	SAAC AT AAAAAA	TROCARA TITLE 7	CAASA TILC CAASAS TTLCCTT	7100707	CCTTTTC TARGEDTTTA TYTAS CARAAAC ICAR	-ATA TTOCOCARAS TTIC TEAARAAG SC- CCRATAAA	TCAGAGAGE 78 SI ICAA - AAAA TOUCA TTAAT IT
163. ChLG4_R180280648RC_C6	THE ARGITE TERMERITY	ALACAC A	GITTTT	ABACCAA	LAAT CARGE	-71111	T- CCIGITOTI	ATT ALLCTA	BAC - AAAAA	TACCARA TITLE?	COL AND TRAC CARDA TTREET?	7100783	C TITIC PARCETTA TITAS CALARAC TORS	-ATA TROCOCARA I TROCTARRAG	TING AGAIN TO THE TOP A AND TO CATTANTIT
165. ChLG4 R180280649RC C2	TOC AA GESC DEA GAASS-	ALAC AC	OFFTT?	AGACCAA	AAAT CRAGT	-7222	C- CrossMar	ATT ABAC	CRAC BLAARAA	ATACCEAR 277887	CARAAR BRAC - RAAAAA STELCCTT	22C T2	CCTTTC MASCOTICA TERS CARAAAC- SCAR	-XERTESCOCRARETEC TERRARE	SCARABACZA SU SEAG ANA THACA TTANTIT
168. Child2 R180279845 C2 167. Child4 R180980786 C2	THE AREA OF THE ACAR STR	ARACAC	CHILL .	ACACCAA	AAAT BAGT	-722227	C CERCITATI	ATT ANCTA	CARCE ALARA	TEACTRAL TOPOLT		710	BRCCCTTTA TURC CARRANC UNA	TTA THEORY ARAB TTO TTARA CO. ACC CARTALA.	- BUCCARRATOR SU SUAA - AAA - NOA CA TTURT TT
168. ChLG5_R180282067RC_C4	TOC ANALTS TO ANALTS	GACAC	BETTE	ALCORA	AAAT CAADT	-71087	C- ACTIT	ATT ASSCTS	GAAC -BAAAAA	TCACCARA TTTOS 7	CAAAA BAC CAAAAA ITIACCIT	770	TANGCOTTTA CITAG TABANAC-ICAT	- ITA TIOCOCAGAATTIC TIAARAAGTARACTCAGIAAA	REACABAT 73 23 ICAA AAA AGACA TTA TTR
169. ChLG4 R180280788 C4 170. ChLG4 R180280788 C7	THE CARTEC TARGET IT.	ACAC	GITTTT	- CCLA	BAAT BAAGT	-71111		ATT ALLCTA	BARCELAARRA	TCACCARA TITELT	CGRARS WIRE PRASES AND TAXAT	T1C	TARCETTA TITRE CALARAC ICAL	- TTACTOCOCARABITTIC TTARABACTALOC - CRAINAB	TIACA SATTA IS ICOL AAR TAACAGTA TTIT
171. ChLG4 R180280788 C6	THE AND TO THANK AND	ALACAC	QUITT7	AGACCAA	AAA7 CREET	-72220	C 222721	ATT ALLCTS	CRACCEALAAAA	TACCARS TITOS 7	CGAAAA BEEC BAAAAA BTEATTT	210	TANGCOTTA ANTAS CABAAAC- NCAR	- TTA TIGCOCAAAA TI TITAA PAAG TAACC- TAA BAAA	ECCALATIN SU ECAL ARABICA CAGTA FFET
172. ChilG10 R180277097RC C6	TOC A GTTTTCA CARTER	- AACAC	CHIER P	CCCCCCC.	AAA7 DA GA	2222223		ATT ALLCTA	-CARCEARAAA	TCACCARA TITICA		25C 7A	ACCONTA THAC CALLARCES	A TTA TTA COCARA TTA CORAA A TA ACCAR TA A	SCACABARTER SCICAA - ARA - NOA CATTA FFFF
174. ChLG10_R160277087RC_C2	TOC AAGTATIGAGEAITTA	-ACAC	BITTT	ALCORA	SAAN ICTAG	TTTTTT	TC TGITTOI	ATT ASSCTS	GLACGLAARRA	TCACCARE TTTT	ALAAA DC: CAAAAA ITIACCTT	TTCTA	AGCOTTTA CITAG CABARACICA	SA ITA TICTOCARAS- TITCT PARASAG TRACCERS INAS	RECARDAT TO BE ICAN AND C-ACATTA TITE
176. ChLG10 R180277097RC C3	THE ARGENTING ANALYSIS	- ACAC	GETTTT	ABBCCLA	AAAB TOABG	TITIT		ATT BEECTA	BACGAAAAAA	TCACCARA TTTTE	COLAR TRAC CAARA TTECCT	TICTA	ASCOTTA TITAS CARARCEYA	A TTA TTOCOCARA - TT TCA PARAA 6 TRACTICA AAA - TTATCA -	TRACADERT IN THE SAR ARE THE CATTA TITT
177. ChLG8 R180253365 C4	TOC AN ANTINO CARA STER	-ACAC	GETTT7	ABACCAA	AAAT CRAGT	2222022	CG TOTTTT	ATT ALLCTA	CALL BLANARA	TCACTARA TITTE?	CGAAAA BRAC CAAAA TTEACATT	250 75	ASCOTTA TECAS CARAAA	A- SCOTTONARARA TINCO PLARES STRAECCARERAR	SCACASAAT IN SU SCAL AAA MALCATTA TIT
178. Chi Cel R180263368 C6 179. Chi Cel R180263368 C1	TOC ARTITUC CAR ITTA	-AACAC	CHITT?		ACAT BAGT	22350 57		ATT AMOUTA	CARCEASAAAAA			710 73	ACCOUTA TECAS CAARAATTA	A DECTRIFICARRA TIPE PARAGE TARECCRABAA	- SCACAGAAT 25 SC SCAA - AAA - STA CA TTA TFFF - SCACAGAAT 25 SC SCAA - AAA - TACA TTA TFFF
160. ChLG6_R180263366_C2	TOROAR ITTA	-ACAC	BITTTT	BACCRA	AAAT CAAGT	TINGT	TGITICI	ATT ASSCTS	GLACGAAAAAA	TCACCARA TITET?	CAAR HAL CAAR TINCATT	TTCTA	ASCOTTA TELS CARARAGE	S- ICA TITTEAARAA- TITCE PARAAAG TRAADCR CA BAA	FEACAGAAT 7A 25 BCAA AAA TOACA TTA TT IT
181. ChLG10 R180277619RC C3	THE ARGINE THREE THE	-ACAC	GITTTT	ABACCAA	AAAT CARGT			ATT AMACTA	BACGLAARA	TCACC DA TTTAAL	THAR THE CARREN TTECT	TTC TA	ACCOTTA TICAS CALARA-CT	A TTA TTOCOTARRA- TTI TOTARRAA () TAAGOORA TAAA	TRACAGAA 77 TO BEAL AAAA TOREA TTA TTATT
183. ChLG10 R180277819RC C2	TOC ARGENC TO A GUARTER	-AC AC	GRITT'T'	AGACCAA	AAAT CRAGT	0 7 3 3 C 3 7	C CORTELL	ATT ALLCTA	GRAC GAAAAAA	TCACC PAR TTTAAS	BAARA 2900 CAARAA STEACOTT	210 75	AUCOTTA TECAS CARAAA-CET	AL PER TROCOTIANE - TENTT BAARA GILOSCOAR BAAR	BACASAAT IN ISI ICAA AAA WAACA TTA TTIT
164. CALCAD R160277619RC C4	THE ARGENE TRACEASTER	-AACAC	GETTTT	AGACCAL	AAAT CAAGT	77110	C CGITTII	ATT ASACTA	GAACGAAAAAA	TROCARE TITAL		710 78	ACCOTTA TELES CAAAAA CT	A TTA TTACCURARA THEFT BARRAC INCCCARTARA	- RACAGAATTA DE KAA AAA RAKC- TTA FFIT
186. ChLG8_R180289636_C3	TOC-ALOTTC TOLOGA ITTL	-ACAC	GETTET	TEACCRA	SAAC CARGT	TIME	CT XGITIT	ATT ASSCTS	GAACGAAAAAA	TCACCARA TTTAAG		770 73	ACOTTA TICAS COLARA CAT	AN TEA TROCG TARAS - TATCS TAGAAG TRASCCRATAAA	- INACAGAAT TA DI BCAA-AAA- NIACA TTA TTIT
187. ChLG8_R150289836_C6 188. ChLG6_R180282087RC_C5	THE ABSTIC TORMAN ITTL	-LACAC	GITTIT	ABACCAA	BAAT CARGT	TING	CC IGITIT	ATT ALLCTA	BLACGLAAXA	TCACCARA TTTAL	CGAARA HEAC CAARA TIMCUT CGAARA HEAC GAARA TIMCUT	TIC TA	ACCITTA TECAS COLARA-CAL	AL TTA TTOCO TAAA - TATTO TAAAAA TAACCAA TAAL -	- Thatagaat 72 teata arr teats to tta tta ttri Tiatagaat 72 te tiat arr teata tra ttri ti
189. ChLG10 R180277974 C4	TOC ALETTCHAUGAICEA	-LAGAC	GETTT7	ACACCAR	AAAT CAST	TARCET	CT TOTTI	AUX ALLCTA	GRAC BLAAAAA		GAAAA 12ChCTT	22C 77	AUCOTTA CECAS MALAAA-CEE	AN ITS TELCARAS- TEVT-RAASS TRASCCASESS	ECACAGAAT 28.83 ECAL AAA FOR CATTA 77 FF
191. ChLG4 R180277974 C7	TGC AAGTIMUCACCAICTA	-AACAC	GITTTTTCACC	TACACCAL	AAAT AAGAT	TING	IC IGITIII	ATT AAACTT	GAACGAAAAAA	777667	CALC CAAAAA TTACTT	710 17	AGCOTTA CELE TAAAA CI	A TTA TTAC A AAAA TTATTA AAAAA TAACAAA TAACAA TAACAA TAACAA TAACAA TAACAA TAACAAA TAACAA TAACAAA TAACAA TAACAAA TAACAAA TAACAAA TAACAAAAA TAACAAAAAAAA	- REAL AND AND REAL AND REAL THAT THE
192. ChLG4_R180280201RC_C7	TOC-AAGTTS TOARAITTA	-MACAC	GTTTTTTTTARCO	TTAEACCAA	AAAT BAGAT	77	CT XGITIT	ATT ASSCT	GAACGAAAAAA	777007	CGAAAA MBAC CAAAAA- I TIAC TIT	TTCT	ASCATATA CICAS CABARA CI	A TTA TACLE ARAA TINCT CRAAAG TAGCCAATAAA	- REACAGEAT TO RECENT AND TRACE TTA TTAT
194. ChLG10 R180277974 C2	TOR ABOTT TORMATTIC	-ACNC	OTITIT	ABACCAA	AAT CA-MT	TITET	CT IQUITIT	ATT AMACTA	CALL CALARA	TCACCARA TITLET	CAAR TROT -AAAA TTECTT	TICTA	AGGOTTA TECAS CARAGA	- A TTATIOCARAS - TTATITICARAS TRANSCORS TAR	TIALASAAT A CALL TO ARA CONCETTA FFFF
196. ChLG10 R180277974 CB	TOR ABGTINUMARATITA	-MACAC	GETTT7	AGACCAA	AAT7 CR-AR	TITLE	CT TOITTIT	ATT ABLCTA	CALC-LAAAAA	SCACCARA TITUS 7	CARAR SUS -AAAAA STERCOTT	210 75	ASCOTTA TECAS CALARA		ECACAGAAT 78 CS SCAR - AR- FOO CARO TOC
197, ChLG5 R180282884RC C7	TOC AAGTIMUGAGGAITTA	-AACAT	ATTTT	AEACGAA	CAGT CARGA	TING	1 RGATELL	ATT ASACTA	ALC GAAAAAA	ATACCARE TING 7		750 73	AGCATITA TECAS CABAAA CAC	A TTA TIGGE CAAL TITIT AA BAG TAATCAALAAA	TACAGAAT IN SI ICAA AA TAGAATTA TIT
198. ChLG7 R180286115 CS	TOC-AAGIIC TEAABAITIT	-SACAC	GTTTTT	ABACTRA	BAAT CARGT	777700	10 10 10 11 11	ATT ASACTA	ARC BARRA	COSCARA TITOR		777778	ASCOTTT TTCAS CALARA COL	R TTA TROCOCRARA TINCT RACEAG TOACCARAIRAA	TEACAGAATTA DE BCAA - AA - ATTACATTATT
200. ChL07 R180290116 C7	THE ARGINE THANKING	-BACAC	GRITIT	AGAC TAA	AAAT CAAGT	TIXE	IT XGRIEII	ATT ABBCTA	BAC - ARAR	COSCIARE TITOSE	CGAARA HELC CAARA TIMCCIT	TITA	AUGUITT TICAS BARAA-GIC	A TRA TROCOCARA TITO PLACE OF CASCING TAR	TURUSPANT IN HE TURE AN ATTRUE THATTIT
201. Childe R180282067RC C9	THE ALGERT TAKEN THE	- ACAC	899997	AGA CCA	AAA	22110	CT XGECTT	ATT ALLCTA	BAC BRAAA	CACCARA 277007	CARA SRAC		-SCOTTA 75CAS CALARA -COC	ATTRANCOCA CA TETT TAAAAA GTAAGCCAA BAAA	SCARAGEATOR SS SCAR AR - A TO TA TA 7
203. Childe Riac288774RC Ca	TOC AAGTIC TEARSAITTA	ACAC	GTTTTT	AGACCA-	CAAGT	TITET	C IGITOT	ATT ASACTA	GAAC GAAAAAA	TOSCARA TITOST	COARA SAL CAARA TIACCT	21212	AGEGITTA TICAS CANANA CIC	A TTA TIGCGCAAA TTICI PAAAAA TA COAAAAAA	TACAGAAA TA TEACGA AA A TGA ATTA TTA
204. ChLG5 R180282204 C4	TOC GACTTC TO A SAA I TTA	-LACAC	GITTT	ABBCCRA	SAAT CARGT	78		ATT ASSCTA	GAACGAAAAAA	TCACTRAL TITOS 7	CEARN HEAC CARRS TTLCCTT	TTC TR	AS GITTA CREAS CALARS CALARS	A TTA TTAC MARARA CITCL TRAAS GTRASC TRANS	TRACARATTA IN ICAL A. RING TO TA TTY
208. ChLO6 R180282204 C2	TOR ARGITTIGA BAITO	-BACAT	GITTTT	VéxCCVF	LALT CALGT	TITE	IC IGITICI	OTT ASSCTA	GEAC GEALANA	TCATTARA TITOST	COARA TRAC CAARA TTIACTT	TINTA	ASCOTTS TOCAS CALARA-CT	A TTA TIQUGARAN TITUT PARANO TRACCARTAR	ICACAL ATTA TACAL AS A TON TATTATT
207. Chi Ga Riao283777 C2	TOC AAGESC THAGEASTEL	-ARCAC	C THE T	AGACCAA	AAAT CAGT	77 22 22	C 2325211	ATT ALLCTA	CALLAR AND A CALLAR AND AND AND A CALLAR AND A CALLAR AND A CALLAR AND A CALLAR AND A CALLAR AND A CALLAR AND A CALLAR AND A CALLAR AND AND AND AND AND AND AND AND AND AND	TCACCARA 277007	CAAAAA STEACTT	210 78	ASCOUTT TECAL CARACTA	A 1994 TEGCOCAAAA TTEC TIAAAAA9 - TAAGCCAABA6A	SCARARTY, STCAA - AR TON CART, FFF
208. ChLG6_R180263777_C3	OC AAGTIC TEAGAITTE	ACAC	AG TTTT	AEXCOLA	AAAT CTAGT	TITE	C IGICITI	ATT ALCTA	CAACGAAAAAG	TCACCAAL TTTGE 7		710 73	AGEGTITE GICAC CAMARACTEC	A 15A TIGCGCAAAAI TIC TIAAAAGT TAACCAAIAAA	TCACABATTA DAGCAA - ANA TCACABTA TTIT
210. Childe R180283777 C5	THE ALGENTING AGENTING	-AACAC	AG TITT	AGA CAA	AAAT CAGT	TING		ATT ALCTA	DAACGAAAAAA	TCACCARA TITOS 7	CORANNE CORANNA TTINCAT	770 73	ASCARTT TECAL CALARACEA	A 124 TROCOCARA TTC TTARRAG TACACCAR TAAA	TRACARATTA TRACAL - ANA TANARA
212. ChLG7 R180298115 C2	TOC ACCTICUTACENTER	-ACAC	ATTT?	TRACCAR	AAAT CRAGT	TITIC	C 1211111	ATT ALLCTA	BACGAAAAAA	TCACCARA TINGE	CARAR SEC CARARA STR. 7	TTTA	ASSOTTA TECAS CARTACTER	A THE THE CARAGETTIC TIGARAGE - TRASCURE FARE	RCACAGAAT IN MARCAA
213. Chi G7 R180286116 C4	TOC ACCUTUCACCARTER	-ACAC	121112 10107	CACCAA	AAAT CRACT	777772		ATT ALLCTA	CRACCALLARA	TCACCARA TITOCC	CAAAA SEC CAAAAA STRC TT	222.04	ACCOUTTA CREAC CARARCERA	A FEA THE CARAA STIC THARRAN TRACCAR SAA	TRACAGARTON IN ICAA CATTOR CATTA FFF
213. ChLG7_R180266115_C6	TAC AAGTITICA CATTA	-ACAC	ATTTT	BACCAA	AAAT CAADT	TITII	C TAITIT	ATT ASSCT	GAACGAAAAAA	TCACCARA TTTOE	CGRAAN TRC CAANNA TTTCCTT	TTTR	AGCOTTA TINAS CABARACTER	A TTA TTACE ARRAY TTA TTARARA TRASCCRATARA	TTCADAAT 7A 18 TCAA - AAA TGACA TTA TTTT
216. ChLG5 2 R180296099RC C2 217 ChLC9 2 R180296099RC C2	THE ADDIE TO A GRADITE	-LACAC	ATTTT ATTTT	AEXC-AA	BAAT CBBGT	TING		ATT ALLOUT	BACGLAARAA	TCACARA TITOS 7	CGAAN TRAC CAARA TTACCAT	TITIA	ASCOTTA TELA CALARA	A TTA TUAN SCARAATTAC TTARARAA - TAAS CORATAAA A TTA TUAN SCARAATTAC TTARARAA - TA DITTA A TAA A	TRACTOR AND A TRACTOR AND A TRACTOR AND A TRACTOR
218. ChLG3 2 R180299099RC C4	THE ARAFIC DURING SALES	-AC	XTTT7	AGACCUA	AAAT CRAST	22	CC CORTELL	APP ARACT	BACGLARAA	TCACAAAA TTT007	MAAATERAC CAARA STEACCAT	AL A LA	AUCOUTTA TECAL CARAGECE	A FER TOALS, CARAGE TAC TIGAAAAA - TACSCCAA BAAA	SCACADAAT 25 STREAM - ARATSAAA 12A 77 SC
219. CHLG3 2 R180296019RC C3 221 ChLG3 2 R180296098C C5	THE ADDRESS TRACTAL	-ACAC	ATTT7	EACCA C	AAAT CAAGT	7775		ATC CARCT	CAACCAAAAAA	TUACARAA TITOS 7	AAAAA TTLATT	25C 7A	ACCUTTA TEAS AAAAACTEA ACCUTTA TEAS AAAAACTEA	A THE TRUCKCCCARTING THARARA - BACCCARTARA - A THE TRUCKCCCCARTING THARARAA - BACCCARTARA	TCARCAATTA TTCAA - AAATCACATA TAA TTA
221. ChLOS 2 R180296098RC C7	TOC ALLTIC TO COLLINS	-AACAC	ATTTT	TEACCAA	AAAT CAADT	TINGA	C TOTTT	ATS BACT	GAACGAAAAAA	TCACARA TTTOS 7	CGAAATEBAC CAAAAA ITIMTT	TTCTA	AGCOTITA TINAS ABAAACTEA	A TTA TROCOC CCALI TTC TTARARA - TRASCCA TARA	RIANABAT TA TERCAA -ARA TORCA TAR TITE
222. ChLG4_R180280788_C3 223. ChLG4_R180280788_C8	THE AACTIC TRACKATTTA	-LACAC	GINGTT	ARCCAR	BAAT CERGT	TITE		GTI ALLCTA	BACGAAAAAA	AA-CACALITTEET	CGAAR TAC CAARA TTRCCTT CGAAR TAC CAARA TTRCCTT	TINTA	ASCOTTA TECAS CALARACION ASCOTTA TECAS CALARACION	ANTA TROCECARABITIC TIAL BAD- TRACCRAINSE ANTA TRECECARABITIC TIAL BAD- TRACCRAINSE	TIALABATTA TRACAS - ARA TANA TA TATAT TIALABATTA TRACAS - ARA TANA GTA TATA
224. ChLG4 R180280786 C8	TOC AND TO THE OWN TALL	-LAAAC	QTTTT7	ARCCAR	AAAT CRAST	20 22 2-7	C EGETELL	STI ABACTA	CRAC QUARAAA	ATCACAAAA TT99 7	GAAAA MAC CAAAAA ITIACATT	220.04	ACCOUTTA TECOS CABARACECA	A TTR TESC CARAGETTIC THARAGE. TRASCCAREAR	SCACALA DA DA SANCAA - ARA SANCA TTA TETE
228. ChLG2 R180270645 CA	TOC AASTIC TEANAITTEA	-ALACAC	GTITTT	ALACCAL	AAAG CAAGO	TTTTT		ATT AAACAA	CARCERARARA	TCACCARE TITCE?	- CARAA MAC CARAAA CTICC TT	710 73	ACCEPTTA TELACARCE BARTER	A TTA TTAC COAR TTENT TO AAAAAATAC COARAAA	TRACADAAAA TO TAA - AAA TAT A TTTT
227. ChLG2_R180278645_C3	TOC AADTIC TOAGGATTIA	ACAC	GTTTTT	ABACCRA	AACC TAACC	TITIT		ATT ALLON	GLACODARAR	TCACEARA TITELT	CAARA TAC CAARA TTIACCT?	77077	AGCATITA TRIAGCARA-ARATCA	A 100 TTROBURAR - ATT TO TRABAR TRABOURAGA	BACAGAATEA IN ICAA - AAA NIACATTO TTIT
229. ChL02 R180279845 C7	TOT AGOTIC TORONALTER	-CATAC	OTITI	ANCCAR	BAAT CRAGT	TINC	CT XWX TX11	ATT TALCTA	GRAAAAAA	TACCARE TITOST	CARAR TARL CARARA TIMCCTT	TIC 1A	ABLETTA TELEVILA ARTE	A 114 TTE COAR - TTE COARA - TRACE TRACE COARA -	TRANSANT'S TRANSFORMED TO TAKE
230. ChLG2_R180279845_C4	TOC AN OTIC TO A SOAD THE	-ERTAC	OWITIN.	ABACCAA	AAA7 CRAGT	7727	12 2013111	ATT TALCTA	GRACELAS ARA	TCACARA TITAN	CARAR SEC CARARA SCREET	TTC TA	SCOTTA CICALCAR-ARA-A	A CR THECOCAAA - ATT COCAA BAR O'LAGCCAR FARA	CACAGAAT 28 29 ICAA - AA 22 A CATTA TITT

d) alignment of cluster 4

Consensus	1 10 AAAAAAAATTTATAACT-	20 30	40 5	0 60	70 8	50 CCG- TX	90	100	110 ACAACAC	120	130	140	150	160	170	180 190 - TGG TGG ATG CG (200	211
1. ChLG2 R180279507 C1	AAAAAAT TOATAACT		FOGTAG AGCAN TO COG 1	ittgttcca <mark>t</mark> fgaa	TT CASCEGC TCATTTT	CIG-EA-	TCAC	ACOCCATTITI	ACAACAC	TACC1	TCACTOGARA	ACTTAG T <mark>A</mark> ARAJ	AATT	- GTTTA	TTAATTTAAAAAA			т
2. ChLG2_R180279507_C3	AAAAAAT T <mark>C</mark> ATAACT	CAAAAACTAAAAGT	rogtag agcaa <mark>tg</mark> oeg 1	fttgttcca <mark>t</mark> fgaa	TT CAGCEGC TCA TTTT	CIG-TA	TCAC	-aco <mark>g t</mark> catt tt 1	ACAACAC	TACC1	TCACTOGARA	actta <mark>tta</mark> aaaz	AATT	- GTTTA	I TAA <mark>CS TA</mark> AAAA		C RS AATTATTT AT	т
3. ChLG2_R180279507_C5	ARARAAT TO ATRACT	CAAAAACTAAAAGT	FOGTAG AGC AA <mark>DG</mark> OGG 1 FOUTAG AGC AA <mark>DG</mark> OGG 1	FTTGTT CCATENAA FTTGTT CCATEGAA	TT CAGCEGC TCATTTT TT CAGCEGC TCATTTT	CIG TA	TCAC	A TOG COATT TT I	ACAACAC	TACT	TCACTCGARA	A CTTAG TAAAAZ	AAATT	G TTT A	TAACTTAAAAA TAACTTAAAAAA	TOGTOG ATG CG (GAATTATTTAT	T T
5. ChLG3 2 R180296924 C10	TAAAAA	CAARAACTARAAGT	CGTAG AGCAN TO CGG	ITTGTTCCATFGAA	TTCACCCCTTCATC TT	CIG-TA-	TTAC	ACCCATTITI	CAACAC	CACCI	TCACTOGAC	ACTING TACCAS	ATT	- ATTTA	TAACTICAAAA		C-OGAAATAAAAA	Ť
6. ChLG3 2 R180296924 C11	TAAAAA	CAAAAACTAAAAGT	ICGTAG AGCAN <mark>TG</mark> CGG 1	TTTGTT CCA <mark>T</mark> TGAA	TT CAGGGCACATTTT	CIG-TR-	TTAC	-ACCG CC ATT TT I	GCAACAC	CACCI	TCACTOGAC	ACTING TAGGAZ	AA <mark>T</mark> TT	ATTA	f taa <mark>c</mark> f tgaaaaa		OS ARA TAA TAAT	т
7. ChLG3_2_R180296924_C2 8. ChLG3_2_R180296924_C8	TAAAAAATTATAACT TAAAAAATTATAACT	CAAAAAGT CAAAAACTAAAAGT	POSTAGAGCAA <mark>NG</mark> OGG 1 POGTAGAGCAA <mark>NG</mark> OGG 1	FFIGTI CCA <mark>D</mark> IGAA FTIGTI CCA <mark>D</mark> IGAA	TTCAGCGGCTCATFIT TTCAGCGGCTCATFIT	CIG TA	TTAC	ACCOCCATTTT	GCAACAC	CACC1	TCACACGACG TCC CTCGACG	ACTARS TASS AF	la <mark>r</mark> TT la r TT	ATTA	TAACTIGAAAAA		COGAAATAATAAT COGAAATAATAAT	T T
9. ChLG3_2_R180296924_C12	TAAAAAATTATAACT	CARAAACTAAAAGT	ICGTAG AGCAA <mark>IG</mark> CGG 1	ITTGTT CCA <mark>T</mark> IGAA	TT CAGCGGC TCATTTT	CIG-TA	TIM	ACC	GCAACAC	CACCI	TCGCTCGACG	ACTTRG TAAGAZ	ATT	ATTA	TAACTIGAAAAA	-TOSTOS AIG CG		T
10. ChLG3_2_R180296924_C4	TAAAAAATTATAACT	CARARACTARARGT	Fortag ago an <mark>ig</mark> ogg 1	ITTGTICCA <mark>T</mark> IGAA	TT CAGCGGC TCA TTTT	CIG-TA-	TTAC	ACCOCATT TT T	GCAACAC	CACCI	T <mark>CG</mark> CTCGA <mark>CG</mark>	ACTTAG TARGAZ	ARTTT	ATTTA	TAACTIGAAAAA		CORANA TANTANT	T
12. ChLG3_2_R180296924_C0	TAAAAAATTATAACT		CGTAS ASCAN <mark>IG</mark> COG 1	ITTGTTCCA T IGAA	TT CASCING TCATTT	CIG-TA-	TTAC	ACOS CCATTITI	CAACAC	CACCI	TOG CTOGAOG	ACTICC TARGAN	ATT	-ATTA	TAAACTICAAAAA		C-OGAAATAATAAT	T
13. ChLG3_2_R180296924_C9	TAAAAAA TTATAACT	CAAAAACTAAAAGT	Postag ascaa <mark>ng</mark> ogg 1	fttgtt cca <mark>n</mark> tgaa	TT CAGCEGC TCA TTTT	CIG-EA-	T TAC	-ACU <mark>G</mark> CCATTTTT	GCAACAC	CACC1	TCGCTCGACG	acti <mark>g</mark> g t ang az	AA <mark>T</mark> TT	- ATTTA	I TAACITIGAAAAA		C OS AA <mark>A</mark> TA <mark>A</mark> TAAT	т
14. ChLG3 2 R180296924 C5	TRARAR TTATRACT		POGTAG AGC AR <mark>IG</mark> OGG 1	FTTGTT CCATTGAA	TT CAGOGGC TCATTTT TT CAGOGGC TCATTTT	CTG-TA	TTAC	ACCCCATTTT	GCAACAC	CACC1	TCACTCGACG	ACTTGG TANGAR	AATTI AATTI	ATTTA	F RAACTIGARAA A FTRAA C FIICABAAA		C-OG AAA TAA TAAT C-OG AAA TAA TAAT	T
16. ChLG8 R180289350 C1	AAAAAA	CAAAAACTTAAAGT	CTTAG AGCAAAACGA	TTATCCAGTGAA	TT CAGOGGC TCATTTT	CIG-TA-	TAT	-ACOG TCATT TTI	ACAACAC		TTACTOGA	A CTTAG CTAAA	A- TTT	ATGTA	TTAACTIGAAAAA	TGGTGGATG CG	CAATTATTTAT	Ť
17. ChLG8_R180289223_C2	AAAAAATTATAACT	CAAAAACTAAAAGT	CGTAG AGCAAAACGG	TTTGTT CCAGTGAA	TT CAGCEGC TCA TTTT	CIG AA	TAT	-ACCGTCATTCTT	AAACAC	TACT	TIA <mark>T</mark> TCGAG <mark>G</mark>	ACTTAG TTARAZ	ATT TT	ATTA	TTACTIGAAAA2			т
18. ChLG8_R180289223_C4 19. ChLG8_R180289223_C8	AAAAAATTATAAACT	CAABAACTAAAAGT	POTAS ASCARAROGS POTAS ASCARAROGS	ftigti ccastgaa ftigti ccastgaa	TTCASCIGCTCATTTT TTACCCCCTCATTTC	CIG AA	TTAT	-ACCGTCATTTTT -ACCGTCATTTTT	ACAACAC	TACT	TTACTOGAGG.	ACTTRS TTARAS	ATT.	ATTA	I TTACI IGAAAAA I TTACI ICAAAAA		CAATTATTTAT CAATTATTTAT	T.
20. ChLG8_R180289223_C6	ARAAAA	CAAAAACTAAAAGT	CGTAG AGCARAACGG	TTTGTTCCAGTGAA	TT CAGAGE GTTCATTTT	C IG - TA-	TAAT	-A <mark>G</mark> C <mark>G TT</mark> ATT TT I	ACAACAT	TACT 1	TTA CTCG AG <mark>G</mark>	ACTTRG TCARAS	ARTT	ATTA	TTAACT CAAAAA			T
21. ChLG8 R180289224 C5	AAAAAAATTATAACT	CAARAACTAARAGT	FOGTAG AGC ANAACGG 1	FTTGTT CCAGTGAA	TT CAGCG GT TCA TTTT	CIG TA	TAAT	-AGOG TT ATT TT I	TCAACAT	TACT	TTACTCGAGG	ACTTAG TCARAZ	ATT	ATTTA	I TAACIAGAAAAZ		G AATTATTTAT	T
23. ChLG8_R180289224_C6	AAAAAAA		CGTAG AGCAAAACTG 1	ITTGTT T CAGTGAA	TTCAGGGGCTCATTTT	CIG-IC	TAAT	-ACOGACATTTTT	ACAACAT	ACA	TIACTOGAG	ACTTAG TOARAS	a <mark>r</mark> it	ATTA	I TAACI AGAAAAA		C-CAAATTATTTAT	T
24. ChLG8_R180289224_C7	AAAAAA	TAAAAACTAAAAGT	POGTAG AGC AAAAC <mark>T</mark> G 1	fttgtt <mark>T</mark> cagtgaa	TT CAGCEGC TCA TTTT	COS-TA-	TAT	-A <mark>GC<mark>G TT</mark>ATT TT I</mark>	ACAACA <mark>T</mark>	TACT 1	TTA CTCG AG <mark>G</mark>	a ctitag t <mark>c</mark> aba <i>z</i>	AR <mark>T</mark> TT	ATTA	I TAA <mark>C</mark> I <mark>B</mark> JAAAAP		C	т
25. ChLG8 R180289223 C7	AAAAAAATTATATCT	CAAAAACTAAAAGT	FOGTAG AGCAAAACGG 1 FORTAG AG <mark>C</mark> AA AACGG 1	FTTGTT CCAGTGAA	TT CAGOGGC TCATTTT	CIG TA	TTAT	-ACOS TCATT TT I	ACAACTT	TACT	TTACTOGAG <mark>G</mark>	ACTTAG TOAAAZ	ATT ATT	ATTA	I TAA CAA GAAAAA I TAA <mark>CAA</mark> GAAAAA	- TGGTGG AIG CG C	C OG AATTATTTAT	T
27. ChLG8 R180289223 C10	AAAAA	CAAAAACTAAAAGT	CGTAG AGCAAAACGG	ITTGTTCCAGTGAA	TT CAGGGC TCA TT TT	TIG-TA-	TCAT	-ACC <mark>G T</mark> C ATT CT T	ACAACAC	TATC1	TTA CTCGAG	ACTTRG TTANAZ	AATTT	ATTA	I TAA <mark>G</mark> TTII <mark>G</mark> AA AF	TGGTGG ATG CG (T
28. ChLG8_R180289223_C3	AAAAAATTATAACT	TAAAAACTAAAAGT	CGTAG AGCARAACGG	TTTGTT TCAGTGAA	TT CAGCGGC TTATTT	CIG TA	TAT	ACCGTCATTTT	ACAACAC	TATCI	TTACTCGAG <mark>G</mark>	ACTTAG TTARAZ	ATT	ATTTA	TTACTIGAAAA2	TOGTOG ATS CS (CAAATTATTTAT	T
29. ChLG8_R180289223_C5 30. ChLG8_R180289224_C2	AAAAAATTATAACT	CAAAAACTAAAAGT	FUSTAS ASCARARUSS 1	FTFGTTCCAGTGAA FT-GTTCCAGTGAA	TTCAGGGGCTCATTTT TTCAGGGGCTCATTTT	CIG TA	TTAT	-ACCATCATTTTT	ACAACAC	CACCI	TEACTOGAGG	ACTTRS TTARAS	ATT	- ATTTA	I TAACITIGAAATA I TAA TITIGAAA		COLARTTATTTCT	T
31. ChLG8_R180289224_C6	ARARAR	CARARCTARAGT	CGTAG AGCANAACGG	TTTGTT CCAGTGAA	TT TAGCGGC TCATTTT	CIG TA	TAT	-ACCGTCATTTT	ACAACAC	TACT	TTACTCGAG	ACTTRG TTANAZ	AA <mark>T</mark> TT	ATTA	f TAA <mark>G</mark> T TG <mark>C</mark> ACG7		OG AATTATTTAT	T
32. ChLG8_R180289224_C4	AAAAAATTTATAACT	CAAAAACTAAAAGT	CGTAGAACAAAACGG 1	ITTGTT CCAGTGAA	TT CAGOGGC TCATTTT	CIG TA	TTAT	-ACOG TT ATT TT I	ACAACAC	TACCI	TAACTCGARG	ACTTAG TCAAAZ	ATT	ATTA	T TAA <mark>A</mark> T TG CACAZ	TGTIGG AIG CG (C OG AATTATTTAT	T
34. ChLG8_R180289343RC_C3	AAAAAATTTATAACT	- CAAAAACTAAAAGT	CGTAG AGCAAAACGG 1	TTGTTCTGAGTGAA	TTCAGCGGCTCATTTT TTCAGCGGCTCATTTT	CIG-IA CIG-IA	TTAC	-ACOGTCATTTTI	ACTACAC	TCTCT	TCACTCCAGG	ACTTAG TTANAZ	AATT	ATTA	I TAACI'IGAAAAA		- CAAST DATITAT	T
35. ChLG8_R180289348_C5	AAAAAAT TTATAACT	CAARAACTAAAAGT	CGTAG AGC AA AACGG 1	TTTGTT C <mark>T</mark> AGTGAA	TT CAGCEGC TCA TT TT	C T G-TA-	TTAC	- A CO <mark>G T</mark> C ATT TT I	ACTACAC	TCTC1	TCACTCCAG <mark>G</mark>	а сттасттала з	AATT	ATTA	I TAA <mark>C</mark> I TGAAAA?			т
36. ChLG8_R180289343RC_C4	AAAAAAT TTATAACT	CAAAAACTAAAAGT	FORTING INCOMPANY OF T	FTTGTTCTAGTGAA	TT CAGCEGC TCATTTT	CIG IA	TIAC	ACCONTRACTOR	ACTACAC	TCTCT	TCA CTC CAGC	ACTING TIANAS	AATT	ATTA	I TAACI TGAAAAA I TAACI TGAAAAAA	- TGGTGG AIG CG (C CAAATTATTTAT	T
38. ChLG8_R180289343RC_C7	AAAAAATTTATAACT	CARABARCTARAAGT	CGTAG AGCAAAACGG 1	TTTGTT CTAGTGAA	TT CAGOGGC TCA TTTT	CIG-TA-	TTAC	ACOGTCATTTT	ACTACAC	TCTCT	TCACTC CAG	ACTTRG TTANAS	AATT	ATTA	TTARCTIGARAA	TGGTGG ATG CG (- CAATTATTTAT	T
39. ChLG8_R180289343RC_C9	AAAAAATTTATAACT	CAAAAACTAAAAGT	CGTAG AGCARAACGG	TTTGTT CTAGTGAA	TT CAGOGGC TCATTTT	CIG TA	TTAC	ACOGTCATTTT	ACTACAC	TCTCT	TCACTCCAGG	ACTTAG TTARAZ	AATT	ATTTA	T TAACT TGA BAAS	TGGTGG ATG OG O	CAAATTATTTAT	T
40. ChLG8_R180289343RC_C6 41_ChLG8_R180289343RC_C10	AAAAAAT TTATAACT AAAAAAT TTATAACT	CAAAAACTAAAAGT CAAAAACTAAAAGT	Postas ascaraross Postas ascaraross	FTIGTI CTAGTGAA TTIGTI CTAGTGAA	TTCAGCGGCTCATTTT TTCAGCGGCTCATTTT	CIG-IA-	CTAC	ACOG TCATT TT 1 ACOG TCATT TT 1	ACTACAC	TCT TCTC1	TCACTCCAGC TCACTCCAGC	Α CTTAG TT AAA3 Α CTTAG TT AAA3	AATT	- ATTTA	I TAACI'IGAAAAA I TAACI'IGAAAAA		C-CAAATTATTTAT C-CAAATTATTTAT	T T
42. ChLG8_R180289343RC_C2	AAAAATTTATAACT	CARARACTARARGT	CGTAG AGCANAACGG	ITTGTTCTAGTGAA	TT CAGCEGC TCA TTTT	CTG-TA	TTAC	ACCGTCATTTT	ACTACAC	TCTT	TCA CTC CAGG	ACTTRG TTANAZ	AATT	ATTA	I TAACITIGAAAAA	TOGTOG ATG CG (T
43. ChLG8_R180289348_C4	AAAAAAT TTATAACT	CAAAAACTAAAAGT	CGTAG AGCANAACGG 1	IGTGTTCT AGTGAA	TT CAGOG AC TCA TTTT	CIG IA	TTAC	GCOGTCATTTT	ACTACAC	TCTT	TC-CTCCAGG	ACTTAG TTAGAZ	AATT	ATTA	I TAACI TGAAAAA	TGGTGG ATG CG (C CAAATTATTTAT	T
45. ChLG8_R180289344RC_C21	AAAAAATTTATAACT	CAAAAACTAAAAGT	CGTAG AGCAAAACGG 1	FTIGTI CCAGIGAA FTIGTI C <mark>T</mark> AGIGAA	TT CAGCEGC TCATTIT	CIG-DA	TTAC	ACCACCATTITI	ACAACAC	TAO	TCATTCCAGG	ACTTRG TTARAX	AATT	ATTA	I TAACITIGAAAAA			T
46. ChLG8_R180289344RC_C2	AAAAAAT TTATAACT	TTAAAACT <mark>G</mark> AAAGT	e og t <mark>o</mark> g a <mark>a</mark> c aalaalogg 1	ITTGTT C <mark>T</mark> AGTGAA	TT CAGCGGC TCATTTT	C G TA	TTAC	ACC <mark>G T</mark> CATT TT I	ACAACAC	TACCI	T <mark>C</mark> A CT <mark>G C</mark> AO <mark>G</mark>	A CTTAG TT AAA3	AATT	ATTA	I TAA <mark>C</mark> I TGAAAA?	TGGT G AIG CG (C CAAATTATTTAT	т
47. ChLG8_R180289350_C6 48. ChLG8_R180289344RC_C6	AAAAAAT TTATAACT	TTAAAACIC AAAGI	FOGTAG ANCANANOGG 1 FOGTAG ANCANANOGG 1	FTTGTTCTAGTGAA	TTCAGCGGCTCATTTT	CIG IA	TIM	-ACOS CATT TT I	ACAACAC	TACCI	TCACTCCAGC	ACTTAC TTAAAA	AATT	ATTA	I TAACI TGAAAAA I TBB CITCA BB SE		C-CAAATTATTTAT	T
49. ChLG8 R180289344RC C10	AAAAAATTTATAACT	TAAAACTGAAAT	CGTAG ALCAAAACGG 1	ITTGTT CTAGTGAA	TT CAGCGGC TCA TTTT	CIG-TA-	TTAC	ACOGTCATTTT	ACAACAC	TACCI	TCACTCCAG	ACTTAG TT AAAZ	AATT	ATTA	TTAACTIGAAAAZ	TGGTGGATG CG	CAATTATTTAT	Ť
50. ChLG8_R180289344RC_C15	AAAAATTTATAACT	TT AA AACTG AAAGT	FOGTAG ANCARARCGG 1	ITTGTIC <mark>I</mark> AGTGAA	TT CAGOGGC TCATTTT	TTG-TA	TIAC	-ACO <mark>G T</mark> CATT TT I	ACAACAC	TACCI	TCACTCCAGG	acttre ttabas	AATT	ATTA	I TAA <mark>C</mark> I TGAAAAA	TGGTGG AIG OG O	C-CAAATTATTAT	т
51. ChLG8_R180289344RC_C20 52. ChLG8_R180289344RC_C17	AAAAAAT TTATAACT AAAAAAT TTATAACT	TAAAACIG AAAGI	FUGTAG ANCAAAADUG 1 FUGTAG ANCAB AADUG 1	FTTGTTC T AGTGAA FTTGTTC T AGTGAA	TTEAGEGGCTEATITT TTEAGEGGCTEATITT	TG TA	TTAC	ACCONCATTITI	ACAACAC	TACCI	TCACTCCACC.	ACTTRS TTAAAA	AATT	- ATTA	I TAACI IGAAAAA TTAACI TIGAAAAAA		- CARATTATTTAT	'T
53. ChLG8_R180289344RC_C8_	AAAAAAT TTATAACT	TTAAAACT <mark>G</mark> AAAGT	CGTAG AACAAAACGG 1	ittetic <mark>t</mark> agtgaa	TT CAGOGGC TCATTTT	TTG TA	TTAC	ACO <mark>G T</mark> CATT TT I	ACAACAC	TACCI	TCACTC CAGG	ACTTRS TT AAA7	AATT	ATTA	f taa <mark>c</mark> f tgaaaas	TGGTGG AIG CG (CAAATTATTAT	T
54. ChLG8_R180289344RC_C12	AAAAAAT TTATAACT	TTAAAACIGAAAGI	FOG TAG AACAAAACGG 1	FTTGTTCTAGTGAA	TTCAGCGGCTCATTTT	TTG-TA-	TTAC	-ACO <mark>G T</mark> CATT TT T	ACAACAC	TACCT	TCACTCCAGC	ACTTAG TTAAAA	AATT	ATTA	I TAA <mark>C</mark> I TGAAAAF		C-CAAATTATTTAT	T
56. ChLG8_R180289344RC_C14	AAAAATTTATAACT	TTAAAACIG AAAGI	CGTAG ALCARAACGG 1	ITTGTTCTAGTGAA	TT CAGCEGC TCA TTTT	TIG TA	TTAC	ACOG TCATT TT	ACAACAC	TCCCT	TCACTC CAGG	ACTTAG TTARAZ	AATT	ATTA	TAACTTAAAAA	TGG GGG ATG CG (CAATTATTAT	T
57 ChLG8 R180289344RC C18	AAAAAT TTATAACT	TTAAAACT <mark>G</mark> AAAGT	ecgtag a <mark>a</mark> caaaacgg 1	ITTGTIC <mark>T</mark> AGTGAA	TT CAGCEGC TCATTTT	C G TA	TIM	ACC <mark>G T</mark> CATT TT I	ACAACAC	TCCT	TCACTC CAG	ACTING TIANAS	AATT	ATTA	TAACTTAAAA	TGG GG AIG CG (C-CAAATTATTTAT	т
58. ChLG8_R180289344RC_C13 59. ChLG8_R180289344RC_C7	ARAAAT TTATRACT		FOGTAG ANCANANCOG 1 FOGTAG ANCANANCOG 1	ITTGTIC TA GTGAA ITTIGTIC T AGTGAA	TTCAGCGGCTCATTTT TTCAGCGGCTCATTTT	CIG-EA CIG-TA	TTAC	-ACOG TCATT TT I -ACOG TCATT TT I	ACAACAC	TCCC1	TCACTCCAGG	ACTTRS TTARAS	LAATT	- ATITA	TAACTIGAAAAA		C-CARATTATTTAT C-CARATTATTTAT	T
60. ChLG8 R180289344RC C19	AAAAAATTTATAACT	TTAAAACTG AAAGT	COTAG AACAAACGG	ITTGTT CTAGTGAA	TT CAGOGGC TCA TTTT	CIG TA	TTAC	ACOG TCATT TT I	ACAACAC	TCCT	TCACTCCAGG	A CTTAG TTARAS	AATT	ATTTA	TAACTIGAAAAZ	TGG GGG ATG CG (CAAATTATTTAT	Ť
61. ChLG8_R180289344RC_C9	AAAAAAT TTATAACT	TTAAAACIS AAATI	FOGTAG ANCARARCGG 1	ITTGTTC <mark>T</mark> AGTGAA	TT CAGGGC TCATTTT	CTG-TA	TTAC	ACOS TCATT TT I	ACAACAC	TOCCI	TCACTCCACC	ACTTRS TTARAS	AATT	ATTA	ATAACTIGAAAAA		C-CAAATTATTAT	т
62. ChLG8_R180289344RC_C11 63. ChLG8_P190299344RC_C4	AAAAAATTTATAACT BBBB AATTTATB ACT		PCGTAG ALCAAAADEG 1 PCCTAC CORB BBCCC 1	PTTGTTC <mark>R</mark> AGTGAA PTTGTTC <mark>T</mark> AGTGAA	TTEAGEGGCTCATTTT TTEAGEGGCTCATTTT	CIG-EA CIG-TA	TTAC	-ACOG TC APP PP 1	ACAACAC		TCA CTC CAGG	A CTITAG TT AAAA A CTITAG TT AAAA	1441"" 2441"	- ATTTA	TAACI'IGAAAAA TTAACI'IGAAAAAA		C-CRAATTATTTAT CRAATTATTTAT	"T "T
64. ChLG8 R180289344RC C5	AAAAAATTTATAACT	CANAAACTAAAAGT	TGTAG TGTAAAACGG 1	ITTGTI C <mark>T</mark> AGTGAA	TT CAGCEGC TCATTTT	CIG TA	TTCC	ACOG TCATT TT I	ACAACAC	TACCI	TCACTCCAGG	ACTTAG TTANAS	AATT	ATTA	T TAACT TGAAAAA	TGGTGG AIG CG	CAATTATTAT	Ť
65. ChLG8_R180289344RC_C3	AAAAAATTTATAACT	CAARAACTAAAAGT	e <mark>t</mark> stas <mark>t</mark> ecaaaaces 1	ITTGTTC <mark>T</mark> AGTGAA	TTCAGCGGCTCATTTT	CTG-TA-	TIAC	-ACO <mark>G T</mark> CATT TT I	ACAACAC	TACCI	TCACIC CAOC	ACTTAG TTAAAJ	AATT	ATTA	I TAA <mark>C</mark> I IGAAAAA			т
67 Chi G8 R180289340_C2	ARAAAAT TTATRACT	CAAAAAC DAAAAG I	CGTAG AGCANAACGG 1	ITTGTTCTAGTGAA	TT CAGOGGC TCA TTTC	CIG TA	TTAC	AGOGTCATTTT	ACAA TAC	TACCI	TCACTCCAGG	ACTTAG TTANAA	AATT	ATTA	I TAACTIGAAAAA	TGGTGG ATG CG (CAATTATTAT	T
68. ChLG8_R180289350_C3	AAAAAAT TTATAACT	CAAAAACTAAAAGT	COT AG AGCARAROGG	ITTGTIC <mark>T</mark> AGTGAA	TTCAGGGCTCATTTT	CIG-TA-	TIGC	-ACO <mark>G T</mark> CATT TT I	ACAA <mark>T</mark> AC	TACCT	TCA CTC CAG	ACTTAG TTARAS	AATT	ATTA	I TAA <mark>C</mark> I TGAAAAA		C-CAAATTATTTAT	т
69. ChLG8_R180289348_C3	AAAAAATTTATAACT	CAAAAACTAAAAGT	FORTAG AGCARAACES I	FTIGTIC <mark>T</mark> AGTGAA	TT CAGCGGC TCATTTT		TTAC	ACCONTANT TTI	ACAACAC	TACCI	TCACTCCAG <mark>G</mark>	ACTING TTAAAA	LAATT	ATTA	I TAACI USAAAAA	- TGGTGG AIG CG (C-CARTTATTAT CARTTATTAT	T
71. ChLG8_R180289343RC_C8	AAAAAATTTATAACT	CAAAAACTAAAAGT	CGTAG AGCANAACGG 1	TTGTTCT AGTGAA	TTCAGGGCTCATTTT	CIG TA	TTAC	ACOGTCATTTT	ACAACAC	TACCI	TCACTCCAGG	ATTANTTANA	AATT	ATTA	TANCTIGAAAAA	-TGGTGG AIG CG (CAATTATTAT	Ť
72. ChLG8_R180289350_C4	AAAAAATTTATAACT	CAARAACTAAAAGT	CGTAG AGCAAAACGG	ITTGTI C <mark>I</mark> AGTGAA	TT CAGOGGC TCATTTT	CTG-TA	TTAC	ACOGTCATTTT	ACAACAC	TACC1	TCA CTC CAG	ACTTNG TTANAS	AGTT	ATTA	I I <mark>G</mark> ACI IGAAAAA	TGGTGG AIC CC (C-CAAATTATTTAT	T
73. ChLG9_R180290079_C4 74. ChLG9_R180290079_C9	AAAAAAAATTATAACT AAAAAAATTTATAACT		ILGTAG AGCAAAACGG 1 FORTAG AGCAA AACGG 1	FTT A FTC <mark>T</mark> AGTGAA FTT A FTC T AGTGAA	TT CAGOGGC TCA TITT TT CAGOGGC TCA TITT	CIG BA	TTAC	-ACCGACATTITI	ACAACAC	TACC1	TCACTCGAGG	ACTTAG TAAAAA ATTTAG TAAAAA		- ATTA	I LAACI'IGAAAAA Taacii IGAAAAA			T.
75, ChLG9 R180289936RC C2	AAAAAAT TTATAACT		FORTAS ASCARAR	ITTGTTCTAGTGAC	TTCAGCEGCTCATTTT	CIG TA	CIAC	ACCCCTATTTT	ACAACAC	TACCT	TCACTOGAG	ACTICC TRANAS	ATT	ATTA	TAACTICAAAA	TOGTOG AIC CE (C-REARTATTICT	T
76. ChLG9_R180290569_C2	AAAAAATTTATAACT	CAAAAACTAAAAGT	Postas ascaaaa <mark>t</mark> es 1	fttgtt c <mark>t</mark> agtga <mark>c</mark>	TT CAGCGGC TCATTTT	CIG-EA	CTAC	ACCCCTATTTT	ACAACAC	TACC1	TCACTCGAG	ACTICC TAAAAA	AATTT	ATTA	I TAACITIGA AA AA		C R G AATTATTT <mark>G</mark> T	т
77. ChLG9_R180290569_C16 78. ChLG9_R180290569_C7	ARARAAT TTATRACT ARARAAT TTATRACT	CARARCTARRAGT CARRARCTARRAGT	CGTAG AGCARAATGG 1 FCGTAG AGCARAA	FTTGTTCTAGTGAC	TT CAGOGGC TCA TTTT TT CAGOGGC TCA TTTT	CIG TA	CTAC CTAC	-ACCCCTATTTT -ACCCCTATTTTT	ACAACAC	TACC1	TCACTOGAGG	ACTOG TAAAAA ACTITIC: TAAAAA	ARTTT	- ATTTA	f taa c f tiga aa aa F taa <mark>c</mark> f tiga aa aa		GAATTATTTGT GAATTATTTGT	T.
79. ChLG9 R180289936RC C3	ARARATTTATAACT	CARAGETARAGE	CGTAG ASCARAACES	ITTGTT CTASTGAA	TTAAGGGGCTCAATTT	CIG-EA	CTAC	ACOGCTATTI	CAACAC	TACCT	TCACTCGAGG	ACTICC TRAAAS	ATT	ATTA	TAACTICAAAAA	-TGETGE ALC CE	C CE AATTATTAT	T

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80. CI	1LG9 R180290569 C3	ARAAAAT TTATRACT-	CAAAAACTAAAACTOSTASASCAAAACOSTITETICTASTSAATTAASOSGCCTCAATTTCT	G-TIA-	- CTAC ACCCCTATT TT ICCAACAC	TACCTCACTCGACCACTTCC TAAAAAATTT	- ATTTAT TAACT IGAAAAA	-TEGTEG AIG OG C-	- OG AATTATTTATT
- 81. CI	LG9 R180290569 C17	AAAAAAT TT ATAACT	CAARARCTRARAGTOGT AG AGCARARCEG TITE TI C T AGTGRATT RA GOGGC TCA R TTC T	-TA-	- CTAC ACCCCTATT TT TCCAACAC	TACCTCRCTCGAOGACTTCGTAAAAAATTT	- ATTTAT TARCTIGAAAAA-	TEGTES ATC CC-	- OG AATTATTTAT
82 C	Co P190200560 C9	3333337TT3T33CT		2-72-	- CTAC - BOOK CTATT TT TAC BACAC		A TTT BT TBB	TOCTOC ATC CC-	02 337737777
	LOB 1100280308 00	33 33 33 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0							
83. ÇI	1LG9_R180289936RC_C4	ARARAAT TTATARAUT		5 T.M.	TTACTATO COSTITITACAACAC	TACCICACITE ASCACITAS TAAAAABT	ATTTAT LAACTIGAAAAA	Teerenale C	G AATTATTTAT
84. CI	1LG9 R180290569 C9	AAAAAAT TTATAACT	T AAAAACTAAAACTOGTAS AGCAAAAC <mark>O</mark> G TTTGTTC T AGTGAATT TA GOGGCTCATTTTC T	G-TA-		TACCTCACTCACCTCACCACTTAG TAAAAAATGT	ATTTAT TAACT TGAAAAA	-TGGTGAAIG C-	GAATTATTTAT
85. Cl	LG9_R180290569_C13	AAAAAATTTATAACT-	CAAAAACTAAAAGTOGTAGAGCAAAACCG TITIGTI C <mark>T</mark> AGTGAATT <mark>TA</mark> GOGGC TCATFITC T	S-TA-		TACCTCACTTGAGCACTTAGTAAAAAATGT	- ATTTAT TAACTIGAAAAA-	-TGGTGAIG TG C-	-GG AATTATTTAT
86 0	CO P190200560 C18	333333777373377377	C2 2 2 2 2 C C2 2 2 C C2 2 C C2 2 C	2-72				TOCTON TO TO C-	C BETRETT
100. O	LOB 1100200308 010								
87. C	1LG9_R180290569_C4	ARARAATTTATRACT	- CARARCIAARS TOJIRS ASCARACUS TITGITCERSTGAATTERSOGGCICA TITTCE	9 - TW	TTACCATO COSTITITACAACAC	TACCICACITS AGCACITAS TARAAADST	ATTTATIAA	TGGTGALAIG	GATTATTAT
88. C	LG9 R180289936RC C6	ARAAAT TTATAACT	Caaraac taaaag tos tas arcaa aaces titg ti c t as tsaatt c r sce go toa titto t	G-TA-	T TACTA TOG COG TT TT TACAACAC	TACCTCRCTCSAGCACTTAGTAAAAATTT	ATTTGT TAACI TCAAAAA	TEETEE AIG CE C-	- CE AATTATTTAT
89 01	G9 R180290569 CT1	AB AA AAT TT ATB ACT	CAABAACTA AAAGTOSTAG A S CABAACES TITGTI C <mark>I</mark> AGTGAATI C A SOGGC TCA TITTC U	-TR		TACCTCACTTGAGCACTTAG TABAAAATTT	- ATTTOT TARCT TO ARAAA -	TRETES ATS CEC-	OG ARTTATTT ATT
00 N	1 C0 B100200026BC C0	BB 33 33TT 33TB 3CT	CARAGE AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED AND ARACTICATED	2 778	TANK TO CONTRACT TO THE TACK TO CAR	TA COMPACTOR ACTING TO BE A READ TO THE	ATTENT TABLE TO A BADA	TOOTION NTC OS C	12 33773777 BT
- 		BROODEL IN STROUT		3 LA			ATTICI DOGLI ICHARAS	1001002000	00 AST LAT TINT
- 91. CI	1LG9_R180289936RC_C12	ARAAAAT TTATAACT-	CAARAACTAAAAGTOGTAGAACAAAADGGTITIGITCOAGTGAATTOAGGGCCTCATITICO	S-TA-	ATAT TATIC COGTT IT TACAACAC	TACCTCACTCGAGCACTTAGTCAAAAATTT	ATTICT TAACTTARAAAA	TGGTGG AIG CE C-	OG AATTATTTATT
92. C	hLG9 R180290569 C14	AAAAAAT TTATAACT	CAAAAACTAATAGTCGTAG AGCAAAACGG TTTGTTCTAGTGAATTTAGCCGCCTCATTTTCT	3 – T <mark>C</mark> – – –		TACCTCACTTGAGGACTTAG TAAAAAATTT	ATTICI TAACITICAAAAA	TEGTES AIG CG C-	OG AATTATT
03 0	L GO P190200560 C10	BB BB BB BB TT BT B BC T	CARABARTA A T AGTIGTAG AGCAR BARGE TITIGTT C T AGTER ATT TA GGGC TCR TITITC T	2 - TE	- TTAC COCCETT TT TACAACAC			TRETES ATS CS C-	CG AATT
- NA C	L CO_D400200560_C5	35 33 530 mm 2 mm 2 000	AS AS ASOURS STRATEGY THE MERCES ASOC DETECTION OF SOME SAME TO COMES THE THE					macmac and an a	02 2 2 0 0 0 2 0 0 0
94.0	ILU9 R100290009 C0	ARABASI ITALAS I	CARAME TA ASTOTAS ASCARAESS INTOTICE ASTORATILA SCAGE LATITICE	3 10	TING GOOD CONTINUES AND A	THEE TENET TONOTAGE THE THURMAN IT	ATTICI LABOL LOBAAAA	100100310030	03 3331 1 1411
95. CI	hLG9_R180289936RC_C7	AAAAATTTATAACT-	CAAAAACTAAAAGTOGTAGAGCAAAAD G GTITGTIC <mark>T</mark> AGTGAATT <mark>TA</mark> GOGGCTO <mark>G</mark> TITTCO	S-TA-	T TAC - A COC CTC TT TT TACAACAC	TACCTCACTOGAGGACTTCG TAAAAAATT	ATITAT TAACT TAAAAAA	-TGGTGG AIG CG C-	- OG AATTATTTATI
- 96. CI	N G9 R180290569 C12	ARAAATTTTATRACT	CAAAAACTAAAAGTOSTAS ASCAAAACOS TITGTI C T ASTGAATT TA SOSGC TO <mark>S</mark> TITTCO	S-TA-	T TAC-ACOG CTG TT TT TACAACAC	TACCTCACTCGAGGACTTGG TABBABAATT	ATTTAT TARCET ARAAAA	TEETEE ATE CE C-	- OS AATTATTTATI
07 C	LC0 P180280036PC C10	BB AB ATT TT ATS ACT	- CARA BECTA BERTIST AS ASCERE ADCTO TITIST CTAGTICS ATT TASCESC TO TITITOO	5 - T20	TTAC ACCOUNT TT TACAACAC	TACCTOR CTCS AGE CTTRE TABLE A ATT	ATTTATTATTAR	TIGGTIGG ATG CS C	OS ABTTATTATI
06 C		3 8 7 7 8 8 10 10 7 10 8 7 10		7 000					
90. U	ILG9_K100290309_C0	HERBELLINGS I	-CARAAT LAAMSIGILS ASCREAMED HIGHLIGASIGARII INGGGCIGRIIIIGG	2 TU	- I ING ROUGOALI II INLANGAC	THUS TOROT SHOW AGT THE TRANAMAT	ATTIAL DAGT INDAAAA	-166166 MIG 08 C	- OG MAL LAL IIGI
- 99. CI	nLG9_R180290569_C15	AAAAAATTTATAACT	CAARA <mark>G</mark> CTARAAGTOGT <mark>O</mark> G AGCAARA <mark>TO</mark> G TTTGTTCT <mark>TG</mark> GTGAATT <mark>TA</mark> GOGGCTCATTTTCO	S-TA-	TTAC-ACCGCCATTTTTACAACAC	TACCTCACTCAGGACTTAGTAAAAAAT	- ATTTAT TARCTTARAAAA	TGGTGG ATG CG C-	- OG ARTTATTT <mark>G</mark> TI
100.0	Chi G9 R180289936RC C13	AAAAATTTATAACT	CAARABCTARABGTOGTAG AGCARABCOG TITGTT CTAGTGARTT TAGOGGC TOG TTTTCO	J-TA-	T TAC A CCC CT ATT TT TACAACAC	TACCTCACTCGAGGACTTCG TABABABATT	ATTTAT TAACT TGA BAAA	TGATGG	AATTATTTGT1
101 0	L CO D190290036DC C5	AB DD AAT TT BTB DOT		- TTD	TTAC A TO CO ATT TT TAC A A CAC	TACOTO ACCACO CUTAC TTAR A A ATT		TROUTION WITH CO. C.	C SSTRATT ST
400.2		A R R R R R R R R R R R R R R R R R R R							
102.0	HLG9 R100290009 C10	ARARAAT TTALRALT	-CARRAGITATRETOSTAS ASCARAGIAS TITETTCERETGARITERISOSCIULATITIC	i-IA-	TTAC ATO CTATTITI TALARCAC	TACCITACIOSAS ACITAS TIARARATIT	ATTTAT LERUT IGARAAR	TGGTGGRIGGC-	GRATTATITAT
103.0	ChLG9 R180289936RC C8	ARAAAAT TT ATRACT	CAAAAACTAAAAGTGGT <mark>G</mark> G AGCAAAAC <mark>G</mark> G TTTGTTC <mark>T</mark> AGTGAATT <mark>TA</mark> GGGGC TCATTTTC T	S-TR-	T TAC	TACCTCACTCGAGGACTTAG TTAAAAATTT	ATTTAT TARCT IGA BAAA	TGGTGG AIG CG C-	-GG AATTATTTATT
104 (ChLG9 R180289936RC C11	ARARAAT TTATRACT	CAARARCTARARGTOGTAG AGCARARCOG TITIGTICTAGTGARTTAGOGGCTCRTITTCT	G-TA-	TTAC ACCCCTATT TT TACAACAC	TACC TCACTCGAGGACT TAG TT AAAAA TTT	ATTTAT TARCT IGARAAA	TGGTGG ATG CG C-	GG AATTATTTATT
105	Chi CO R180200079 C5	ABABABT TTATE ACT	- CAAAAACTAAAAGTOTTEGAGCAAAACCGTTTGTTCTANGAATT	G-TA-	TTAC ACCOCCATTTTTACAACAC		ATTTATAAACTIGAAAAA	TGGTGGAIG CRC-	G AATTATTT ATT
122.5	N CO D100200070 CO	22 22 23 23 20 20 20 20 20 20 20 20 20 20 20 20 20	CARAGE ARACELO PACES AND AND A TAKEN AND A	- 972			A DEED ST. A STREET S & S & S	INCOMPANY AND AND A	OC SERVICE STOR
175.2		ABARARI TTATAACT	CARDON LANSAUTOR AS AS AS AS AS AS AS AS A A A A A A A	A 10	A A A A A A A A A A A A A A A A A A A	INCA INCLUSION OF THE TAABABATT	ATTIATASTUTUAAAAA	Tota Tata Allta CarC-	A ANT DAT TTAT
107.0	nLG9_K180290079_C3	AAAAAAT TTATAACT	CARARRUTARRETOGTES RECERERED STITETTCE ASTERATIONS CONCERNING	s IG	-TTAT ACUG CTATT TT TACAACAC	TACCICACTAGAGGACTIAG TAAAAAAATT	ATTATTAACTIGAAAAA	TG - GG AIG G C-	- CAAATTATTTAT
108.0	ChLG9 R180290079 C7	AAAAAAT TTATAACT	- CAAAAACTAAAAGTOGTAG AGCAAAACAG TITATTCTAGTGAATTCAGOGGCTCATTTTT	s I <mark>s</mark> -	TTAC ACCCCATTTTTACAACAC	TACCTCACTAGAGGACTTGG TABAAAATT	ATTTAT TAACT TGAAAAAT	TGGG AIG TG C-	-CAAATTATTTATI
100 0	L CO P180200070 C2	AB BB BATTT BTE BCT	<mark>BR</mark> AA BACTA AABGT IN THE BIC AS AB <mark>C I</mark> N THY IT IN ACTES AT CARGE IN ATTITUT	3-73		TA CONTRACTOR ACTOR OF TAGE TA A & A ATT		TG-GGATG C-	- (T: BETTETTET AT)
198.3									
110.9	ILG9 R1002900/9 C0	A AAAAT TTATAAL T	- CAAAAACTAAAAGTUGTASASCAAAACUS TITIGTICTASTGAATICAISUGGCTCATITICU	a TA	TTAL AUX CLATTITIALAACA.	TAGET ACTUS AS A CITING TARAAA TIT	ATTAACTIGAAAAA	TGG TGG ATG Co C	CTARTIAT TAT
111.0	ChLG5 R180282447RC C2	ABBATAAACTATBACT	CACAAACTAAAAGTCATAG AGCAAAACGG TTTATT CCAGTGAATT TAGCGGC TCATTTTC	5-TA	- T TAC A CCC CT ACT TT TACAACAC	TACCTCACTCGANGACTTGGTARAAA-TTT	ATTTAT TACTTIGA BAAA	TGGTGG ATG CG C-	- OG AATTATTTATT
112 (Chi G5 R180282447RC C14	AAAAAAAA TTATAACT	CAARAATTAARAGTTAFAG AGCARAACOG TITATI CCAGT TAATT IG GOOGC TCA TITTC T	G-TA-		TACCTCACTCGARAACTTCC TRATAAA ATT	- ATTTAT TAC TTTGAAAAA	TEGTES ATC CC -	- OG AATTATTTATT
445.7	bl C5 D100202447DC C4	22223337777272372377		2		TACCOMESCENCES BES CONTRACT TALES 33		TRACTINGE WITH CEL	12 2200200002000
113.2		AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		3 105				10010010000	GIAST LAL TINT
114. (ShLG5_R180282447RC_C7	AAAAAAT TTATAACT	CAARACTAAARGTOGTAGAGCARAAC <mark>A</mark> GTIT U IT CCAGTGRAFT <mark>TA</mark> GOGGCTCATFTTC	j – TA —	-TTAG ACCOCCAGT TT TACAATAC	TACCTCRCTCGARGACTICGTARAAAA TTT	ATTTAT TAC TTIGAAAAA	TGGTGG AIG CS C-	- OS AATTATTTATT
115. (ChLG5 R180282447RC C9	AAAAAAT TTATAACT	CAAAAACTAAAAGTOGTAGAGCAAAACAGTTTATTCCAGTGAATTAGOGGCTCATTTTT	S-TA-	T TAG A COG CCAGT TT TAT AACAC	TACCTERCTCGARGACTEGG TARRARA - TTT	ATTTAT TACTT TGARAAA	TGGTGG AIG CG T	- OG AATTATTTAT
116.0	ChLG5 R180282447RC C8	AAAAATTTTATAACT-	CAARARCTARARGTOGTAGAGCARARCAGTITTATTOCAGTGRATTAGOGGCTCATTTTC	-TA-	T TAC -ACCC CT ACT TT TAC AACAC	TACCTCACTCGAAGACTTCGTAAAAAA - TTT	- ATTTAT TACTT IGAGAAA-	TGGTGG AIG CG C-	- OG AATTATTTATT
1177	bLC5 P180282447PC C12	22 22 2 7 7 77 272 277		- TR		TACCOR CONTRACTORS AND CONTRACT AND AND AND THE	A 1111 BT TB	TRETER ATE C-	03 35773777 377
116.3								moomoo amo oo o	100 3 3 3 mm 3 mm 3 mm
118.0	ILG5_R160262447RC_C5	AAAAA	-CARARCTARRSTOTAS RECARACTS TITETTOCASTERATTERSOSCE TCATITIC	i TA	TTAC AUGCTAUTTTTALAACAL	TAGE TRACTOS AREACTING TRARAAA -TTT	ATTTATIA	TGGTGG ALG CS C	US AATTATTATT
119. (ChLG5 R180282447RC C8	AAAAAT TTATAACT	CAARARCTAR T RETOGT <i>RER</i> ECARARC R ETTT R TFOC <i>R</i> ETGRATT TR EGGECTCRTTTTC T	S-TA-		TACCTEACTOGANGACTERS AAAAAA - TTT	ATTTAT TAACT TGAAAAA	-TGGTGG AIG CG C-	- OG AATTATTTATI
120.0	ChLG5_R180282447RC_C13	AAAAAT TTATAACT-	CAAAAACTAA <mark>T</mark> AGTOGTAG AGCAAAAC A G TIT A IT CCAGTGAATT <mark>TA</mark> GOGGC TCATITTC T	-AT-E		TACCTTACTCGA <mark>AG</mark> ACTTAG <mark>AA</mark> AAAAA	- ATTTAT TAACTIGAAAAA-	-TGGTGG <mark>G</mark> IGCGC-	- CG AATT <mark>T</mark> TTT TA I
121.0	bl G5_R180282447RC_C10	ARARART TTATRACT	CAARBECTARATGT OF TAG AGC BARRON TO TAG TO CONSTRAINT TAGOGGC TO TITTO	-TA-		TACCTERCTCGARGACTERG ARABAAA -TTT	- ATTTAT TABCTIGAAAAA-	TEGTES	- OG AATTATTAATT
122.2	NI CE D100202447DC C11	335 33 33 577 375 307	CS 35 35 CTL 55 5 CTL CTL 3C SCC 35 35 CCC TTT ATT CC 30 TC 3 TTT CC 30 CC TC 3 TTT CC 30 CC 10 C 10 C	2 10		THE COLUMN CREW & NO. 1 COLUMN AND BEER AN - THE	A THEFT BUT THAN STORE & B.B. 7.7.	meaner and core	CC SSTRATTERT
122. 2		MARAANA I MIRACI		3 151	TING ACCOCCASITI LATANCAS	TAGG TINGTOGRAPHICT THE REALING AND THE	ATTIAT LANGT IGAAAAA	19919999199090	OB ANT INT TINT
123.0	ILG5_R180282447RC_C3	ARAAAAT TTATRACT	CARARCTARRGTOGTRERECARACTE TITATTACRETERATTACGECTCATITIC	i -TA-	-TTAG ACCOCCASTITITA	TACCTERCICUARSACITES AAAAAA AIT	ATTTAT LAACT IGAAAAA	-TEGTEGAIG CS C-	- US AATTATTATT
124. 0	ChLG9 R180291487RC C5	AAAAAATTTATAACT	CAAAAACTAAAAGTOGTAG AGCAAAACGG TTT <mark>AG</mark> T CCAGTGAATT C <mark>A</mark> GOGGC TCATFTTC T	S-TA-		TACCTCACTCGCAAACTTAGTAAAAAA-TTT	- ATTTAT TAACCIGAAAAA	-TGGTGG AIG CG T	- OS AATTATTTATI
125.0	ChI G9 R180291490RC C14	BRARAST TTATRACT	CAAR BECTARARG TOG TAG AGO BARACOG TIT EG T COAGTG RAFT C R GOG GO TOR TFTTO	G-TR-		TACCTCACTCGCARACTTAGTARAAAA-TTT	- ATTTAT TAACCIGAAAAA-	TEGTES ATC CF	- OG AATTATTTATI
420 /		B D D D D D D D D D D D D D D D D D D D	OT AS ABOTT STATE TO THAT NOT AS ABOTT THE ATT OT STATE AS A DECTION OF THE PROPERTY OF	7 778			A STATE BUT THE & COUNTY & B.B. A.B.	INCOMPANY AND AN AL	CT S STUDIES STO
120.5	AILOS 2 RIDU290309RC 03	AAAAA III		2 LU		INCOLORCICONNACTING INTRAMAN -III	ATTIAT LANGE IGARAAA	-166166A1666-	OSANI IAL IIAI
127.9	ILG3_2_K180295309RC	AAAAAA	- CAAAAACTAAAAGTCGTAGAGCAAAACAGTTTGTT <mark>TTAT</mark> TAATTCAGGGCTCATTTTC	a-ra-	TTAC ACCOCCACITTTACATITT	TAUS CACITISANSANTITIS TAAAAAA TIT	ATTTALLASTTIGAAAAA	TGGTGG ATG CG C-	- US AAT TATGT AT
128. 0	ChLG3 2 R180295309RC	TAAATTTTTAACT	CAAAAACTAAAAGTOGTAG AGCAAAAC <mark>AGG</mark> TT AC ICCASTGAATT <mark>TA</mark> GOGGCTCATITTC I	5-TR		TAC-TERCTEGARGA	- ATTTAT TARCTIGAAAAA	AGTIGG ANTITI	- CTAATTTTTTT
129 (C5 C5 C5 C5	ARARAAT TTOTRACT	CAARARCTARARGTOSTAG AGCARARCOG TIT AG T COAGTG O ATT C A GOGGC TOR TITTO D	TA	ATAC A TOG CT ATT TT TACAACAC	TACCTERCTCGAGGACTERG TARAAAA - TTT	ATTTAT TAACTIGARGAA	TGGTGG ATG CG C	OG AATTATTTATT
130 0	CO R180201400RC CR	AB AB AAT TTOTA ACT	- CAABARTABAARTIST IS ISCABARSS TT AT COASTS ANT CROSSENS TO TTTT	-T'A-	- ATAC A TOC CT ATT TT TAC AA CAC		- ATTT AT TAB CTTC A 20 44 -	TRETER ATC C-	CT: BETTETTET
182.3									
131.0	ILG9_R18029148/RC_C-3	AAAAST TTATAALT	-CARABETAR-GTESTRE ASCARABLES TIT <mark>RE</mark> TECASTSCATTCASESCTCATITIC	L'TA	ATAC ATO CTATTITTALAACAC	TACCTCRUTCGARGACTTRS TRAAAAA TTT	ATTATTATTGAAAAA	Tuli Tuli Allo To C-	- USARTTATTATT
132.0	ChLG9 R180291490RC C9	AAAAAT TTATAACT	CAAAAACTAAGTOGTAG AGCAAAAOGG TIT AG T OCAGTG <mark>G</mark> ATT O <mark>A</mark> GOG GC TCATITTC	A TA	ATAC A TCG CT ATT TT TACAACAC	TACCTCACTCGARGACTTAGTAAAAAA-TTT	ATTTAT IT ATTIGA BAAA	TGGTGG ATG TG C-	- OG AATTATTT ATT
133.0	ChLG9_R180291487RC_C-2	AAAAAAT TT <mark>G</mark> TAACT	CAAAAACTAAAAGTCGTAGAGCAAAACGG TIT <mark>AG</mark> TCCASTG <mark>C</mark> ATTC <mark>A</mark> GCGGCTCATTTTC	A-TA-	- ATAC A CCC CT ATT TT TACAACAC	TACCTCACTCGA NG ACTTAG T R ARAAA	-ATTTAT TATTGAAAAA	TEGTES ATC CE C-	- OG AATTATTTATT
134	Chi Ga B18020140000-00	AAAAAT TTOTA ACT	- CA AA AACTA AAAGTOGTAG AGC AA AACOG PPP ACP CC ACTO AAPP CA COCCOCA TOP TOP TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP COCCOCA TOP TOP COCCOCA TOP COCCOCA TOP TOP COCCOCA TOP TOP COCCOCA TOP COCCOCA TOP TOP COCCOCA TOP COCCOCA TOP TOP COCCOCA TOP COCCOCA TOP TOP COCCOCA TOP COCCOCA TOP TOP COCCOCACA TOP COCCOCACA TOP COCCOCACACACACACACACACACACACACACACACACA	A-T2-	ATAC A TOG CT APP PP TAC AACAC		ATT ATT ATT A A A A A A A A A A A A A A	TEGREG ATC CC.	CI AAPPART AND
102.5	SH CO D400004407DO O	NO NO NO NO NO NO NO NO NO NO NO NO NO N							
135.6		AAAAAAT TI ALAALT	- UNANAMA LANAMA LOT NA NAVANANJAA TIT NA TUUN	IA	ALL ALL CALLER TITLE ALARCES	INCOLONGIA AND CTING TRANSAR TT	ALLIAT LEAST 19AAAA	Trate Male Wills Ce Of	AS ANT METTAT
136.0	JNLG9_R180291490RC_C7	AAAAAAT TTATAAKT	CARAARTAAAAGTUSTAS AGCARAARDIG TITI <mark>AG</mark> TUCASTGURTTU <mark>A</mark> GUIGCTURTTTTU	A TA	ATAC A C CTATT IT TACAACAC	TACCTCACTCGARG CITTAG TARAAAA - TTT	ATTTAT TAACTIGAAAAG	TGG GGG AIG CF CG	G AAT AAT TAT
137.0	ChLG9 R180291487RC C3	AAAAAT TTATAACT	CAAAAACTAAGTOGT <i>N</i> G AGCAAAACGG TIT <mark>NG</mark> T CCASTG <mark>C</mark> ATTO <mark>A</mark> GOGGC TCA TTTTO <mark>T</mark>	A-TA-	ATAC A CCC TATT IT TACARCAC	TACCTCRCTCGARCACTTAGTRAAAAA-TTT	- ATTTAT TAACTIGAAAAA	TGGTGG AIG CG C-	- OG AATTATTTATT
138 0	Chi G9 R180291490RC C12	AAAAATTTATAACT	CAARAACTARGTOGTAG AGCARAACGG TITI <mark>AG</mark> T CCAGTG <mark>C</mark> ATT C <mark>A</mark> GOGGC TCA TTTTC	A TA	- ATAC - A TOG CT ATT TT TACAACAC	TACCTCGARGACTTAGTARAAA -TTT	ATTTAT TARCT TGA BB AB	TEGTES ATS CS C-	OF ARTTATTTATT
190.7	H G0 P180201487PC C	BAAAATTTRTRZ	CABB BACTA BABGT (STAC BC BB BACCC THE REP COACHES BUT COACHES BUT TO	2 778	TTAC ACCONCATATIZACAACAC	TACCTCACTCE ASA CTTAC TARABAA	A data bu data sa ya	TRETTER ATTACK	OC SATIFATION STOR
138.		ADDRESS I MARRIE T		- Art			A DESCRIPTION OF A DESC		TRALL AND ADDRESS OF
140. (TLG9_K180291490KU_C4	AAAAAAT TTATAACT	CARABRITA ARS TUSTRS AS CARARIES TIT ATTUCASTS ANT CASOS CONTATTITO	-TA-	-TTAC ACLE CATATTTACAACAC	TAGE TEACTCERAGACITAG TEARAAA -TTT	-ATITATI ATTIGAAAAA	TGGTGGAIGCGC-	- OS AATTATTTAT
141.0	ChLG9 R180291487RC C6	ARRART TTATARCT	– – <mark>T</mark> a aa aac ta aang t <mark>g</mark> g t <i>n</i> g ng k aa aace <mark>t</mark> titt a tt ccae tga att c <mark>a</mark> ece gc tca tt tt c <mark>i</mark>	S-TA-	T TAC - A COC T CATT TT TACAACAC	TATCTCRCTCGA RG ACTTRGT R ARARA-TTT	-ATTAT ITATIGAAAAA	TEGTES AIG CG C-	OG ARTTATTTAT
142	Chi G9 R180291490RC C15	AAAAAT TTATAACT	- TABABACTABABGTGGTAG AGRABAACGT TTT ATT CCAGTGA ATT CAGGGC TCA TTTTC	-TA-			ATTATI	TGGTGG ATG CF C-	OG ARTTATTT ATT
145 2	H CO D180201487DC C	B B B B T T T AT B BCT	TABABABCTA BABGTCOTAG AGABABABCOTTT ATT COAGTGA ATT CACCAC TOR TOTOC	- TB	TTAC BOOM BTTTTTACABORC	TA CTCA CTCG A BCA CTTAG TA BBA AZ -	A TIT BT TA TIT A BE AN	TOCTOC & TO CS C	CC 22 THE REAL PROPERTY AND
113.5		ROOM I INTROVI		3 1.11				10010020000	CO MAL LOL LINI
<u>199</u> (ULOS KI00291490KC C1/	AAAATTTTATAACT	INAMASI INAMS TUSTAS AS ARARISTITTATTOLASTGAATTCAGOGC TCATTTTC	a - 12A	TING AGUETCATTTTTALAACAC	INCLOSED AUTOSANACITAS TRABARA TIT	ATTATTATTGAAAAA	TGGTGGAIG C	- OS ARTTATTTAT
145. 0	ChLG9 R180291487RC C-4	AAAAATTTATAACT-	CAAAAACTAAAAGTCGTAG AGCAAAA TC G TTT A TTC T AGTGAATTC A GCGGCTCATTTTC T	3 - C A		TA CCTCA CTCGA AGA CTTAG TA AAA AA -TG T	ATTTAT TAACI TCAAAAA	TEETEE ATE CE C-	- OS AAT AATTT ATT
146	chLG9_R180291490RC_C5	ARAAAAT TTATRACT-	CRARARCTARARGTOSTAS ASCARAR <mark>TO</mark> S TIT <mark>R</mark> TT C R ASTS ARTT C R SOS SC TCR TTTTC R	3 - C h		TACCTCACTCGARGACTTAGTARAAA-TGT	ATTAT TAACTTCAAAAA	TEGTES ATS CF C-	OG AATAATTTATI
117 7	bl G0 R180201497DC C.0	3 3 3 3 3 T T T T T T T S T S C T	CARABARCTARRAGTOST AGRECCARRAGTE TUTISTT CTRACTER ANTER CONCERNING	- TB-	TTAC BOOG CORTETINA BARON	TACCTCACTCGACGACTTACTTACA AS _ TT	ATT CTTRATICA BE AR	TIGGTIGG ATTA CO.C.	OG AATTATTAT
176 2		AND AND AND AND A STATE							COLUMN AND A A STATE
140. (ILG9 K180291490KC CZ	AAAAAAT TTATAACT	- CARARASTRARSTUST AS ASC <mark>G</mark> ARALES TITGTT CHASTGARTT <mark>HA</mark> SCASC TCATTTTCH	a TA	TIAL ACCOUNT TARACAC	TAGE TERCTOSAGAGUTTAS TTAGARA -TTT	ATT-GTTEATTIGAAAAA	TOR THE ALLS OF C	G ARTTATTTAT
149.0	ChLG9_R180291487RC_C7	ARAAAAT TTATRACT	CRARARCTARARGT OF TAG AGO <mark>G</mark> RARCEG TITG TT C <mark>T</mark> AGTGRATT C <mark>R</mark> GC <mark>R</mark> GC TCR TTTTC <mark>T</mark>	s-TR-	T TAC A COC CC ATT TT TACAACAC	TACCACACTCGAGGACTTAGTTAGAAA-TTT	ATT-ATTATTGAAAAA	TRETEGATE CE T	OG AATTATTTATI
150 0	ChLG9 R180291490RC C16	ARARAAT TTATRACT	CAARAACTAAAAGT CET AG AGO <mark>G</mark> AAACEG TITE IT C <mark>T</mark> AGTERATT C <mark>A</mark> EC <mark>A</mark> EC TCA TITITC T	G-TA-	TTAC A COG COATT TT TACAACAC	TA CCACACTCG AGGA CTTAG TTAGA AA -TTT	ATT-ATTATTGAAAAA	TAGTGG ATG OG T	OG AATTATTTATT
151	Chi G0 R180201400RC C2	AB AA AAT TT ATA AA AA	- CARABARCTARRAGTCOTICS RECORD RACES TITIETT CTREETS ART CREETE TO TO A TREETE A	-T78-	TTAC - ACCCCTTTTTTACAA CAC	TACCARA CTOGACA CTTAC TTACA A A - TTA	ATT-ATTATTAAAAAA	TOOTOG ATC CL-	C AATTATT ATT
12-1-2		a a a annual a statistic d					A DUE - A DUE A DUE A A A A A A A A	mercines and of c	OT SAUDADUT STO
152.0	TLG9 K18029148/KC C-/	AAAAAT TTATAACT	- CAAAAAGTAAAAGTUGTAGAGOGAAALKGTITGTICHAGTGAATTCAGCAGCTCATTTICH	a TA-	TTAC ACCOCATTTTTACAACAC	TAGGACACICGAGGACITAG TIAGAAA -TIT	ATT-ATTATTIGAAAAA	TUG TGG ATG CG C-	LI ARTTATTTAT
153. 0	ThLG9 R180291487RC C4	ARAAAAT TTATRACT-	CARABACTABARGT CET AG AGC <mark>G</mark> ABACES TITETT C <mark>T</mark> ASTEBATT C <mark>A</mark> SC <mark>A</mark> SC TCA TITTC <mark>II</mark>	J-TR-	T TAC	TACCTCACGACGACTTAGTTAGAAA-TTT	- ATT-ATTATTGAAAAA	TGGTGG ATG CG C-	OG AATTATTTATT
154 (ChLG9 R180291490RC C13	ARARART TTATRACT	- CAAAAACTAAAAGTOGT NG AGO <mark>G</mark> AAACGG TITGTI C I AGTGAATI C <mark>A</mark> GC <mark>A</mark> GC TCA TITTC I	G-TA-	T TAC ACCC CCATT TT TACAACAC	TACCTCACTCGAGGACTTAG TTAGAAA-TTT	ATT-ATTATTGARAAA	TGGTGG ATG CG C	OG AATTATTTATT
166 2	H C3 2 P18020520000 C2	ZZZZZTTTTZZZZ	-CARABRETARRETOTING BCCARES TOT BODA STORES AND CREATED ON A DECEMBER OF	3 - T2-	TTAC A CTC CT ATT TT TAC AA CAC	TACCTES CTC SACCA CTTAC TT CA & & TT	ATTATAT TAR TTTLA AS SO	TRATICS CT C	TS BATTATITY AND
133.5	DILOG 2 RIDU280008RC C2	AND AND AND AND AND AND AND AND AND AND		- 10				The reader of the out C -	CONTRACTOR CONTRACTOR
136.0	TLG3 2 K180295309KG C4	ABABAAST TT ATBACT	- CAAAAA TAAAAST <mark>TT</mark> FASASC <mark>S</mark> AAAL A STTT AC FCCASTGAATT TA SCSGCT T ATTTTCT	p-TA-	TTAT AUXOUSAITTTIGCAACAC	TAGCICACICAMA CTTAGAAA TTT	ATTATIAA	-Tole L Re C IC C -	- us ABTTATTTAT
157.0	ChLG3 2 R180295309RC C7	ARAATT TT TRACT	CARAARCTARARGT CET NE AEC ARARC <mark>A</mark> E TI <mark>E RC</mark> E CCAETER AFT C <mark>A</mark> ECE SCIERT TTTC <mark>E</mark>	G-TA-	T TAC A COC CCATT TT TACAACAC	TACCICACTCAAGGAGTIAGTIAGAAA-TTT	ATTTAT TAACTTAAAAAA	TGATAGCIG CG C	OG AATTATTTATT
	Chi C3 2 R180295309RC C9	ABAATT TTTTBACT	CTAAAACTAAAAGTOGT <i>NG A</i> GCAAAAC <mark>A</mark> G TI <mark>G AC</mark> T CCASTGAATT C <mark>A</mark> GOGGC TCA TTTTCT	-TA-	T TAC-A COC CCATT TT TACAA CAC	TACCTCACTCACCACTTACTTACAAA-TTT	ATTTAT TAACTTABBBBB	TGATAGCIG CG C-	- OG AATTATTTATT
158.1									
158.0	C3 7 P180205300PC C9	BRAR TTTTTTTTTTTT	─────────────────────────────────────	3 - TTB				- THE ATT DIS COTO (TO CO-	، تن بر منظم عليه 10 ملغ على 12 2 2 1 1
158.0	hLG3_2_R180295309RC_C8	AAAATTTTTTAACT	CAARAACTAARAGTOGTAS ASCARAAC <mark>A</mark> S TI <mark>G AC</mark> T COASTGAATT C <mark>A</mark> SOGGO TCATTTTO <mark>I</mark>	S-TA-	TTAC ACCOCATT IT TACAACAC	TACCTCATCAAGGAGTTAGTTAGAAA-TTT	ATTTATTAACTTAAAAAA	TGAT AGGTG CG C-	CAATTATTTAT
158.0 159.0 160.0	ChLG3_2_R180295309RC_C8 ChLG3_2_R180295309RC_C6	AAAA <mark>TT</mark> TTT T TACT AAAA <mark>T</mark> TT <mark>GT</mark> TRACA	Caaraactaraagtog tas ng caraac a s ti g ac t coastga att c a sos go tcatttto r Caaraactaraag tog tas ag caraac a s tt aac t coastga att c a sos go tca tttto r	S-TA	TTAC ACCOCCATTITTACAACAC TTAC ACCOCCATTITTACAACAC	TACCTCATCAAGGAGTTAG TTAGAAA - TT TACCTCACTCAAGGAGTTAG TTAGAAA - TTT	ATTTAT TAACTTAAAAAA ATTTAT TAACTTAAAAAA	TGATASCIGCSC- TGATASCIGCSC-	- CRAATTATTTATT OG AATTATTTATT

162	CHIGG R	19020149780 02	AB AB ABT TT ATS SCT	-CA AN ARCTA ARACTICCT AC ACCAR ARCCC TTT	CORTER ATT CACCOCCTCA TUTTIC C - 12	а — — тта <mark>с</mark> а со	CACATT TT TACAC CAC		ATTTOT TAACTTCA AA AA	TOCTOS ATS OS C OS AATTATTT ATT
482	CHLOD D	19020140000000	22 25 25 TT TT TT A 5 5 5 5 5 5	CARA SAFTS BRACKTONIC BUCKS SAFTS TT		A			A 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TOTAL AND A COLOR AND AND AND AND AND AND AND AND AND AND
403.		49029024200-044	TRANSPORT NUMBER							
104.	CHLGO R	100209343RC_C11	ARRANT TTATARL T	TRANSL'IS ARRETUSTAS AR. ARABIDAS TITUSTI	CTASTGAATTCASCIGC TCATTTTC IS -12		CTATICI TALAACA.	TACT ACTO AND ACTING TRAATATIT	ATTALIAN	TGGTGG ALG C. CG APT ATT
105.	CULCO K	C180289344RC_C22	ARAAAAT TTATAACT	CARAAACTAAAAGTUSTASASCAAAACASTITISTT	CTASTGAATT CASUSGC FCATTTTTOS - 17	A TTAC ACO	GCTATTOT TACAACAC	TAICICACITIGANAACITAS TTAATATIT	ATTTAT LAACITIGAAAAA	TGGTGG AIG US C US ATT ATT
166.	ChLG7_R	(180286162_C4	AAAAAAT TCATAACT	-TAAAAACTAAAAGTCAFASAACAAAACCS TTTGTT	CCATIGAATICAGCEGCTCATITIACE-IC	G T TAT - ATC	ATT TT TACAACAC		ATTTAT TAACT GAAAAA	TGGTGG AIG CG C CAAATTATTTATT
167.	ChLG7 R	180286162 C11	AAAAAAT TOATAACT	- T AAAAACTAAAAGTC <mark>A</mark> FAGA A ACAAAAC <mark>O</mark> G TITGTT	CCATIGAATT CAGCGGCTCATTTTACE - T	G — — T TAT – A <mark>T</mark> C	TACAACAC		ATTTAT TACCT GAAAAA	TEGTES ATS CG C CAAATTATTTATT
168.	ChLG7 R	180286162 C2	ARARACT TCCTRACT-	-CAARAACTAAAAGTCAFAGAGCARAACCGTTTGTT	CCATIGAATTCAGCGGCTCATTTACG-T	G	AATATT TT TACAACAC		ATTTAT TAACT GAAAAA	TGGTGG ATG CG C CAATTATTTATT
169	ChI G7 R	180286162 C7	AAAAAT TTATAACT	TAAAAACTAAAAGTCATAGAACAAAACCG TITGTT	CCAGTGAATT CTA-GACTCATGTTACG-T	G TIAC ACC	ATT TT TACAACAC	TG CCCCACTCGAGGACTTAG CARAAAATT	ATTTAT TAACT GAAAAA	TGGTGG ATG CG C CAAATTATTTATT
170	CH C7 R	180288182 C3	AR AR ART TO ATA ACT	CARA BACTA BAACTINT AC BOCAS BACK TTWOTT	CACTER A REPORT OF A CORE PERMIT		TA ATT ATT TAC AA CAC	TR COTTA OF BOARDA CEPTAG CAAAAAA	ATTT AT TAA CTTL A AA 30	TOCTOR ATC CL C ARTTATT ATT
444		400200102 00								
14.			AAAAAAT ISADAAL I	GARARE TRANSTON TA ASCARRENA TITOTT	CASIGAATICIA GALTLATITIALS I	TIMI ACC	AND ALL THE ANG AL	I COLONGITANS ACTING CANADARTIT	ATTALLAS	TOG TOG ALLS US C. US ANT DAT IT ATT
1/2.	ChLG/_R	(180286162_C8	AAAAAAT TCATAACT	TAAAAACTAAAAA CATAG AGCAAAACOG TTTGTT	CASTGAATTCTA-GACTCATTTTACG-T	G TTAT ACC	AAT ATT TT TACAACAC	- IG CCTCACTTGARGACTTRG CARAAAATTT	ATTAT TAACTIGAAAAA	TGG AGG AUG CG C OG AATTATTTATT
173.	ChLG7 R	R180286162 C15	AAAAAAT TCATAACT	-TAAAAACTAAAAGTCA FAGAGCAAAACCGTTTGTT	CCAGTGAATTCTA-GACTCATTTTACG-T	G	ia at att tt tacaacac		ATTTAT TTACTTARAAAA	TGGTGG AIG CE C CG AATTATTTATT
174.	ChLG7 R	180286162 C12	AAAAAAT TCATAACT	- TAAAAACTAAAAGTCAFAGAGCAAGACCGTTTGTT	CCASTGAATTCTA-GACTCATTTTACE-TC	G	ATATT IT TACAACAC		ATTTAT TAACT GAAAAA	TEGTES AIG CG C CAATTATTTATT
175	ChI G7 R	180286162 C13	AS AT AAT TO ATS ACT	TRABARCTA ARAGTCATAG AGCARARCOG TITGTT	CCASTGAATT CTA-GGC TTT TTTACG - T	G	ATATT TT TACAACAC		ATTTAT TAA TTGAAAAAA	TGG AGG ATG CG C CG AATTATTT ATT
176	CHLOT D	190296162 05	35 33 33T TO 3TS 30T	TA AN ART TA ARACTCOTIC SCORE ARACON TENSOR	CORONA ANT CTA COCO TO A TELEVISION - TO	2 TTAT ACC	A BURNETT TAC SS CAC	TO COMPACT TO A DOB CONTROL TO A BAR AS THE	5 TETE BT TR 8 TETE 2 8 8 8 8	TOCTOC ATC CC C ARTINTER
477		100200102 00							A NUMBER OF THE ADDRESS IN A DECK	
144.			AAAAAAA INA INA INA INA INA INA INA INA	BARARD IRAARS I CAL AS AS CARARDOS III 1011	CONSIGNATION - SGCTCAL TINGS - R		AM ATTTLALAN AC		ATTALLATIKAAAAA	TOG TOG ALS OF C OS ANT TAL TIATT
1/8.	CILG/_R	(180286162_C9	AAAAAAT TCATAAC	TAAAAACTAAAAGTUTAAGASCAAAACUG TITUS	CCATFGAATTCASCSSCTCATTTTACS-T	G	AATATT TT TACAACAC		ATTAT TAA TIGAAAAA	TUGT SAIG COC-CIANTATTATT
179.	ChLG7 R	(180286162_C14	ARARAAT TCATRACC	TAAAAACTAAAAGTCCAAGAGCAAAACGGTTTGCT	CCATFGAATTCAGCGGCTCATTTTACG-T	G TTAT ACC	A ATT TT TACAACAC	- IG CCCCACTTGAGGACTTAG CARAAAATTT	ATTTAT TAACT GAAAAA	TGGTGG AIG OG CCAATTATTATT
180.	ChLG7 R	R180286162 C16	ARAAAAT T <mark>C</mark> ATRACT	- <mark>T</mark> AAAAACTAAA <mark>C</mark> GTC <mark>CA</mark> AG <i>A</i> GCAAAACEG TTTC <mark>C</mark> I	CCATIGAATICAGCEGCTCATITIACE-IC	G T TAT -ACC	ia <mark>at</mark> att it iacaacac		ATTAT TAATTIGAAAAA	TGGTGG AIG CE C CAAATTATTTATT
181.	ChI G7 R	180286162 C17	ACAAAT TCATAACT	TA AAAACTA AAAGTO <mark>CA</mark> AG AGCAA AACGG TTTG <mark>C</mark> T	CCATTGAATTCATCGGCCCATTTTACE - TC	G TIGT-ACC	ATATT TT TACAACAC		ATTTATTAACTIGAAAAA	TEETEE ATE CE C CE AATTATTT ATT
182	Chi G5 R	180283147 C5	TA AA AAT TOACA ACT	CABABARTA ABAGTINTAG ASC BABARES TITISTI	CASTGA ATT CTSCAGC TCAGT TTACS - 17	a	CONTRACTOR TO TACAA TAC	TA C TTA TTOG A BAA CT TA TT ABA AB ATT		TGGT ACATS CS C CATTATT ATT
105	CHLOS P	190293147 09	TAAAATTAAAAA	CARABODO BRACTICITAC BOCAB BBOCC TTROTT	Cacing a are creacaco ecacinere a co-re	B		ייייים גם גמב דיייים מעייים את מיייים את מיייים את מיייי		TOOT NO ATC OC C CATTATT ATT
463.		400203147 00								
104.	CULCO K	C100283147_C4	TRARAAT ICALARST	-CARARETRAAASTUSTASASCARARIAS TITGTI	CASTGARTICISCISC ILAS TITLOS - IN	A TIAI ACC	ALCOTTTTT LALAATAC	TARCTIRTICSARAACITATITTAAAAAIT		TGGTGG RIG CS C CRTTATTTATT
185.	CULCO K	(10028314/_CZ	AAAAAT TOACAACT	ARAAALTRAAAGT <mark>T</mark> GTAG AGCAAAACGG TTTGTT	CASTGAATTCTGCGGCTCAGTTTACE-T	A TTAN ACC	ATLATTTTACAATAC	TAKATATCGARAACTTATTAAAAAATT	-Ang Taattigaaaaa	TGAT ANG CG C CATTATTTATT
186.	ChLG5 R	(180283147_C6	TAAAAAT TOTOAACT	-CARARACTAR AGT CCTAG AS CARRACGG TT GTT	ST AGTGAATTCTGCGGCTCA <mark>G</mark> TTT <mark>A</mark> OG-T	A TGAT ACC	AGC TT TT TACAA AC	TAACATATTCGAAAACCTATTTCAAAAATT		TGGTGG AIG CG C CATTATTT
187.	ChLG5 R	R180283147 C9	TAAAAAT TOTOAACT	-CAAAACTAATAG TO <mark>C</mark> FAG AGCAAAACEG TITG TI	T retgaatt Ctegegc tea <mark>c</mark> ttt <mark>a</mark> ge – 19	a — — T <mark>g</mark> at – acc	ia <mark>go t</mark> iti ti iacaa <mark>t</mark> ac — —	TAACATATTCGAAAACCTATTTCAAAAATT		-TGGTGG AIG CE C -C ATTATTT <mark>T</mark> TT
188	ChLG5 R	180283147 C3	AAAAATTOGCAACT	CA AA AACTA A <mark>T</mark> AG TO <mark>C</mark> FAS AS CAA AACSS TITG TI	CRASTGAATT CPGCGGC TCATTTTACS-TC	G	ACTIT TT TACAATAC	TAACATATTCGAAAACTTAG AFAAAAATT		TEETEE AIG CE C CATTATTT ATT
189	Chi G5 P	180283147 C7	TAGA AAT TOACA ACT	TAAAAACTAAAAGTOGTAGAACAAAACGG TTOGTT	CASTGAATT CTGCGGC TCAGTTTACS - T	A TTAT ACC	BGCTTT TT TACAATAC	TARCATAT TOGA AAACT TAG AT AAA AATT	- GTGT TAA TT TGA AA AA	TGGTGG ATG CG C CATTATTT ATT
100	CHI GS D	180283147 010	TAGA AAT TOADA ACT	TAAAAACTAAAAGTCUTAGAACAAAACCU TTACIT	CAGTIGA ATT CTGCGGC TCAGTTTE CC T	B TAT BOO	AGCITT TT TAC AG TAC	TANCTER TOSCARAN TETATTERA AS A STOP		TRACTICS ATS CS C CATTATTTTTTT
101	2023	100200147 010	A REAL TRANSPORT	TALBACTARA CONTRACTOR OF THE CARD AND THE CONTRACT OF THE CARD OF			TA DO AUT UT AUTO A A CAC	TA ACTURE CONTRACTOR AND A ACTURE A A REPLACEMENT I	CIPPPINE A CONTRACTOR	
191.	SULST K	100200350_02	AMARAMANI IN TANGT	A REAL AND A REAL AND				AND ILLOW CARACTERATIC CIA	TRACK ISAAAAA	THE THE ALL OF COLORATINE TATTATT
192.	UNLGY_R	00285990_C3	AAAAAAAA	TCAAAALTACAAGTUGTAG AGCAAAACAG TITATT	CLARING ATTCTGCGGCTTATTTACE - T	A TARC ATC	ARCAITTTTTTAACAC	TASCTITCTCCARATTTTATTTATTGCTA	GTTITTAACATIGAAAAA	TGASTGAS ATACG C CRAATTATTTATT
193.	ChLG7_R	R180285990_C7	AAAAAAAT T <mark>CG</mark> TAACT	TTAAAACTAAAAGTCITAG AGCAAAACAG TITAT	CCACIES ATT CIECESC TATTTA CE-T	A TAAT ATC	ACATTTTTAACAC	TAGCATACT TA AGA T IG TA T ITAA T IG CTA	GT TTAACA TGAAAAA	TGGTGG AIG CG C TAAATAATTATT
194.	ChLG7 R	R180285990 C5	TAAAAAAT T <mark>OG</mark> TAACT	TTAAAACTAAAAGTOGT <i>NG N</i> GGAAAAC <mark>N</mark> G TITATT	CCA <mark>CICG</mark> ATICIGOGGCT <mark>T</mark> ATITI <mark>A</mark> OG - T	T TAAT -A TC	ia <mark>a</mark> catt tt t <mark>tt</mark> aaca <mark>a</mark> — —			TGGTGG AIG CG C CAAATTATTTATT
195	ChI G7 R	180285990 CB	AAAAAAT TOOTAACT	TTAAAACTAAAAGTCGTAGAGCAAAACAGTATAT	CTACIES ATTCIESSECTATITACE - T	T	ACATT TT TT AACAA	TAGCTTACTCAAGATCTTATTTAATTGCTA		TGGTGG ATC CC C CAATTATTTATT
106	ChLG7 R	180285000 C8	GAR AR ART TO ATS ACT	TTANAACTA AAAGT (GTAG AGC AA AACAG TATATT)	CTACING ATT CTRCS GC TTATTING OF - 17	A	ACATT IT -TRACAC	TAGCT CACTC AGAA CTTATT AGA AA ATT		TIGGTIGG ATG CE C
407	CHLO7 D	1002000000000	BB 33 ST TT 3 TB 3 OT	TABLE ADDRESS ADDRESS OF THE ADDRESS ADDRE				TRACTOR AND A BRACK AND A RANGE		
100		100203070 02	ARAMANI II ALANGI							
198.	CILG/ R	(180285677_C3	ARAACAT TTATAACT	TAAAAACTAAAAATCOTAGAGTAAAAACGAATTGTT	CCRETARATT TIGCATCING TIG CA-14	A TAAT AAC	ACTAPT PERABAACTC	TG TCTTAGTCARAACTTTTTT - AAAAACTT		TGATGGATAGGC - AAAATTAG TTATT
199.	ChLG7_R	(180285677_C5	ARAT AAT TTATAACT	TACAAACTA AAAG TOG TAG AG <mark>T</mark> AAAACGG TITIG TI	CCAST AATT CIGCAGCIES TITIG CA-12	A	A CTATT TT TACA <mark>G TC</mark> C	TAGCTTAGTCAABAACATTTTT-AAAAACTT		TG TGG AIG CG C AAATTATTTAAT
200.	ChLG7 R	R180285677 C7	ARARAAT TTATRACT	CAAAAACTAAAAGTCGTAGAGTAAAACGG TITGTT	CCAGT A AATT T FGC C G T T T ATTTT G C A -T7	A TTAT A AC	ACTOTI TI TACAA	TAGCTIAGTCABAAACTT		TGCIGG AIG CG C AAATTATTCATT
201.	ChLG7 R	180285677 C9	AAAAAAT TTATAACT	CAARAACTAARAGTOGTAG AGTAARAOGG TITGTT	CCAGT AAATT TIGOOG TITA TITIG CA-TZ	A	IAC <mark>T C</mark> TT TT TACAA <mark>T</mark> AC	TAGCTIAGTCARAAACTT		TGCIGG AIG CG C AAAATTATTCATT
202	ChI G7 R	180285877 C11	AAAAAAT TTATAACT	-CARAGETARARGTOSTAS ASTARARCAS TITETT	CCAST AAATT TIGCAST TTATTTIG CA-12		ACTTITITIACAATCC	-TAGT TIAGTCABAAACTT		TECTERATE CE C
203	ChLG7 R	180285676 C5	ABB BB ABT TT ATB ACT	CABABACTA ABAGT (GTAG BGTAB BACKS TOTGTT	CASTGA CTT TOSCS GC TTAGTTTS OF - TR	B	ACTATT TT CACAA INT	TAGC BUTCHICK A BAA CTTOCHT TTA AA ABT		TIGGTIGG ATG CE C OS CTTATTT ATT
203.	CHLOT D	100200010_00	33 33 337 77 375 377	CAR ARCES BASSECTION AC NOT A BASCOC TOTOL					TAR AND ADDRESS BA 22	
204		100203070 07	ARAMANI II ALAM I	CANANAL INNANDI COTAD IS MANACOG IS 1011				The off the rest o		IGGIGGALGOC USSOI IAI ITATI
200.		(1002030/0_00	AAAAAA	CARAMACTRAARSTOSTAS ASTAAAAADGG 16 TOTT	CASTGAUTTESOSGCTERS TTIS OS - 14		ACTATITICALARITA	- TROCKLADING ANALY CITACITICANANT		TGGTGGAIG GSC- USGTIATTATT
206.	CILG/_R	(180285676_C8	AAAAAATAACT	CAAAAATTAAAAGTUSTAGASTAAAALAIGT	CASTGACTT CSCSGCTTAGTTTGCG-12	A ATAT - AAC	CACTAINT IT CARAA TOT			TGGTGG ALG CG C CG GG PTATTTATT
207.	ChLG7_R	R180285676_C3	ARAAAT TTATAGCA	TG AAAACTAAAAGTCGTAG AG <mark>T</mark> AAAACSG T <mark>G</mark> TGTT	CASTGA OTT TOSCIGC TTAG TTTG OS - TI	R ATAT-AAC	ACTATT TT CACAA TCC	TAGCETAGTCGAEAACTTACTT TTT AAA <mark>A</mark> T		TGGTGG AIG CG C OS <mark>GG</mark> TTATTTATT
208.	ChLG7 R	180285676 C4	AAAATAAT TT TAACT	CAAAAACTAAAAGTOGTAGAG <mark>T</mark> AAAACGG I <mark>G</mark> TGTT	TCASTGACTT TCGCGGCTTATTTACG-T2	A ATAT A AC	ACTATT IT TACAA TOT	TACCATACTCGARAACTTACTT TATAAAAT		TGGTGG AIG CG C CG <mark>CG</mark> TTATTT ATT
209	ChLG7 R	180285677 C2	AAAAAAT TCATAACA	-TAAAAACTAAAAGTCETAS ASTAAAACSE TITETT	CASTGA OTT TPSCGGCT TATTTIG TS - 12	A ATAT A AC	ACTATT TT CACAA TCC			TEGTES ATS CS C CS CG TTATTT ATT
210	ChLG7 R	180285677 C4	A AA AAT TT ATA TC	TABA AGETA AAAGTESTAS ASTAB AACSATAT	CASTIGA THE DESCRACTER THE TAG OF -17	3	CTATT TT CACAA TCC			TEGTES ATS CEC OF SC TTATET ATT
511	CHI G7 D	100205677 CG	BBBBBTTTBTBC	TA 38 330TTA 33 TOTOTO 3 AA 38 330 ST TACTT	THE ROTAL & CONTRACTOR AND THE OWNER CONTRACTOR	B TTTAT BAC	2010111111110222020	TACCOTA TOWNER BAR CO TATT TAN AN ANA ANA	- TT BE STT ATT A TT A CA SS	TOCTOC ATC CC CC CC CC CC CC CC CC CC CC CC CC C
543		100200077 00	N Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z	AN AN ANTICA S AND DOT THE STATE AND AN AN AN AN AN AN AN AN AN AN AN AN AN				CALC NUMBER OF TAXABLE AND AND AND AND AND AND AND AND AND AND	TTAN AND ADDRESS AN AR	
<u> </u>			MARARI II GIRAL	SARAAL LEAR STOTAS AS MARAALOG TITOTT			ROMITICALAROAL			
213.	CULCI K	(180283677_C12	AGAAATTIGTAALA	TAAAASI TAAATI TUSTUSTUST	FRATEACTIC FACE ATTATTATE CA - 12	A TTAT ARL	ACTATI IT TALAACA.	TASCHIRATOSAHAAC-TAATTTEAAAAHTT	TTTTTATTAATTGAAAAA	TGIATGIA ARA CA C CIA GG PTATTTATT
214.	ChLG7_R	180285677_C8	AAAAAT TIGTAACA	TG AAAACTAAATGTCGTAG AGTAAAACGG TTTGTT	GAGTGATTTTGCGGTTTATTTGCG-TZ	a — — TTAT – A <mark>A</mark> C	ACTATT IT TACAACTC	TAGCATAATCGAAAACTTA-TT T AAAAAAAA	TTAARTTATIGAAAAA	TGGTGG AIG CG C CG GG TIATTTATT
215.	ChLG8 R	R180289322RC C2	AAAAAAATTATAACA	-CAAAAACTAAAAGTCGCAGAGCAAAACCGGCTTGTT	T CAGTGAATTCT <mark>A</mark> OGG <mark>G TT</mark> ATTTT <mark>G</mark> OG - TA	a — — T tat – a <mark>a</mark> c	IACT ACT TT TACAAC <mark>T</mark> C	TA <mark>G</mark> CTT <mark>CG</mark> TCG C A AA <mark>T</mark> FTA T TT -A T AAA A F T		-T R STGG AIG CG C OG <mark>CGA</mark> TATTT ATT
216	ChLG8 R	180289322RC_C49	TRAAAAT TTATAACA		T CAGTGA ATT C CA CGG <mark>G T</mark> A TTTT <mark>G</mark> CG — 14	A	CTTTCTTTACAA	TAGCTTAGTCGARAATTTATTT-AAAAAATT	AG TT ACA TT IGA AA AA	TGATGAATG CG C TG TCPTTPT ATT
217.	ChLG8 R	180289322RC_C9	AAAAAAAT T <mark>C</mark> ATAAC <mark>A</mark>	-CARTAACTAATAGTCGCAGAGCARAACGGTTTGTT	TTAGTGAATTCTAGGATTATTTG OG - TI	A TAA ACA	ACTACT TTCACGACTC	TAGC TIR <mark>G</mark> TCGAGAA <mark>IIG</mark> TA T TT -AAAAA <mark>A</mark> TT		TGGTGG ATG CG C OS GAATATTT ATT
218	ChLGA R	180289322RC C19	AAAAAAT TOATAAC	CARTAACTAATAGT CO CAG ASCARAACSS TTTGTT	TAGTGAATT CTACGGATTATTTC	A TANA ACA	ACTACITICACGACTC	TAGC TIAG TOGAGAA TG TAT TT - AAAAAATT		TGGTGG AIG CG C CG GANIATTT ATT
210	Chi GA P	18028932280 023	TARARART TOO TARCE	CARTAACTAATAGTCOCAGAGCAAAACCC TTCTT	CASTGAATTCTACEGATTATTTCC	A	ACTACTTCACCACTC	TASCTTASTSCACAA TO TATTT - AA AA AAT	- TE TE TAATT AAAAAA	TOGTOG ATC CC C CC AAA TATTT ATT
330	CHICA P	18028032280-027		CARTARCE A COLOR OF ACTION ACTION			ACT ACT TT CALL ACT	TAC TTRACTICACES TO TRANSFERENCE		
<u>22</u> 7.		10020032210 021			CACING & BUILDING CONCERNMENT OF THE CONCERNMENT OF THE					MOCINO AND CO. C. CO. 2 TRATT
<u> </u>	KULGO K	100208322RC_C33	AAAAAA TIYTAAL	CARACAS LASTASTUS AS ASCARASISS TITISTI	CASIGNATICIAGE TRATTING OF -12	A TRAN ALA	ACCESSION OF THE REAL OF C	INT ILST US BOAR IS LANT - AAAAA	- TOTT LAST ASAALA	TOO TOO AND CO C. CO AND INTTATT
222.	UNLG8 R	CI00289322RC_C36	AAAAAAAT TCATAAC	-CATRAACTAATAGTUS CAG AGCAAAACGG TTTGTT	CASTGAATTCTAUGGATTATTTG OG - TH	a TAAT ACA	ACTACITICACGACTC	TAGCTIAGTOGAGAATGTATTT-AAAAATT		TGGTGGAIG CGCCGAAATATTTATT
223.	ChLG8_R	(180289322RC_C31	TAAAAAAT T <mark>og</mark> taac <mark>a</mark>	-CAATAACTAATAGTOGOAGAGCAAAACGGTTTGTT	CASTGAATT CTACGGATTATTTIC CS - TA	а——Т ала -Ас <mark>а</mark>	ACTART TTEACEACTC	TAGCTIAGTCGAGAATGTATTT-TAAAAATT		TGGTGG AIG CE C CE <mark>CCC</mark> TATTTATT
224.	ChLG8 R	180289322RC_C38	ABB BA AAT TCATA AC 🔒 —	-CATAAACTAATAGTCGCAGAGCAAAACGGTTTGTT	T CAGTGAATTCT <mark>AT</mark> GG <mark>A</mark> T <mark>T</mark> ATTTT <mark>G</mark> OG-T2	А — — ТТАТ – АС <mark>А</mark>	AC-ACTTTCACAACTC	TA <mark>G</mark> CTTA <mark>G</mark> TCGA B AA <mark>TG</mark> TA <mark>T</mark> TT-AAAAA A TT		TGGTGG ATG CG 👗 — CG 😋 TATTT ATT
225	ChLG8 R	180289322RC C41	AAAAAAAT TCATAAC	CATAAACTAATAGTCGCAGAGCAAAACGGTTTGTT	CASTGAATTCTATGGATTATTTIC OG - TA	A TTAT ACA	AC-ACTTTCACAACTC	TA <mark>G</mark> C TIA <mark>G</mark> TCGA R AA <mark>IG</mark> TA T TT - AAAAA A FT		TGGTGG AIG CG 🗛 — CG GGG TATTTATT
226	Chi GA D	18028932280 044	TARARART TOGTAGCA	-CAATAACTAATAGTOGGAGAGCAAAACCG TTIGTT	CASTGAATTCTACEGATTATTTCC - 77	A	AC-ACITICACAACTC	TAGCTIAGTOGRAAA TG TATTT - AAAA AAT	IG TI TAACI AABAA AAB	TGGTGG AIG CE C CE CG- TATTT ATT
227	CHICK D	10020012200-02	22 22 22 TO TO AT 2 2	-CARA AACTA AT ACTIC AC ACCAR AACTC PERMIT	TANK IN A REPORT OF A CASE OF A DEPENDENCE OF A CASE OF A	a	ACT ACT TT CAC AACT	TASCITTASCATASA ALA TATTA A A A A A A A A A A A A A A	TR. TP 1 TRA 1999 A 2 2 2 2	TRICTICS ATC CC CS CCC TATTER ATE
556		10020332200 03		CARD BACTER A DAGE OF A CARD BACTOR AND A CARD AND A CARD						BOORDON AND CE C
<u>~~0</u>		100200322760_00		CALL AND LANDING LOSS AND AND AND AND AND AND AND AND AND AND	The second state of the se	- INT AUG			THE TRACT THE ARA	LOUIS AND AND AND A CONTRACTOR
229.	UNLG8 R	CI00289322RC_C7	AAAAAAAT TCATAACA	CARCHAUTAA RETUSCAS ASCARACES TITET	TRANSARTUTALSG TRATTING CA	A TIAT ACC	AGTACITICACCACTC	TAGCTIASTOSAGAN IG TATTT-TAANATT		TGG TGG ALG GS C - OG GGG TAT TT ATT
230.	ChLG8_R	(180289322RC_C29	AAAAAAAT T <mark>C</mark> ATAAC	-CAATAACTAATAGTCG CAG AGCAAAACGG TTTGTT	TTAGTGAATTCTACGCGTTATTTCCA	A	ACTACITICAL CACTO	TAGCTIAGTCGAGAATG TATTT-TAAAAATT	IC II TAATTTAAAAA	-TGGTGG AIG CG C CG <mark>CGG</mark> TATTT ATT
231.	ChLG8 R	(180289322RC_C11	aaraaaat t <mark>c</mark> atrac <mark>a</mark>	-CAATAACTAATAGT CGCAG AGC AA AACGG TTTG TT	TT AGTGAATT CT <mark>A</mark> CGG <mark>G TT</mark> ATTTI <mark>G</mark> C <mark>A</mark> -TI	A	ACTANT TTCACGACTC	TA <mark>G</mark> C TIA <mark>G</mark> TCG AGAA <mark>TG</mark> TA T TT - AA AA A A T <mark>T</mark>		TGGTGG AIG CG C CG CANTATTT ATT
232	ChLG8 R	180289322RC C13	ABBABAAT TCATBAC	CANTAACTAATAGT COCAG AGC ANAACGG TITG TI	TTAGTGAATTCT <mark>A</mark> OGG <mark>GTT</mark> ATTTT <mark>GCA</mark> -TI	A TTAT ACC	ACTANT TTCACGACTC	TA <mark>S</mark> C TIA <mark>S</mark> TCGAGAA <mark>TS</mark> TA <mark>T</mark> TT – AAAAA A TT		TGGTGG ATG CG C CG GANTATTT ATT
233	ChLG8 R	180289322RC C21	AAAAAAAT TCATAACA	CAATAACTAATAG TOGOAG AGCAAAACGG TITGTT	TAGTGAATTCTACGGG TATTTTG CA-T	ATTAT-ACC	ACTANT TTCACGACTC			TGGTGG AIG CE C CE CANTATTATT
234	Chi Ca -	18028032200-074	AAAAAAATTAATAAAA	CAAAACTAAAAGTOCAGAGAGAAACTOCTU	TRAGTICA ATT CTRACECCO TRATTER TO THE CAL	A	ACTACTTCACSACT	TAGCTTAGT GAGAA TO TATT - 33 23 3 TO		TEETES ATS CS C CS CARTATION AND
225	ALL CALL	100000000000000000000		CBBBBBCTS BRACK BC SC SC BBBBBCT STORE						
230.				OF AS A AGENT CONCERNENCE OF A CASE AS A CONCERNENCE OF A CASE AS A CONCERNENCE OF A CASE AS A C						MODELS AND ALL
230.	CULCO K	CIOU269322RG_C50	AAAAAAAT TCATAACA	CRARASS TRET RET CHERE AS CARRANGE TTTGTT	CASTGRATICIALSGATERTITIG OG - TI	A TTAT ACC	ACTICITITACAAOOC	INS. INSTANSANS TATIT AAAAATT	- IS TI TAA TATABAAAA	TGGIGG AIG GC C GGCAAATTTATT
23/.	CILG8_R	C180289322RC_C37	AAAAAATTOGTAAC	-CAAAAACTAAAAGTCACAGAGAGAGAAAACGGTTTGTT	CASTAAATTCTACGGG TTATTTIG CA-TA	A	ACCACITECACAACTC	TAGE TTAETCEAGAA IG TATITT -TATAAATT		TAAINGG AIG OG COG TOFTATTTATA
238.	ChLG8 R	180289322RC_C40	TAAAAAT T <mark>CG</mark> TAAC A	-CAAAAACTAAAAGTC <mark>AC</mark> AG AGCAAAACGG TITGTT	CAGTARATT CTACGG <mark>G T</mark> ATTTI <mark>G</mark> CA-TI	A	ACCACITCCACAAC <mark>T</mark> C	TAGG TIAG TOG ARAA TG TAT IT -TATAAR T		TATTTAT
239.	ChLG8 R	180289322RC_C35	TAARAAAAT T <mark>og</mark> trac	CARAACTAAAAGTC <mark>AC</mark> AG AGCARAACGG TTTG TT	CAGTAAATT CTACGG <mark>G TT</mark> ATTTI <mark>G CA</mark> -TA	A TTAT ACC	ACCACTTCACAACTC	TA <mark>GG</mark> TIA <mark>G</mark> TOGAGAA <mark>TG</mark> TA <mark>T</mark> TT - TAT AA A T T		TGATGG ATG CG C CG TCT ATT ATA
240	ChLG8 R	180289322RC C25	AAAAAAAT TCATAAC	-CARTAACTAATAG TOO CAS AS CARAACES TITG TI	CASTAAATT CTACEG <mark>C TT</mark> ATTTI <mark>C CA</mark> -TI	A	ACCACITOCACAAC			TGGTAAAIG CE C CE TCTTATTTATT
241	ChI G8 R	180289322RC C4	TARARAAT TOGTRAC	CARARACTAR TETCS CAGAGCARARAGE TITGTT	CAGTEGATT CTACEGG TATTTE CE - 🖬	A-TTAT-ACC	ACCACT TCCACAACTC	TAGC TIAGTCGAGAA TG TATTT -TATAAATT		TGGTGG ATG CG C CG TCT ATT ATT
242	Chi GA D	180289322PC CC	TABABAAAT TOG TA AC	CANAAACTAAAAGTOG GAGAGCAAAACGG TTYGTT	CASTGART CTACAGE TER TTTE OF T	A TTTL ACC	ACCACT TCCACAACAC	TAGC TIRGTOGAGAA TO TATTT -TATA A	- TGTTTAATTTGAAAAAA	TGGTGAATG CG C CG TCPTATTT ATT
545	Chi Con C	10020022200	TAB DO ANT TO A				18 00 8 0F TO 0 8 0 8 0 2 0		A REAL PROPERTY AND A REAL	
2.40.	VILOD K		THE REPORT OF A DAY O	COMPANY STATUTE LOS COMPANY STATUTE	an an an an an an an an an an an an an a		arwaren han an an an an an an an an an an an an a	STORE THE TOOLOGING THE TT THE TRANSMENT		200 20 m 200 00 0 - 0 200 101 11 11 11 1

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244	. ChLG8 R1802893221	RC C10 TAAAAAT TOGTAAC	Caaaaactaaactog c ag ag caaaacgg titg ti <mark>t</mark> cagtgaatt ct <mark>a</mark> c	AGC TTATTTC OG -TA-		TACCTIACTOGAGAATGTATTT -TATAAAT	T	-TGGTGAAIG OG COG TCI	TTATTATT
245	ChLG8_R180289322	RC C18 TAAAAAAT T <mark>CG</mark> TAAC	CAAAAACTAAAAGTOG CAGAGCAAAACGG TITGTT CAGTGAATTCTAC	AGG TTATTTE CG -TA-		TAGCTERGTCGAGAATG TATTT-TATAAAT	T	-TEGTGAAIG CG C CG TCI	FTATTTATT
246	Chi C0 B100200220								
270	OILOO RI002003221				I I I ROUSCOMI I CONCARDA				I LAL HIGH
247	ChLG8 R1802893221	KC C16 TAAAAAAT TCG TAAC	CARCARCTARCERGTOGCAR ASCARARCEGTTIGTTCASTGRATTCIAC	AGG TTATTTIG OG TA	TTT ACCACCACTTCACAACAC	TAGCTIAGTCGAGAAGG TATTT-TATAAAT		TEGTERATE CE C C C C	TTATTTATT
248	. ChLG8 R180289322	RC C24 TAAAAAAT TOG TAAC	CAATAACTAATAGTOOCAG AGCAAAACGG TTTGTT CAGTGAATT CTAC	AGC TTATTTC CC -TA-		TACCTEACTOGAGAATC TATTT-TATAAAT	T	-TEETGAAIC CE C IE TE I	FTATTTATT
240	Chi CB D180280322			ALL THE TRANSPORT		TAR AND A CONTRACT ACT AS TO TRATING THE ADDRESS OF		TRACING A AVEC CO. CO. TO THE	The second second
675	OILGO RIOUZO3322			and a state of the					L LOLL X X PSA A
250	. ChLG8_R1802893221	RU_UZU	CAAAAACTAAAAGTUGUAGAGCAAAADGG TITIGTTUCAGTGAATTUTAL	ASS TRATITIS OS -TA	TITI-ACCACCACTICCACAACAC-	- TAGCTIASTOGAGAATGTATTT-TATAAA	T	-TGGTGAALG US C US TAT	PERTTATT
251	ChLG8 R180289322	RC C14 TAAAAAT TOG TAAC		GGG TTAG TTTACG - TA	-TTAT ACCACCACTTCCACAACAC-	TAGCTEAGTGGAGAATGTATTT-AAAAAAT	T	TEETEE ATE OF C G AA	ATATTTATT
262	Chi Ce B100200222			TANK THE PROPERTY AND A DECK	TTAT A OCS CONCETTINGS CAA CAC			THE REPORT OF A 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	STATITY ATT
202	. CILGO R 1002033221		CARRAND IRRANGI CHICAS HIS CARAALOG III GIII CASIGAATI CIIICA	SOUTHING -IN-		INCLUS DIGNORNIN IN IT - REARING	- 19 TI TAK II MANANAN	-199169 MD9 09 C 09 MM	THE PARTY
253	. ChLG8 R1802893221	RC C34 TAAAAAAT TCG TAAC	CAAAAACTAAAAGTC <mark>AG</mark> AGAGCAAAACGG TITGTT <mark>T</mark> CAGTGAATTCT <mark>A</mark> C	GGG TTATTTACE -TA		TAGCTTAGTCGAGAA <mark>IG</mark> TA <mark>T</mark> TT-AAAAACT	T	-TEETEE ATE CE C CE AA	ATATTTATT
254	Chi G8 R1802893221	RC C39 TAAATAAT TTGTAAC		GGG TEA TETTIG OF TA	- TAT A CCACCACT TCCACAACTC	- TAGC TTAGTCG AGAA TG TATTT - AA AA AGT	T	TEGTES ATS OF C-OS AN	ATATTTATT
222									
200	CILGO_R100209322	KU_UA3 TAAAAAAT IKU TAACI	CAR ARCIAN RETURN AS ASCARARISS TITETI CAS TGARTICIAN	GG ITATITIG US -IA-		- TACTIRG TURAGAALG TATIT - AAAAACT		-166166 Mile Or C 05 161	PLAPTATT
256	. ChLG8 R1802893221	RC C30 TAAAAAATTOGTAAC	CAAAAACTAAAAGTCGCAGAGCAAAACGG TTTGTT <mark>T</mark> CAGTGAATTCTAC	AGG TTATTTIG CG -TA-		TARCTIAGTCGAGAAIGTATTT-TACAAAT	T	-TGGTGG ATG CG C OG <mark>GGG</mark>	TATTATT
257	Chi C8 R180289322	PC C32 TAAAAATTOGTAAC		AGG TTA TETTE CG - TA		TARCITTARTOGAGAA TG TATTT-TARAAAT	T	TRETES ATS CS C	TATTATT
250	CHLOB D400000000							maamaa ama ar a	
200	CILGO R1002093221	KU UZO ANADADAT TUNINAS	CRAMPS INAMS TO TAS AS CRAMPS STITUTI	ASS INATITIES OF TH	TINI ACCACIANTITUNCARCAC	INNOTI-GIOGREANIGINTII-INGANNI	JSET INETT IGRAAAA	199169 MB 05 C 05 06	, ALTIATI
259	. ChLG8 R1802893221	RC C45 TAAAAAT TOGTAAC	Caaaaactaaagtcasag recaaaaceg titg ti cagtgaatt ci ax	GG NIT ATITI <mark>G</mark> CG – TA —		TAGCTEAGTCGAGAA IG TAT TT -TA CAAN	T	-TEETGE AIG CG C CE <mark>GGG</mark>	TATTTATT
280	Chi G8 P1802803221			GER THE PERMIT CE - TR -		TAGCTTA ATCGAGAA TG TATTT-TA CA AAT		TRETES ATS CS C OS GGG	TATT ATT
2004								BOORDO 200 00 00 200	
201	. UNLGO_R1002093221	KU_U4Z TAAAT TIGTAACI	CARADIC TARANG TOCOMS AS TRANSMISS TTTO TITCAS TORATTOTOG	GG ITATITIGOG TA	TTAT ACCACCACT TTOACAACAC	TASCTLASTOGASAATSTATTT-TACAAAT	16 TI LASTI GAAAAA	TGGTGG ALG CS C- OS AN	TREFTATT
262	. ChLG7 R1802856851	RC C8 AAAAAAT TT <mark>C</mark> TAAC	o g ag aactaaaaag og tog agcaaaaceg tittatt <mark>t</mark> ca c igaaci ctaci	GGCTTATTTTCA-TA-	-ATAA ACTITIATT ATT TT TACAACTI	TA <mark>GT</mark> TIA <mark>G</mark> TCGA R AACTTA TC FAAAA <mark>CT</mark> TT	A G IG TAA TT IGAAAAA-	-TGGT AG AIG CG C CT AAT	TTATTAATT
267	ChI C7 P180285685			C. (. C. 1997) A 1979 1979 1970 (- TRATE AND CO. C C AND	TTATT ATT
222	OHLOT 1(100205005								
204	. GNLG7_R1802898891	KU_GIU AAAAAATTTGTAAL		SGCI <mark>T</mark> ATITICA TA	ATAA ACCUTTATITITACAACTT	TAGT TIRG TUG A RAAUTTAT TAAA AGUTT	ACITIAATTTAAAAAA	Too Too Allo Co C	PLATTATT
265	. ChLG7 R180285685I	RC C2 AAAAAAATTATTAC	OCAC ARTTARARG TOST AS ASCARAROSATT ATT TO ACTGRATT CTAC	GGTTTATTICCCA-TA-	- G TAA A CCTTT ATT TT TACAACTC -	TA <mark>GT</mark> TIA <mark>G</mark> TCGA N AA CTTA <mark>T TA</mark> AAAA <mark>G C</mark> TT	A	-TGGTGG AIG ÓG C C <mark>A</mark> AAT	FCGATTATT
288	Chi G7 R1802856851	RC CA AAAAAATTTETAAC		GGCTCATTTG CG-TA-		TACTTTACTCAAAAACTTATTTAAAACCTC		TECTED ATC CC	TTATTAATT
200	ONLOT D400200000								a section of the sect
20/	. UNLG/_R1002050051	AAAAAATTTCCAAC	TA AS ASL TAAAS STUFT IS ASCAASALASS TIT STTUCACIGAATTCT C	Tax. TTATTTIC GG -TA-	AUGTTATTTTACAACTC	TAGT TIAGTURABAAUTTATTAAAACCTT		Tata Told Alle Us C OF AAT	LT. T. BAATT
268	. ChLG7 R1802856851	RC C11 AAAAAAT TTCTAAC	OG PG AACTG AAGG T CG T AG AG C AA AACGG T TT ATT TT AC I G AATT CT AC	AGC TCATTTIC OG - TA	ATAA ACC <mark>G TT</mark> ATT TT TACAAC <mark>T</mark> C	TA <mark>GT</mark> TIA <mark>G</mark> TC A AAACTTA <mark>T</mark> TTAAAA <mark>CC</mark> TT	A G T TAT TT IGARARG	TGGTGG ATG CG C CAA	TATTATTAT
280	Chi G7 R180285685	RC C7 AAAATTTTTTAAC		EGCTCATTTECE-TA-	-ATAN ACCOTTATT TT TACAACTC	TRGTTIAGTCGRAAACTTATCTABAAACT	A	TEGT AGAIG OF C	TTATT AATT
572	CH 07 B400005000	BO 042 333350							mmamme -
210	. <u>cnrg/_r(80285685</u>	AAAAATTTETAAC	IN AVAILTRANSTOTAS ASCAAALISS TIT ATT TACISAATTCTAC	SGUTLATTINCS TA	ALAS ALLATTATTTTALAACTC	TASTTIASTUSASAACTCATCTAAAACTT	GIGTAATTIGAAAAA	THE THE ALL OF C CAAT	CLATTAATT
271	. ChLG7 R1802856851	RC C3 AAAACAT TT CTAAC!	CARGAACTAAAAGT CETAE AEC <mark>G</mark> AAACEE TTT <mark>E</mark> CA <mark>C</mark> EEAATT <mark>T</mark> F <mark>A</mark> C	IGGC TTA TTTTG OG - TA	-ATAA ACCGTTATT TCAACAACTC-	TAGTTTAGTCGARAACTTATTAAAACTT	AG IG TAA TT IGAAAAA	-TGGTGG ATG CG C 🖬 G AAT	CTATTAATT
272	Chi G7 R180285685	RC CS AAAAATTTOTAAC	TG 2G AACTA AAAG TOYTAG AGCAA AACSG TTT ATT TO ACTG A ATT OT AC	GACTRATTTS OF TR	ATAA ACCGTTATT TOTACAACT	TAGTCIAGTCGA BAACTTATT ABA ACCTT	A	TGGTGG ATG CG C	PCATTT ATT
516									
213	. CILG/_R1002056651	RU_UIJ AAAAATTTEIAAC		S BO IGATITITE OS -TA-	ACIG TTATT TO LACARCTC -	INGT TERSTONA RAGITERTITARA ACCTT	GIII TRATTIGAAAAA	THE THE ALLS US C-CAAAT	LEATTATT
274	Chi G7 R180286088	CZ AACCCTTGTAAC	CAAAAACTAAAAGTCGTAG AGCAAAACGG TTTETTCTATIGAATTCTGC	GGCTCTTTCTACA-TA-		TAGCTTTCTCGAGAACTTAATAAACGAAAC	TTAT TAT TAA AAAAA	-TEETEE ATE CE C CE <mark>CCA</mark>	ATAG TTGTT
276	Chi G7 D190396099	6 8 3 3 3 6 7 1 1 1 1 1 1 1 1 1 1		CALC BC BOTT CT A CAL TRA	TTAT BROZECSTITTT-SCALCEC	TRACTOR CONCERNING ACCESS CONTRACTOR AND A SALE	TAT TAT TAB CT TAB A A A A A A A A A A A A A A A A A		TTATT BTT
210	OILG7 R100200000								
2/6	. ChLG7_R180286088	C8 AAAACCITGTAAC	CAAAAACTAAAAGTIGTAGAGCAAAALGG TITATICTAALGAATICIGU	GCTCTTTCTACA-TA		- TAGCTLACICGAGAATITLAAIG AACGAAA	TINITICAACCI-AGAAA	-TGGTGG ALG G5 C OG GGA	TAATTATT
277	. ChLG7 R180286088	C5 AAACCCTTGTAAC	CAAAAACTAAGTOTTAGAGCAAAACGG TTTATTCTATIGAATTCIGC	GGCTCTTTCTACA-TA-	-TTACAACAC	TAGCTTACTCGAGAACTTACTAAACGAAAC	TING TI CAACTIGAAAAA	-TEGTGAATG CG C CG CGA	ATAATTATT
279	ChI C7 P180286088			CCCTCS BACTACC -TR			TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TREATING ATTA CT. C	STOC TT BTT
210									
2/9	. GhLG7_R180286088	G/ AAAAGGGTGTAAG	CAAAAGTAAAAGGG TAS ASCAAAGGG TITETTGTAGTGAATTGIGG	GGCTCA AAC IACG TA	TTATACTAS CATITTA ACAACAC	TASCICACICGAGAACITAAIG AACAAAA	TIMITITAGAAAA-	TGGTGG ALG CS C CG GGA	TA TTATT
280	. ChLG7 R180286088	C6 ARAAGCCTTGTRAC	CAARAACTAREGTOST <i>IS R</i> ECARAACES TIT ATTCEATIGAATTCISC	ggctca aac tacg-ta-	-T TAT ACCAG CAT IT TA ACAACAC -	TACCTEACTCGAGAACTTAATAAACGAAAC	TTAT TAT CAACTIGAAAAA	-TG -TGG AIG CG C CG <mark>GGA</mark>	ATAG TTGTT
284	CH C7 D190298098				TTAT BCC2CCBTTTTE ACAACAC	TRACTOR CONCERCING ANTINA TRANSPORT	TTER TRANSFORMERS CONTRACTS	TRETTOR ATE CAC	STOC TT BTT
201	OILO7 R100200000								STOR THREE
202	. ChLG7_R180286088	_G10 AAAAA	CARAARCIARARGTUSTAGASTARAARCASTITTATTUTATIGAATTUIGU	GCTCATICIACA TA	-TTCTACUGA TACTTTT -ACAG CAC	TAGT TLACICAS ASS TLASTI AS - ASU	TINTTICAGCINGAGAAA	TGGTGG ALIG US C CAGGT	TTACTTATT
283	ChI G8 R180289409	RC C2 ARARART TTATRAC:	CAAAAACAAAAGTOGTAGAGCACAACAG TITATTCCAGTGAATTCTAG	GGCTCATTCICCA-TA-	-TTATATCAC CTATTTT-ACAACAC-	TAGCTTACCCGAGAACATATTTAATAAAA-	TTAIGT TAG CITIGG AA AA-	-TEETEE ACC CC CE CC T	PATTTATT
294	CH C9 P1902904001			TAR - TRA 171 - 172 - 178 -	THE REPORT OF STREET ACAS CAC	TAC THE CONTRACTOR AS A CONTRACT AS A SA	TAUX TAUX TO TAC TO TAKE A SA SA	TRACTIVACE AND CT. C. TT. CO.	TAST TTATT
204	CILGO R 100209409			AGGIGATION IN					
285	. ChlG8_R1802894091	KC_C9 AAAAAATTTATAAC	CAAAAACAAAGT GTAGAGCACAACAG TTT TT CCAGTGAATT CTAG	GGCTCATICICCATA	TTACATCAG CTATTTT-ACAACAC-	TAGCTIACCCGAGAACATATTAATAAAA	TATGT TAG CTIGA AAAA	-TGGTGG Alig CG C CG <mark>GG</mark> T	PATTATT
286	. ChLG8 R180289409I	RC C13 AAAAAATTTATAAC	CAAAAACAAAG AGT GTAG AGCACAACAG TTT ATT CCAGTGAATT CTAC	GGCTCATICIGCA TA	-TTACATCAGCTATTTT-ACAACAC-	TAGCTIACCCGAGAACATATTTAATAAAA-	TTATGT TRG CF IGA BAAA	-TGGTGG AIG OG C OG <mark>GG</mark> T	PATTTATT
297	CH CB B180280400			CALCERCA TO COLCE TA	TTACATOR CROMMENT - SCARCAC	TAC SSTRATE STRATES CONTRACTS TO THE SSTREET SS SS	Tana rate rate rate as a sa	TRACTICAC WITH CO. C	Taarraarr
201	CILGO RIOUZOSHUSI			BGCIGATI	I INCHICAS CENTITI TABAACAC			199199719.090 090	1001 11 MILL
266	. ChlG8_R1802894091	RC_C1/ AAAAAATTTATAAC	CAAAAACAAAGAGTIGTAGAGCAGAACAG TTTATTCCAGTGAATTCTAG	GGCTCATICIGCA TA	-TTACATCAG CTATTTT-ACAACAC-	TAGCTLACCCGAGAACATATTTAATAAAA	TING TING CITIGAGAAA	-TGAIGG Alig CG C CG CG I	PATTATT
289	Chi G8 R180289409i	RC C7 AAAAAATTTATAGC		GGCTCATTCTGCA-TT	-TTAT ACCAG CTATT TT -ACAACAC -	TAGCTTACTCGAGAACATATTTAA-AAAA-	TTAGGT TTG CTTGG BABA	TEGT S ATG CG C CG CGT	TAATTT ATT
200	CH CP D1903904001								
290	CILGO KIOUZOSHUSI			GCICALICIGCE IL		INCITACIOS NORA CA INTITAR ANAR	THE LINE IS ANAL	-1661 Ma Mile Ca C 06 66 1	THUT TIMIT
291	. ChLG8 R1802894091	RC C14 AAAAAATTTATAGC	CAAAAACAAAAGTCGTAGAGCAGAACAGTTTATTCCACIIGAATTCTAC	ggctcatt c igca-ta-	-TTATACCAG CTATTTT ACAACAC	TAGCTTACTCGAGAACATATTTAA-AAAA	TING AAAA	-TGGTGG AIG CG C CG <mark>GG</mark> T	PAATTTATT
292	Chi G8 R1802894091	RCC3 AAAAAATTTATAAC	CAARABCARABAGT OF TAG AGC ACABCAG TTT ATT CCACTGA ATT CTAC	GGCTCATTCIGCA-TA-	CTAT ACCAG CT ATT TT -ACAA CAC	TAGT TTA CTCG AGAA (G TGT TT AAT AA A	TTATGT TAG CT TGG BABA	TEGTES ATS CS C CS CGT	PARTTTATT.
202	Chi G9 D190390400	BC CA BABASTITIATEACT	CARA ARCE ARACECTERS ACCORDANCES FOR ANTICIDES ANTICIDES	CALCHER DECK PROVIDE AND	T TAT BOOM (TA ATT TT - 7 (13 5 (26 (TRACTORIA CORCACINA CONTRACTOR AND AND AND AND AND AND AND AND AND AND	THE TRUE TO A BEAR	TRACTIVIC BUTC CC C CC CC	TA STOTE BOT
293	CILGO R 100205409			AGCIGATION IN	I TAL NO AND ALL I ACARONS	INCOLLACT SUSARCE LATIINE AGAI	THIGT LAGE IGHNAM	199199779.090 09991	1001 11MII
294	. ChlG8 R1802894091	RC C8 AAAAATTTATAAC:	CAARARCARAAG TO TAG AGCARARCAS TITATI COACTGART CIACI	GGCTCATICICCA-TA-	T TAT ACCAG OG ATT TT ACAACAC	TAGCTIACCAGAACATATTTAATAAAA	TAIGT IS CTICAAAAA	-TEETEE Alle ce c ce <mark>ce</mark> t	PATTATT
295	. Chi G8 R180289409i	RC C11 AAAAATTTATAAC	CAARARCARAAAGTOGTAGAGCACARCAGTTTATTCCACTGAATTCTAC	GGCTCATTCIGCA-TA-	-TTAT ACCAG OG ATT TT -ACAA CAC -	TAGCTTACCAGAGAACATATTTAATAAAA-	TTATGT TRG CTTGA BA AA-	-TEETGE ATE CG C CE <mark>GG</mark> T	PAATTTATT
200	Chi CB D100200400		CARABASC AN ASSCRIPTING SCORESSON FOR STRUCTURE	GCCTCS TTOTAL TO	TAT BCC BC CS ATT TT _ AC 33 CBC	TAC TTA CTAC ACRE CAPTANTERS AND A ST	TATA TO TAC DUTE 3 3 5 2 2	TRACTICES ATTA CT. C. C. C.	TA APPART NOT
280				AGGIGATINIA IN			THIGH HAVE IGAINAS	100100210000 000	1001 11 MIT
297	. GRLG8_K180289409I	KU_UG AAAAAAT TTATAAC	CARARCARARGTUST AS ASCACAS TTTATTCCACTGARTCTAC	LGCTCATTCICCA-TA-		TAGCTIACTOGAGAACAICTITAATAAAA	TINIGT TAGC TIGAAAAA	-TGGTGG AIG CG C CG <mark>CG</mark> T	TRATTTATT
298	ChLG8 R180289409	RC C12 AAAAAATTTATAAC	CA AA AAC <mark>A</mark> A AAAG TOO TAG AGC A <mark>C</mark> AAC <mark>A</mark> G TTT ATT CC A <mark>C</mark> IGA ATT CT <mark>A</mark> CI	GGCTCATTCTCCA-TA-	T TAT ACCAG OG ATT TT -ACAA CAC	TAGCTTACTCGAGAACATGTTTAATAAAA-	TTAIGT TAG CITICA AA AA	TEETGE ATE CE C CE CGT	TTATTTATT
200	Chi G8 R180280400	RC C16 SEARATTTETE	CARARAC ARARAGE COT AG AGC AT ARC AGE TET ATT CORACTE A ATT COTAC	GGCTCATTCTCCA	TTAT ACCAG OG ATT TT -ACAACAC	TAGC TTA CTCGAGAS CATGT TT AND AN AND	TATGT TRACT TRACE	TEGTES ATS C. C. C.	PATTATA
200	CH 00 D400000000							mormor and on a	mmamper a set
200	CILGO K1002098921	Ku ve Anananan TATAA	TANANA LANANG TESTAS ASCARARISS TITSTICCASTGAATTCASC	ASCIGATITICA US TA	- INS CRICE PARTA I TT INCAACAC	ASCTLACED AT A CITATIT TAAAAA	-ATTELAS-TTESASAS	-199 199 MIS 05 C 06 GAT	LISTTATT
301	. CnLG8_R180289892I	KU_CO AAAAAT TTATAAC	TTARAACTAAAAGTOGTAGAGCAAAACGGTTTGTTCCAGTGAATTCAGC	AGCTCATTICA CG -TA-				-TGGTGG AIG CG C CG <mark>G</mark> AT	LTAT TATT
302	ChLG8 R180289892	RC C6 AAAAAATTATAAC	TT AAAACTA AAAGT CGTA <mark>A</mark> AG - AAAACEG TITE TT CCAGTGA ATT C <mark>A</mark> GC	ASC TCATTTCA OS -TA-		TGGCTTACCCGATAACTTATTTAAAAAA	TTT TTASTTTS AAAAT	-TEETGE ATE CS C CE GAT	FTATTTATT
202	Chi G8 R180280902	RC C1 BRABAS	TRABARCTA ABAGT (STAG ABC AR BBCCCC TTRATT (CACTC & NOT CACTC	ASC TCA TTTT ACC TR	- TAC TA TCA AA TAT TT TAC AA CAC	TRACTOR COLOR AND TRACTOR AND A SAME	- ATT TT A	TRACERS ATS CLC	THE THE ATT A THE A
000	OLLOD D40000000								
JU4	. CULGO K1002898921	AAAAAATTATAAC		ASCOUNTITICAUS -TA-	- 1AS TRUCK MATRIT TT TAGAACAC	TACTING BARACTIATT AAAAA	ALT BAATUTAAAAA	-166 166 Mile Gi C Ui <mark>G</mark> AT	TATTATT
305	. ChLG8 R1802898921	RC C8 AAAAAATTTATAAC	TT AAAACTAAAAGTOGT <i>I</i> IG IIGCAAAACIG TTTGTT CCIIGTGAATTC <mark>A</mark> GC	AGCTCATTICACE-TA-		TA <mark>G</mark> CTIA OCOGA <mark>T</mark> AA CTTA <mark>T</mark> TT T AAAAAA	TT <mark>TG</mark> AAAA <mark>T</mark>	-TGGTGGAIG CG C OG <mark>G</mark> AT	PATTATT
306	Chi G8 B180280902	RC C2 вакакая ттатьас		AGC TCA TTTCA OG - TT		TAGC TTACTOGA TAACT TATTT TAA AB AB		TEGTES ATS CS C	PTATTTATT.
37-	CHI CO DI COCOCIO	• • • • • • • • • • • • • • • • • • •		No. No. Office State Street St				TRACTIVIC BUT OF C	THE REAL PROPERTY AND INCOME.
307	UNLOG K10020943/	AARAAT TOATAR	TOWARS INAASTUTIALASCARASUS TITATTTASTAATTCIAG	ATA ICATO TTAUS TA	TIAL AUTTAATITTTTACTACAC	TAACTIACA: ATAAACAAATITAAAAA	TINI DI LATATIARAAAA	199 199 KI9 C9 C 06 <mark>99</mark> I	L'LENTINTT
308	. ChLG8 R180289437	C13 AAAAAT TCATAAC	Tog aractaraagto <mark>t</mark> fa c agcaracces titatt <mark>tt</mark> ast <mark>a</mark> aat <mark>a</mark> ct a u	e <mark>ng</mark> tea i <mark>g</mark> tt an g — ta —	T IGT -ACTTART TT TT TACTACAT		A	-TECTEC AIC CC C EC <mark>CC</mark> T	CTANTT TT
305	Chi G8 R180280417	C7 AAAATTCATAAC		G AT PCATE TTACE - TA	TTAT-ACTTAATTTTTTACTACAC-		A	TEETE ATE TO C OR COT	PTANTTOTT
346	CHICA BARADO	-Cin 8333300 - 201		T BUT TO B TO THE AVE AND				TRACTICE STR. C. C. C.	Think Share
310	CILCO C 100508431	-XIV Assact Testast:	AND ADDRESS OF A DECK AND A DECK ADDRESS OF ADDRESS OF ADDRE	A PAR LOAD IN THE CASE OF	LIAL ACTION TTTTAL ACAC-	- ABA TIOVA ATORA TRATTINA - ABA	A A A A A A A A A A A A A A A A A A A	100 100 ALIA 10 V - Vi 00 1	TIVELAN
311	. ChLG8 R180289437	C5 AAAAT TCATAAC	TTG ARACTAAAAGTC T TA C AGCAAAACGATTTATT <mark>TT</mark> AG CA AATTCT A C	g at tca i <mark>g</mark> tt <mark>a</mark> og - ta	TTAT - ACTTAATTT TT TACTACAC-	TAACTIACAGAGACTAATITAAAAA	TTAT TT TAT TTTGARAAA	-TGGTGG AIG C3 C CG <mark>GG</mark> T	CTANTTGTT
312	Chi G8 R180280437	CA ABABAT TOATABC		e ne tea t <mark>e</mark> tt a ce -ta	TTAT-GCTTARTTTTTTTACTACAC		A	TEGIES ALC CC CE CC I	TTANTTGTT
345	CH C0 B100200437	C11 B B B B B B B B B B B B B B B B B B	THE RADIES AND COMPANY AND A COLOR AND ADDRESS OF A DREET OF A DRE					moonvolt amo to como	and a state of the state
513	GILGO R 10020043/	AAAAAT TOATAAL	TIMASE LASSINGTITI ALSO ASSAULTS TITETTERSTAATTCIRE	AT THE LAST THE THE TAKE THE	TIME COMMENTERIAL MACAL	INCTINCTING CIMPETTAN AND	TIMITI INTIGAAAAA	Tota Tal Milla Ila C (19 66)	LINGTIGTT
314	. ChLG8 R180289437	CH AAAAAT TCACAAC!	TOGA AACTACAAGTCTTACAGCAA AACGATTTATTTTAGTAAATTCTAC	G AG TCA IG TTAOG - TA	TTAT ACTTCATTTTTACTACAC	CARCITIA CAGATARA TRAATITAAAAA	TTAT TTAT TACTTIGA BABA	TGGTGG ATG CG T	CTANTTGTT
315	ChLG8_R180289437	C12 AAAAAT TCACAAC	TOGAAACTACAAGTOTTACAGCAAAACGATTTATTTTAGTAAATTCTAG	C AC TCATC TTACE - TA		CARCTINCES ATAAATTAATTAA	A	-TGGTGG AIG CG T TG GGT	TTANTTGTT
34ĕ	CHI CO B100200437	222 202 202 202	TO A A A STORE A A A STORE OF A A A STORE THE A STORE A STORE A STORE AND A STORE A				S S S S S TRUE DI LO DI	TREETINGS ATTE CT. C	ana ang ang
Sib	ULCO R 0020943/	Assast Tustast	MODOOL LANSAUL CEL AND ASSAULT TITETTANT AATTUTAL	A BO LOOM ITA	I IAI -ACTINATITTTALTACAC-	INSTITUTE ASS	THE OT IS TT IS A SASA		- ABLITOTT
317	. CnLG8_R180289437	C4 AAAAAT TCATAAC	TTGA AACTAGAAGTCTTCAGCAAAACGG TTTGATTAGTAAATTCTAC	ig a c tca i <mark>g</mark> tt <mark>a</mark> og – ta —		TARG TIACAAATTAACTAATTAACAA	TTAT TT TAT TAT TAT TT TGA NG AA	-TGGTGG ATG TG C OS AAT	CTANTICTT
318	ChLG8 R180289437	C6 AAAAAT TCATAAT	CATTOGAAACTAAAAGTOTTACAGCAAAACGG TTTGAT TTAGTAAATTCTAC	GACTCAIGTTACE-TA-	TTAT ACTTAATTTTTTACTACAC	TARS TEACAAATTAACTAATTAA CAA	A TAT TAT TAT TAT TATA A A A A	TGGTGG ATG TG C CG AAT	TTANTTGTT
210	CH CA P180280427	C4 ZZZZZTZTZZZ	A DE DE LE REPORT DE LE REPORT DE LE REPORT DE LE REPORT DE LE REPORT DE LE REPORT DE LE REPORT DE LE REPORT DE	TATE AND THE COLUMN	TTAT ACTTAT TT -30 PACAC	TAZCTTA BAC LT BAA TT BATTAA	TAT TAT TAT TA TAT TA A A A A A A A A A	TRACTICAS BITS OF C	TTANT TO THE
212	- CILCO R 10020043/			- 18 19 19 19 19 18	LIGA BOLLMANTITI - AT BURN		LINE DE LE MARARA		A LONG LA COLLEGE
320	. CnLG3_1_K18029228	CD AAAAAAT TCATAAC	CAAAAAUTAAATGATTITAAGGCAAAADGG TITGITITCAGTAAATTCTAG	ggci <mark>ni</mark> t-Ti <mark>gg</mark> g- ig		TAGICITITGAGAACTTATITT - TTABA	ATTTERARAAA	-TGG TGG ATG CG C OG <mark>GG</mark> T	PLATTATT
321	ChLG3 1 R1802022	89 C6 AAAAAT TCATAAC		ggct <mark>tt</mark> t-tt <mark>gg</mark> g-t <mark>g</mark>	TTAT ACTACT TTAT ACAACCC	TAGT CITTIGAGAA CITATITI TTAAA	ATTT AAAAAAA	TGGTGG ATG CG C CG CGT	FCATTTATT
222	CH C1-1-D1902022	80 C7 BABABTT ATBAC	CA AS 33CT 3 STORE STORE SALES CAS 33CT TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		TAT ACTACT TO TAC ACTAC	TACTO PERFORMANCE ACLES (TPUTA PERFORMANCE)	A THE BAA THE A A PARTY		TO ATT ATT
322		nanani Tuataac	CHAMING LIGHT THE AND CREATED IT FIT CAST ART CINA		I IMA NORICE II MI INDRE COL	INTELLET SPRINGLINGT	ATTI TANTI ON NAA		TIME LINE
323	. CnLG3_1_R18029221	by_c4 Araaaat ccataac	CAAAAACTAAATGACTTGAGGCAAAACATTTTGTTTCAATAAATTCTAC	GGCTTTTTGGG-TG	T TAR ACTACTTTT TTACAACCC-	TAGTCITTIGAGAACTIATITTATA	ATTT TAATT AAAAAAA	-TGGTGG ATG CG C CG <mark>GG</mark> T	FCATTATT
324	ChLG3 1 R1802922	89 C2 AAAAAATTTATACC	CAAAAACTAAATGT TTTA <mark>AG</mark> GCAAAATGG TTTG TT TCAGT AAATT CAAC	G CTTTT-TTTAG - IG	TTAT GCTACTTTT TACAACCC		ATTT TAAAAAA	TEGTES ATS CS C C CE CGT	FCATTTATT
225	CHI C2-1-D10020020	00 09 35 35 35 30				TRACTOR TO A DATE OF THE OWNER AND A DATE OF THE OWNER			To A data the second
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326	ChLG3_2	R180295520RC C2	ARARAT TOATRATT	- CAARAACTAAATCAACTAAAGCAARACCG TITAIT TCATIGA CATTIACGGC TCATITIC CA-TA-				- OG CC TTATTTATT
327.	ChLG3_2	R180295520RC_C6	AAA <mark>TT</mark> AT T <mark>CC</mark> IAACT				TTATCI TTATTIGAAAAA TGGTGG AIG CG C-	- OS A <mark>G</mark> TTATTTAT <mark>C</mark>
328.	ChLG3 ²	R180295520RC C4	ARARAAT TCATRACT	- T AAAAACTAAAAGT <mark>A</mark> GT <mark>A</mark> G GA CAAAACEG TITG <mark>CI T</mark> CA <mark>T</mark> IGAATT C <mark>CA</mark> CGGC TCATITI <mark>G</mark> OG – TA —		A-G CTIA <mark>T</mark> T B AGAACTTA <mark>T</mark> TTAAAT <mark>G C</mark>	T T <mark>N</mark> T C T TAA T <mark>G</mark> TG AAAAA T AA TGG ATG CG C-	- T G A <mark>G</mark> TTATTTA
329.	ChLG3_2	R180295520RC_C7	AAAAAAT TCATAACT	- C T ARAACTAAAAGT TA TAG GA CAAAA <mark>G A</mark> G TITIGIT TTAT IGAATT CIGOG A CTC T ITIT <mark>IG</mark> C A -TA	TTAT - ACCACTATT TO TACAACCT	ARGCTIATTEGAGAATTTAGTTAAAIGC	TTAT OF TAATT IG AAAAT	T G AGTTATTT
330.	ChLG3_2	R180295520RC_C5	AAAAA TTATAACT	CAATAACI <mark>G</mark> AAAGTOGT <i>A</i> GGGCAAAAOGG TITGIT TTATITA ATT <mark>CG A</mark> OGGCTCATTITCC A GA	-TTAC ACCATCATATCAACAACCT		TTALCI TAATTIGAAAAT TGGTGG AIG CE C-	- COAGTTATTTATT
331.	ChLG3_2	R180295520RC_C3	AGAAAATTCACACCT	- CTAAAACTAAAAGACGTAGGACAAAACGGTTTGTTTCATTGACTTGTGCGGGCTTTTTTACA CA	-TTAT-ACCATCATTICIAGAACCTCA	AGTACTTAGAG TACCTGAGAA OG TATTT AAAAG C	TTAT OF TAATTIGAAAAA TGGT AG AIG TG C	- OS AGTTATTTATT
332.	ChLG6 R	180283243RC_C3	AAAAAT TCATAACT	OS TARARGTOSTAS ASCAALSCOSTTIGTT CCALIGAATT CTAOSGC TCATTTIAOS - TA	-TTAC ACCAGE TITTT GTAATAC		TINTET TATTTIGAAAAATGGTGG AIG CG C-	- OF OGT TATTTACTA
333.	CHLG6 R	180283243RC_C6	AAAAAAATT TCATAACT	- OF ARAACTAAAAG TUSTAS AS CARTELISS THIGHT COAT IGAATT CHAUSGCTCRTTTTAUS - TA	TTAC ACCASE TITTISTAATAC	TAGCTIAGCUTGAAATITTTTAAAAA	TIME TATTTIGARAAA - TGGTGG AIG US C	CG CGTTATTTACT
332.		100203243RC C12	ABBR 33 33T TO BTR 3CT				THE TELEVISION OF C	
336	Chi G6 R	180283243RC C10	ARABART TCATRACT	- ORGA AACTA AAAGTTATAG AGC AA TACGG TITGIT CCATGA ATT CTAGGGC TCATTITAGS - TA	TTAC ACCAGE TTTTTTTTTAAAAAC	TAGCTTACCTAGAA	TAT TT TAT TT TAT TT TA AA AA - TGGTGG ATG CG C	- CG CC TTTTT ATT
337	Chi G6 R	180283243RC C15	AAAAAAAT TCATAACT	- OF ARAACTAAAAG TOG TAG AG CAN TO OGG TITG TE COATEGAATE CTACE AC TOATETTAOG - TA-	-TTAC ACCAGE TITTTGTGATAC		TTALT TATT GAAAAA TGGTGG AIG CE C-	- OG GGT TATTTACT
338.	ChLG6 R	80283243RC C19	AAAAAAA					OG GG TTATTTACT
339.	ChLG6 R1	180283243RC C5	AAAAAAAT TCATAACT	O <mark>g</mark> ar arcta arret og tag ag car <mark>tig</mark> ogg tittgit oc a <mark>r</mark> tgartt ot <mark>r</mark> og oc tor titte <mark>r</mark> ogtr			TINT IT TATIT GAAAAA TGGTGG AIG CG C-	- og <mark>gg</mark> ttattt a <mark>c</mark> t
340.	ChLG6 R1	180283243RC_C16	AAAAAAAT TCATAACT	O <mark>S</mark> AAAACTAAAAGTOS A AG ASCAA <mark>TSCA</mark> S TITGTI CCA <mark>TTA</mark> AATI CT A CGGCTCATTIT <mark>A</mark> OG – TA	T TAC ACCAGC TTT OT IGT AATAC	TAGCTIAOGCTAGAAATTTTAAAAAA	TTAT TT TAT TT TGAAAAA TGGTGG ATG CG G	og <mark>gg</mark> ttatttatt
341.	ChLG6_R1	180283243RC_C20	AAAAAAAT T <mark>C</mark> ATAACT	C <mark>E</mark> ARAACTARAAGT CE <mark>R</mark> AG AGCAR <mark>TECA</mark> E TITETT CCA <mark>TER</mark> ARTT CT <mark>A</mark> CEGC TCATTTE <mark>R</mark> CE - TA			T TAT T T TA T TT TEAAAAA <mark>A</mark> - TEETGE AIC CE <mark>G</mark> -	- CE <mark>GG</mark> TTATTTATT
342.	ChLG6 R	180283243RC_C7	AAAAAAAT TCATAACT		-TTAC ACCAGE TIT CITCE AA TAC		TTAT IT TAT TT IGAAAAATGGTGG AIG CG C-	- OG <mark>OG</mark> TTATTTACT
343.	ChLG6_R1	180283243RC_C4	AAAAAAAT TCATAACT	- O <mark>G</mark> ARAACTAAAAGTOSTAG AGCAA TS OGG TITGTI CCA T IGAATT CTAOSGC TOATTITAGG - TA	TTAC ACCAGC TITCI IGTAA TAC	TAGCTIAOGCTAGAAATITITTAAAAA	TTATT TATTTGAAAAA TGGTGG AIG CG C	- OG <mark>GG</mark> TTATTT <mark>G</mark> TT
344.	CHLGE R	180283243RC_C8	ARARAAATCAARACT	- CCARAACTAAAAGTOGTAGAGCAATCOGGTITGTICCATIGAATICTACGGCTTATTTIACG-TA-	-TTAC ACCAGE TITET IGTAATAC		TTATTTTAAAAAA TGGTGGAIG CG C-	GGTTATTTATT
345.	ChLG6 R	180283243RC_C22	AAAAAAAT TCATAACT-	CI ARAACTARAAGTIGTAS ASCARTIGUSS TITIGTI CORTIGAATT CTALISISC TEATTTTALS - IS	-TTAC ACCACC TTTTTGTAATAC		TAT IT TATAT TARAAA TEETEE AIG CE C-	- CE CC TATTCATT
340.	CHLGO R	190293330 00	ABBABAAT TUTAM, T	US ARAR, TRARRET TOT THE RECORD OF THE TOUR TITE TOUR ATTUINED TO A TTUE OF A TOTAL OF THE OF A TOTAL OF TRA	TTAL ACCASE TITETAR AC	TAGO TIALGUGAGAAATITTTALAAA		CONTRACTORY AND
348	CHLGG R	18028324380 013	ALAGAMAI IGALEACI	- CA AN AND A ANGTOT AS AS CAN THOSE THE TO CAN TO ANT CHARGE TO ATTITACE - TA	TTAC ACCASC TTTTTGTAATAC			- COCCTTATTATT
340	Chi G6 R1	180283243RC C14	AAAAAAAATTCATAACT	- CE ANANCTANNAGTOFTAG AGCAN TO CEG TITETT CCATTERANT CTACEGC TCATTERACE	-TTAC ACCAGE TTTTTTGTAATAC	TAGCTTACGCGAGAA	TAT TT TAA TT TGA AA AA TGG TGG ATG CG C-	- OF GGTTATTT ATT
350	ChLG6 R	80283243RC C23	ARARAAT TCATRACT	OF ARAACTAAAAGTOFTAG AGCAATGOGG TITIGTI CCATTOG ATTOAGCAGCTCATTITACA	TCAC ARAGC TITCI IGT AATAC	TAGC TTACGCGARAA	TTAT TT TAT TT TGAAAAA - TGGTGG ATG CG C	OG GG TTATTCATT
351	ChLG6 R	180283243RC C24	ARARART TO ATRACT	O <mark>C</mark> ARAACTA AAAGT OFT <i>A</i> S ASCAA <mark>TS</mark> CEE TITG TI CCA <mark>T</mark> IGA ATT CT <mark>A</mark> CE GC TCATTTE <mark>A</mark> CE - TA			TTATT TATTTGAAAAATGGTGGAIG CG C-	- OG <mark>GG</mark> TTATT <mark>C</mark> ATT
352.	ChLG6 R1	180283243RC C25	AAAAAAT TOATAACT	o <mark>s</mark> ar aacta arag tog tag ag caa <mark>tg</mark> ogg titig ti oca <mark>n</mark> iga att o <mark>ca</mark> og go toa titit <mark>a</mark> og ta			TTAT TATAT TTIGA AA AA TGGTGG ATG CG C-	- og <mark>gg</mark> ttatt c att
353.	ChLG6_R1	180283338_C3	ARARAAT TCATRACT	o <mark>sg</mark> aaac taaaag t <mark>e</mark> g t <i>a</i> s ascaa <mark>ts</mark> des titts ti cca <mark>r</mark> iga att ct <mark>e</mark> ces sc tca c t te <mark>a</mark> ce - ta	-TTAC-ACCAGC TITCI IGTAA TAC		TIAT IG TAG TT IGA AAAA TGG TGG AIG CG C-	OG <mark>GGA</mark> TATTT ATT
354.	ChLG6_R	180283338_C5	AAAAAAT TCATAACT		TTAC ACAAGC TIT CI IGTAA TAC	TAGCTIACGCTAGAAATITTTAAAAA	TTAT IS ING TITGAAAAA - TGGTGG AIG CG C-	- OG <mark>GG C</mark> TAT TT A N T
355.	ChLG6_R	180283338_C6	ARAAT TOATRACT	- CEGAAACTAAAAGTEGTAGAGCAAEGCEGTTEGTECCAETEGAATECTECGGCTCAETTERCE-EA-	-TTAC ACCAGC TITCI IGTAA TAC		TIAT IS INCTITICAAAAA TIGTIGG AIG OG C-	GGGTTATTTATT
356.	ChLG6_R1	180283338_C11	AAAAAAT TCATAACT	CEGRAACTAAAAGTEGTEGAGCAATGCEGGTTTGTTCTATEGAATTCTACEGCTAACTTTACE-TA-	-TTAC-ACCAGC TITCT IGTAAAGC		ATAT TT TAG TT TGA AAAA TGG TGG ATG CG C-	OG CCC TATTTANT
30/.	CHLG6 R	00203338 C4	AAAAAAT ICATAALT	- OSG AACTAAAAST STAS ASCACTS USS THIGHT CRAFTGAATT CHUGGC TCACTTTAUS - TA	TTAC ACCAGE TITETIGTAATAC	TAGCTIAUGUTAGAAATITTTAAAAAA	THE TATTIGAAAAA - TGGTGG AIG UG C	CG CC MEANING
350.		100203330 07	AAAAAA IIALAASI					- CC CC (00 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1
360	Chi G6 R	80283338 C1	A A A A T T A T A A CT	- OF AN ANOTA NANATING THE AND AN OWNER THE OTHER AND THE OTH	-TTAC-ACCAGE TTECT TETAATAC			- OG GGTTATTT ATT
361	Chi G6 R	80283338 C2	AAAAAAT TCATAACT	OSGAAACTAAAAGTTGTAGAGCAATGOGGTTTGTTCCATEGAATTCTTOGGCTCACTTTOG-TA	TTAC ACCAGE TTTET TGTAATAC	TRECTIACECGAGAA	TTAT TT TAG TT TGAAAAA - TGG TGG ATG CG C	OG GG TTATTTATT
362.	ChLG6 R	80283338 C10	AAAAAAT TOATAACT					- CTGGTTATTTATT
363.	ChLG6 R1	180283243RC C9	ARAR CAT TTATRACT	O <mark>s</mark> araactraaagtostas ascar <mark>ts</mark> oss titisti oca <mark>rt r</mark> aatt c <mark>ar</mark> oss toa <mark>r</mark> tt <mark>r</mark> os tr			TINT IT TATITA AAAA TGGTGG ATG CG C-	– og <mark>gt</mark> ttattt att
364.	ChLG6_R1	180283243RC_C2	AAAAAAAT T <mark>CG</mark> TAACT	- CAARAACTAAAAGTOGTAG <mark>G</mark> GCAAAAC <mark>O</mark> GTT <mark>G</mark> GTT <mark>G</mark> CAGTGAATTCTGC <mark>T</mark> GCTCA <mark>AA</mark> TT <mark>G</mark> OG - T <mark>G</mark> -	GAT - A CCA CCCTT TT CATAACAC	TA <mark>G</mark> CTIAC <mark>GCTI</mark> GAA	TTAT TT TATTIGAAAAA	OG GG TTATTT ACT
365.	ChLG6_R'	80283388_C7	ARARAAT T <mark>OG</mark> TRACT	CARARACTARARGTOGT <i>ING INCORRAGE</i> G TITATI COR A IGRATI CI <mark>ACA</mark> GO TORTI <mark>CIA</mark> OG - T <mark>O</mark>		TACCTIACCOGAGAACTTATTTTAAACA	T-R TAT C AACTIGAAAAAIGGT R EAIG OS C-	- OG <mark>GG TC</mark> ATT <mark>C TC</mark> FA
366.	ChLG6_R	180283388_C11	AAAAAAT T <mark>CG</mark> TAACT	- CARABACTARARGTOSTAS ASCARAACTS TITATI CORDEGATI CIRCASCICA TICIACE - TC		TACCTTACCCGAGAACTTATTTTTTAAGA	T-A TAT CARCETIGAAAAA	- CE CGT CATTCTCT A
367.	ChLG6 R	180283388_C4	AAAAAAAT TOG TAACT	- CARARACTRAMAGTOGTAG AGCARARCEG TITLETT COARTGRAFT CTACAGC TCATTITAGG - TC	-TTAT-AGCATC TITTT TACAACAC			- OG GGTCATTCTCTA
368.	ChLG6 R1	180283388_C6	ARARAATCATAACT	- CAARAACTRAARGTUGT NE RECAARACIGE TIT ATT CCATTERATT CTACASCTCATE TTACTAGE - TO	TTAT -AGCATATITTTTTACAACAC	ARCETIG COOGAGAACTTATITTTTTAAAAAA	T AT AT CAACT IG AAAAA TGG TGG AIG CG C	- OF CCCATTCTCTA
370	CHLGO R	100203300 010	ALAAAAA TOALAALI					
371	Chi G6 R	180283388 C9	ARARAA ATCATRACT	- CARA AACTA AAAGT GT TAG AGC AA AACGG TTT NTT CCAR TGA ATT CTACAGC TCA TCTTACG - TC	-TTAT-AGCATATITTTTACAACAC			- OGGATCATTCTCT A
372	Chi G6 R	180283388 C5	AAAAAAATCATAACT	- CAARAACTA ARGT OF TAG AGC ARAACCE TIT ATT CCAT I GAATT CTACA GC TCA TT TTACE - TC-	-TTAT-AGCATE TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT			GATCATTCTCTA
373.	ChLG6 R	80283388 C14	AAAAAA	CAAAAACTARAAGTOSTAS ASCAAAADES TIT <mark>A</mark> TI CCA <mark>T</mark> IGAATI CI <mark>ACA</mark> SC ICATITI <mark>A</mark> CE - T <mark>C</mark>				- CG GG TCATTCTA
374.	ChLG6 R	180283388 C12	ARARAA TCATRACT	CARARACTARARGTOSTAS ASCARAROSS TIT <mark>R</mark> ITICCA <mark>R</mark> ISARITICT <mark>A</mark> CASCTCRITITI <mark>A</mark> OS - T <mark>C</mark>			T-N T AT C AA C ITIGA AA AA TGGT N G ATG CG C-	- og <mark>gg</mark> t <mark>c</mark> att <mark>c tc</mark> t a
375.	ChLG6_R1	180283388_C13	ARARAA	- CAARAACTAAAAGTOGTAG AGCAAAACOG TITATI CCA <mark>T</mark> IGAATI CT <mark>ACA</mark> GCTCATITI <mark>A</mark> OG - T <mark>C</mark>	T TAT - A <mark>G</mark> CA T C T IT TT TACAACAC	TACCTIACCOGAGAACTTATAT TTTTAAAGA	T-AFAT CAACITIGAAAAA - TGGTAG AIG CG C-	OG CGTCATTCTCTA
<u>376</u> .	ChLG6 R	180283388 <u></u> C3	AAAAAAAT COGTAACT			TACCTIACACGAGAACTTATTTTTAAAGA	T-ATAT CAACITIGAAAAAA - TGGTGG AIG CG C-	- CE GATCATTCTC A
377.	ChLG6_R1	180283388_C2	ARARAR	- C <mark>B</mark> ARA <mark>TT</mark> TAAAAG TOG T <i>A</i> G AG OG AAG OG G TITG TI C T AGTG AATT CTACAG C TOA TTTTAOG - TO-	TAT AGCAGC TTT TT AAT AACAC	TACT TAACTC TAAAACAAAT TA TTAAAAAAA	TATAT CAACITIGAAAAA - TGETGE AIG CG C	OG GG TCATTC TTT
378.	ChLG3_2	R180296704_C3	AAAAAT TCATAACT	AAAAAACTAAAAGTOGOGAGAGCAAAAOGG TIT CIT CAAT AAATT CIGOGGC TCATTCAOG - TA	-TTAT-ACCATC TITTIG CATCAC	TAACIE - TABAACTIATITAAAAA -	TTTTTGAGAAA TGGTGG AIG CG C-	G AGT TAT AT AAAT
3/9.	Childs 2	R160290704 Co	AARAAT TOATAACT			TARCING TRAACITATITTAAS -AA		CT 2CHURA NU 222
381	Chi G3 2	P190296704 C4	A AA AAT TO ATA ACT	- ARARAR TERRAR TOPPAG ASCARARDES THE STOCKS TO ATT CLOSE CONTRACT CONTRACT	-TAT-ACCATCATTTTTGCAACAC	TAGCTTA CTCTA BAACTRATTITIC AA AA		- OS 26TTGT AT 388 T
382	Chi G3 2	R180296704 C2	AAAAATCATTACA	AAAAAATTAAAGGTOGCAG AGCAAAACGG TTIGTI CCAGTGAATT CIGOGGCTCATTITAOG - TA	TTAT ACCATATAT TT TS CAACAC	TTGCTAACTCTAAAATTTAAAA -AA	TTAT TAATTIGAAAAA TGGTGG AIG CG C	OG AGTTAT CTATG T
383	ChLG3 2	R180296704 C7	AAAAATGCATAACT	- CAARAACTRAANSTOS AS ASCARAACHS TIT TIT COAST ARATT CTAOS CONTINUES - TR-		TACCTERCTCOC ARA TITA-TT ARA AR CAR		CAAATTATATAAAT
384.	ChLG3_2	R180296704 C8	AAAAAT TCATAACT	CABAAACTAAAAGT C <mark>A</mark> TAG A <mark>AA</mark> AAAACG <mark>A</mark> TITIG TI C <mark>U</mark> AGTG AATT CIGOG G CI CA TI <mark>C</mark> IACG - TA				- OS A <mark>G</mark>
365.	ChLG7_R ²	180285984_C2	TRACTAT TCATRACT	- O <mark>s</mark> araac taa <mark>cc</mark> s t <mark>e</mark> sta <mark>ra ta</mark> araaces te r ite ccast r aa <mark>c</mark> e ct a cssc i <mark>s</mark> a te cta cs – ta —	T <mark>G</mark> ACACCATCTTITT -ACATAAT	TA <mark>GT</mark> TIACT T GA R AA AA T TA TT TT AAA — T	ATAT TTAAAT TGAAA TGGTGG ATG CG C-	og <mark>gg</mark> tta ag c att
386.	ChLG7_R1	180285984 <u></u> C4	ARAR TAT TTATRACS	CAARAACTAA <mark>C</mark> AGTOG <mark>C</mark> A RATA ARAAG <mark>A</mark> TIT A TI COAST A RA <mark>C</mark> I CT A OGGO I <mark>G</mark> AT <mark>COTA</mark> OG - TA		——————————————————————————————————————	ATAT TI TAAAT TGARA TGG TGG AIG CG C-	- OG <mark>CG</mark> TTA <mark>A</mark> TTATT
387.	ChLG7_R1	180285984_C7	ATAATAT TTATAACG	- CE ARAACTRACAGT CE CARATA ARAACEE TIT ATT CCAET ARACT CTECESC TAR TTCTACES TA	-TTACACATCTTITCITCCACAT	TAACTIACTIGAAAAA TAATTITAAA	ATAT TI TARAFTARAARA TGETGE AIG CE C-	OS CCC TAATTATT
365.	ChLG/ R	180285984_C3	AAAATAT TTATAACT-	- ARARAATTAACAGATGTAG AGCARAADGG TITGTT CCAGTGAG TI CIGOGGCACATTITAGG - CA	-TTAGCTARACTCTTTARCAACAT		ATACT TRAAT IGAAAAAAAT GG TGG AIG CG C-	- CG CCTTANTTATT
309.		100200904 C0	AAAATAT TTATAACT	- CARARACTRA RETTOTAS ASCARARUS TITOTI CCASTERS IT CIRCES CALATITI OS - CA	TRACCTRAC TO TT INCAACAT	TABUTIACIBARAAACATATITTTTAA	ATRUTT TRANTIGU AAAAA TABTUG ABG UG C	- OG COTTARTTATT
390.		100200904 00	AAAAAAA ATTTATAAAGT		TIANA CHACE IST IT IS CARCAL			
102	Child? P	180286027 C10	BART CTRACT					
393	Chi G7 R	180286027 C3	ABAT TCATAACT	TAAAAACTAAAAGTOOTAGAGCAAAACGG TTAATT CCAGOGAATT CTACGGTTTATTTTG CG-TG-	TTAT ACAATTTTTT-ACAACTG	CAAT TIATICGARAATIAAATT TAAAA	AAATAATAATAA TA TA TA TA TGA AAAA - TGG TGG AGG CG C-	GGGTTTTGA
394	ChLG7 R	80288027 C15	AAAT IG ATAACT	TAAAAACTAAAAGTOOTAG AGCAAAACEG TTAATT COAGOG ATT CTACEG TTCATTTIC CE - TA-	-TTAT ACTAT TTTTT -ACAAC	CAAT TIATICGA AAATI AAATT TAAAAAA	TAATAATAATAA TAA TO TEAAAAA TEETGE AGG CE C	CG CC TTTCGA
395	ChLG7 R	180286027 C19	AAAT I <mark>G</mark> ATAACT	TA AA AACTA AAAGTOOTAG AGC AA AACGG TT <mark>A A</mark> TT CCAG <mark>O 3G</mark> ATT CT <mark>A</mark> CG G <mark>T</mark> TCA TTTTO CG - TA		CART TTATTOGARAATTRAAARA	TAATAA TA A TAA T <mark>G</mark> TG A AA AA — TGG TGG A <mark>G</mark> G CG C—	- OG <mark>GG</mark> TT <mark>T</mark> TGA
396.	ChLG7 R1	180286027 C23	AAAT I <mark>G</mark> ATAACT	– T ABABACTABABGTO <mark>C</mark> TAG AGCABABCGG TT <mark>AB</mark> TT CCAG <mark>C</mark> GCATT CT <mark>A</mark> CGG T TCA TTTT <mark>5</mark> CG – TA ––	TTAT ACTATTTTT-ACAACTG	CAAT TIATICGARAA TIAAAAAA	TAATAA TA A TAAT <mark>G</mark> TGAAAAA — TGGTGG A <mark>G</mark> G OG C	og <mark>gg</mark> tt ttga
397.	ChLG7_R1	180286027_C11	AAAT TCATAACT	T AAAAACTAAAAGTO <mark>C</mark> I AG AGCAAAACGG TT AA TT CCAG <mark>C</mark> G ATT CT A CGG T TCA TTTT <mark>G</mark> CG TA		CAAT TIATICGARAATIRAATI TAAAAAA	TARTAR TA R T ART <mark>G</mark> TGARAAATGGTGG A <mark>G</mark> G CE C	- OG <mark>GG</mark> TT <mark>T</mark> F GA
398.	ChLG7_R	180286027_C16	AAATTTATAACT	- TABABACTA AAAGTOOPAG AG T AABACGG TT AB TT CCAG OSG ATT CT A CGG T TCA TPTTO CE - T <mark>G</mark>	-TTAT-BCAATTTTTTACAAC	CARTTIATICGA BAATTRAAAA	TAATAATAATAATG IGAAAAA - TGGTGG AGG CG C-	OG CG ITTT DGA
399.	ChLG7 R	80286027_C24	AAATTTATAACT	TAAAAACTAAAAGTOOTAG AGTAAAACSG TT AA TT CCAGOGG ATT CTACGG TTCA TTTTG OG - TG	TTAT - ACAAT TTTTTTACAACIIG	CARTTERTCGARAATTRAATT	TAATAAT AA TAA TG IGAAAAA TGGTGG AGG CG C	OGGTTTCA
400.	CHLG/ R	100200027 012	AGAT TTATAACT	TRARMASTRARAST CAT AS ASTRARASISS TTANTI CLASUSS ATT CTAUS STORE TO TTTT CS - IS	TTAT - ALAATTITTTTALAACIG	CARTING POUL A A A TRANSPORTANCE A A	TANTANI AN LAA 13 IGAAAAA TGGTGG AG CG C	CT CONTRACTOR
401.	SULS - B	180288027 020	AAAITTATAACT-	- The same langer in the second statement of the second statement of the second s			- BASTAN AN LAS IN IGARARS - TRETING AND CO C-	
402	Chi G7 P	180286027 C25	AAATTCATAACT	TARAAACTAAAAGTCETAG AGCAAAACGG TIT CTTCCAGGGAATTCTACG TCATTTACG	TTAT -ACTAT TTTTTTTACAACT	CARTTATCGARAATTAAATTAAAA	AAATAATAATAATAG TG TGAAAAAA TGGTGG 200 CS C	GGGTTTTGA
404	ChLG7 R	180286027 C31	AAAT TCATAACT-	TAAAAACTAAAACTOCIAS AGCACAACES TITUTI COASCAATICIACE ATTCATITICOS - IC	-TTAT ACTGTTTTTTTTTTTACAACTG	CAAT TIATTOGA RAATI AAATT TAAAA	- AA TAATAA TAA TO TGAAAAA - TOGTOG AGO CE C-	- OG CC TTTTAA
405	ChLG7 R1	180286027 C26	AAAT TCATAACT	A BAAACTA AAAGTOCTAG AGC AAAACGG TOT BTT CCAGOGAATT CTROGGTTCA TTTTG OG - TG	TTAT - ACTGTTTTTTACAACTG	CART TTATTCGARAATTRAAATTTAAAA	AAATAATAATAA TAAT <mark>G</mark> TGA AAAA — TGGTGG A <mark>G</mark> G CG C	- CG CG TTTTGA
406	ChLG7 R	180286027 C4	AAAT TCATAACT	- TABABACTABAAGTCOTAG AGCABABCGG TITGTT CCAGOGABTT CTACGGTTCATTITG CG-1G-	TTAT ACA AT TTT TT TACAAC	CART TING TOGA BAATT AAATT TAARA-	AATAATAATAATG TGAAAA- TGGTGG AGG CG C	OG GG T TT GA
407.	ChLG7 R1	180286027 C9	AAAT TCATAACT	<mark>T</mark> aaraactraaacto <mark>c</mark> tas ascaraaces tite teccas <mark>e</mark> s rate ct r oss <mark>T</mark> ica tite <mark>s</mark> os t <mark>s</mark>		CARTTIAC TOGARAATIRAATT TTAAAA	AATAA TA A TAA T <mark>S</mark> TGAAAATGGTGG A <mark>G</mark> C OS C	- og <mark>og</mark> t t <mark>t</mark> p ga

408, ChLG7 R180286027 C6	AAAT TCATAACT	- TAARABEETAAAAE TOOTAS AS CAARAEGES THE TH CORSEGAATH CTREES TO ATTTE CORSEGAATH CTREES TO A TTTT CARAETAA CAETA
409. ChLG7 R180286027 C8	A AAT TCATA ACT	TAAAA-CTAAAASTCE MS ASSAAACES TITSTE COAST SAATT STATEST TO ATTITE (S-15
410. ChLG7 R180286027 C30	A AAT TCATAACT	- TAAAAACTAAAAAGTOTAG AGCAAAACGG TITGTOCCAGOGAATT CTACGGTCA TTTTOCG - IG TAX - ACA-CITT TTTOCAACING
411. ChLG7 R180286027 C14	AAAT TCATAACT	- TANAARCTAAAAGTOTAS ASCAARACGS TITISTI CCASCEAATI CTACGETICATITITICS 16 - TIGT -ACAATITI TITITCAACTIS - CAATITITICS AAAATTAAATTAAAATTAAAAATTAAAAATTAAAAATTAAAA
412. ChLG7 R180286027 C18	AAAT TCATAACT	TAARABETAAAAGTOE ME MECAAAAEGE TITETT COMBESAATT ET MEGETICATTITE CI-IE
413. ChLG7 R180286027 C22	AAATTCATAACT	- TAAAAACTAAAAAGTOTAA ASCAAAACES TITETT CCASCEAATT CTĂCESTICATTITECE - IS TIET - ACAATTIT TITECAACIE CAATTIA TICAAAAATTAAAAATA AATAATTAATAAA TAAAAAAA TESTES AES C OS CEITETE CA
414. ChLG7 R180286027 C27	AAAT TCATAACT	- TAAAAACTAAAAAGTOTAA SICAAAACGI TITGTI CCACGIAATII TTACGA TIGTI CATTITG CI - TGTI - ACAATTITI TI TTACAACTIG
415. ChLG7 R180286027 C7	AAAT TCATTACT	- TRARAACTAAMS CORTAS INCAMPACES INTERTICIAS ANTICATITICS INTERTICIATION OF TACTACING CORTARATIONAL CORTAGE AND AND AND AND AND AND AND AND AND AND
416. ChLG7 R180288027 C13	AAAT TCATAACT	- TAARAACTAAAAGTOE AS ASCAARACES TITETT COASEBAATI CTÂDE ATTCATTITE OF -16
417. ChLG7 R180286027 C17	AAAT TCATAACT	- TAAAAACTAAAAGTO TAG MICAATITI CAAGEAATITI TAG AATICA TITI GI - IG - TIAT - ACTESTITI TI TACAACTES
418. ChLG7 R180286027 C29	AAAT TCATAACT	- TARAAACTAAAAGTOTAS ASCAAAACGS TITGTT COASCEAATT CTÁOS AMTCATTITEOS 16 - TIAT - ACTSCUTT TI TACAACUS - CAATAACAACUS - AATAACAATAAAAA - TESTOS AGS OS C - OS GG TITGTT TI TACAACUS
419. ChLG7 R180286027 C21	AAAT TCATAACT	- TARABACTAAAAGTOORAS AS CAABACEG TITGTI CORCEGAATI CTAAS AUTOCATTITE OG - IC
420. ChLG7 R180286027 C2	AAAT TCATAACT	- TAAAAACTAAAATICG TAS ASCAAAACCS TITG TI CCASCSAATIC <mark>E TA</mark> CES TICATITE CEAT <mark>IG - CLETTI TE - CCASCTE</mark>
421. ChLG7_R180286027_C32	AAAT TCATAACT	- TAAR FACTAAAAG TO TAS ASCAARACES THIGHT CORSEANT CTACES TO A THING IS A AAA- TESTING TO A TAA TA TENTING TO A AAA- TAST IS A AAA- TESTING A AAA-
422. ChLG2 R180279507 C2	AAAAAATTTATAACT	- CRAAACUTAAMAGTOSTAS ASCAC <mark>US</mark> OSS ITIS ITO CARING AS ANTO CASOSS CTCATTING (G - IA TAAA CCARC IT IT TACAAA AA TT TTAA AA SI TITTAAA TTT TAAAA TTTTAAAA TTTTAAAA CCARCAAA ATTTTAA AA CCARCAAA
423. ChLG2 R180279507 C4	AAAAAATTTATAACT	CAARARCTAANGTOF TAS SECRETES THE STOCK THE CARE SAAR THE AND CAREAR OF THE THE CAREAR AND THE TARGE AND THE THE SAARATE THE CAREAR AND THE CAREAR AND CAREAR
424. ChLG6_R180283243RC_C17	AAAAAAAT T <mark>C</mark> ATAAC T	- o <mark>g</mark> ararctranget get as no car <mark>tes</mark> i get content carge get at the second
425. ChLG6 R180283243RC C18	AAAAAAT T <mark>C</mark> ATAACT	– O <mark>G</mark> AAAACTAAAAGTOJTAS ASCAA <mark>IS</mark> COS ITIGIT CCADISAAIT CASOGSC TCATTITS (G - IA — - IAAA CCADIC-III IT AAAAACTAAAAGTOT TAAAGTOT ITIG AAAAATTAAI CIATIG CAATA I CIATAAAATTAAAATTAAAATTAAAATTAATATIG CAATA I CIATAAAATTAATATTAAAATTAATATATAA
426. ChLG7 R180286162 C18	AAAAAAT T <mark>C</mark> ATAACT	CAARABACTAAAAGTOE MS BSCAABACES TITATIC COSTIGAATICASCG COCATTTCES - TA ITACACCEATATTTATAACESCATAAAGTOE MS BSCAABACES TITATIC COSTACES AAABTOE MILTARCA

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628. Chlón R180286488 C10	arreatara 🗸 🛣 rénérica a caracter recerciencies 🔁 errea — 6 al 200	ili ili alla presi di contra ser esta serie di contra di	a 0.00000 armans00 2007000	TERESTING CONTRACTOR CONT	Canadra and Canadra and	Carlona - Carlona - Carlona	DOMOTOR DESCRIPTION OF A DOMOTOR OF A DOMOT	Regel and the second state of the second state
827. Childa (R180285486 C4)	ATTRACT PROPERTY ACTIVAL TITICALCONTATING SAICH	III TATAL MANTEN AND AND AND AND AND AND AND AND AND AN	1 CACLER AT REAL TOTALS	TITOTISCOCTIC CARTERS CIACE - SITI STARCATA-	THE PARTY OF THE P		CENTRAL PROPERTY AND ADDRESS A	ATTAC CONTRACTOR TO A CONTRACT OF A CONTRACT
828. Chl.G8 R180286673 C4	TAXETTATION STATES - TO MANY A LANCED AND THE STATES - 6 10 COM	dhé néw néw 7. ne farangan pané kapanangan ana miné panan anéw ané kapangan panén 🖉 anéh	a curanta armanage agement	CX CX CX CX CX CX CX CX CX CX CX CX CX C	THE & PERFECT MALE AND A PERFEC	Characteristic Car - Zampre State - State Caracteristic	CONTRACTOR AND ADDRESS OF TAXABLE PARTY OF	COMERCIAN AND AND AN ADDRESS AND AN ADDRESS AND ADDRE
529. Chl.GJ R180283673 C11	ATTALANCE STORAGE ACTIVITY AND ADDRESS SHOW	and a state of the	1 dicials 19614 miles	CONTRACTOR OF THE STATE OF THE CARDINGS - BUT AND ADDRESS - BUT AND ADDRESS ADDRE	THE DESCRIPTION OF THE DESCRIPTO		CONTRACTOR AND A REAL PROPERTY.	COTAN CALIFORNIA THE MAN AT SALVE SALVE AN AVAILABLE AT THE AVAILABLE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE AT THE AVAILABLE A
530. Chl.Gil R180286875 C5	ATTALANCE STORTED, ACTIVAL TITICARCONTATION - 5-10 CD	INCOMPARED MERITARIAN INTERNET INTO A CARTALY AND A CARTALY AND A CARTANY	A CAPAZA AVELAND AS TRO-	CARACTERISTIC CHEFTER CARE GITZ GITZ GITZ CAREALANA ANTICATA	THE ADDRESS OF ADDRES	Charles of the second second	CONTRACTOR AND TRACTOR AND TRACK AND ADDRESS OF	CAME OF A REPAIR AND A DAMAGE AND A
831. ChuG8 R180298673 C10	RTTRACTOR CONTRACTOR - ACTIVITIES - CONTRACTOR - CONTRACTOR	1999 yaya ayar 🛛 aliya ya ƙafarata (karyata) yaya 🗤 🖬 🖬 a keya (ya) ya kuta ku yata 🚺 a k 🚥 🖉 ya ku	A CHIMAN AT RAMAND ADD THE	CINERAL PRODUCTION CONTRACTOR CONTRACTOR OF THE REPORT OF THE PARTY OF	THE & PERFORMANCE AND AND ADDRESS OF	Contraction of Automatical Contraction	CONTRACTOR AND ADDRESS AND ADDRESS AND ADDRESS	CHYNNE CAMPERATURY YNLED YN YN YMAR YN YN YMAR YN YN YN YN YN YN YN YN YN YN YN YN YN
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531. Chl.GH_R180286675_CS	ATTRACT TOTOLOGIA, ACTUALLY TITLENERS AND ATTRACT	INCOMPACIAL MUNICIPALITY INTO A TRADUCT IN TAXABLE INTENTIN TAXABLE INTENTIN TAXABLE INTAXABLE INTENTIN TAXABLE IN TAXABLE IN TAXABL	A CAPACITY AND ADDRESS	CARGE STREET, CARACTER STATE OF THE CARGE STREET, SALES STREET, SALES	THE ACCOUNT OF A DATE	Contraction of the second second second second second second second second second second second second second s	CONTRACTOR AND ADDRESS OF ADDRESS	CARGO OF AFTER ALL SO IN A SUBJECT AND A SUBJECT OF A CARGO F
84. CH_G0_B190290673_C12	ATTENAND CONTRACTOR ACTIVITY AND ACTIVITY ACTIVI	IDO NOT BURGE MURIE VALUE AND AND AND AND AND AND AND AND AND AND	A CHICAGA AT REALING AUG	CONTRACTORIZZO CHOPTERS COACO 6272 8 YEE DUTENAMEN ANT MORE AND	TE A JULITUS MARKED	Concerned the Article Areas and the second	CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACT OF A CONTRACTACT OF A CONTRACTACTACT OF A CONTRACTACT OF A CONTRACTACTACT OF A CON	CHEVENE CHEATER MERCENNEL STREAMS THE WEINT AND AND AND AND AND AND AND AND AND AND
335. Ch. Ge R180288673 C2	ATTRIANS THOUGH A MARK TITICALCONNER MICH	and a second statement of the	1 CHORE STRAND AS THO-	INTERVIEW CONTRACTOR CONTRACTOR OF THE CARDINAL AND ADDRESS AND ADDRESS AND ADDRESS ADDRE	THE METTAL BAR MAN		CREWNING CONTRACTOR AND AND AND AND AND AND AND AND AND AND	COTON CAMPAGATAN TANÀN I VINSAN PARANA ARA ARA ARA A
536. Ch.Ge R180286673 C3	ATTRIANS ATTRICTS ACTION TITICALCOUNTER SACO	INCOMPACIAL AUXILIARIA CANTING TY AND A TRADUCTION TO TAXA TAXA AND A TRAD	A CHEMICA AND AND THE	CINETISCOCTO GLOPTES CINC SITI STRUMAN	DEADLINE AND A AND	CLARKE SA CHARLES AND CAM	CHARTER CONTRACTOR AND THE ADDRESS AND THE TA	CYTH CATCERTY IN STATE IN A TIME TO A TIME A
ST7. CN. G9_B190299873_29	ATTRACING STRUCTURA ACCESSION TETTOMACIACIÓ	ICC ICT ICAL IN CONTRACTOR IN CONTRACTOR IN THE ICC. NOT THE TREE IN THE ICC.	A ORDER ATRACTOR ADDRESS	CONTRACTOR DESCRIPTION DESCRIPTION DE LA CONTRACTION CONTRACTICA DE LA CONTRACTICA DE LA CONTRACTICA DE LA CONTRACTICA DE LA CONTRACTICA DE LA CONTRACTICA DE LA CONTRACTICA	-CAURITIANNA (LA	Crosser Ga Anna Anna Cac Gaac	COMPTERSION AND TOWN GROW AND TOWN	OCTOR COMPONENCES THE READ OF TRANSFERRED AND A CONTRACTOR OF TAXABLE PARTY.
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589. Ch. Ga PT30236673 C13	RALATION AND ALACTORY SCHOOL ALACTORY OF ALACTORY OF ALACTORY	INTERACTOR AND A	P CICHER SARAND AD ANY	CUMPANNOBLALC OPONABLE CANCE - 64.45 6 AND DEAD FORMER - ANA REASE FORM	-gapanya waka wa	Characteristics - Langer - Sold Caracteristics	Colorado and successive fraction of the	CANNO CAPANERSKI AND AN AN ANY AND AN ANY AND AN ANY AND AN
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87. Ch. Ch. R 10(2)(1742 C14	ATTRACT CONCRETES ACTIVALLY TYPE ACTIVITY OF A		a cacata available at the	CONTRACTOR CARDENSE COACE - 62 97 COM CARDMAN AND AND - MARAA	THE MACT MARK IG-	General Ch. Collin Very and Child	CLEAR THE MERIDIAN CONTRACTOR OF A DESCRIPTION OF A DESCRIPANTE A DESCRIPANTE A DESCRIPANTE A DESCRIPTION OF	COTTO CALVALANTS TO A REAL OF TAXAN TO A TAXANG A STRATE A
53. ChLGH R180289742 CS	ATTRIANS OF ACTOR ACTORS TOTAL CONCERNMENT		A CREMEN ADDRESS ADDRESS	CONVERSION CONTROL CARE GITZ ON CATALANA AND AND AND AND AND AND AND AND AND	TEANS CONTRACTOR DO NO.	Care and the second second	CONTRACTOR AND ADDRESS OF ADDRESS OF	CAMER CONTRACTOR IN THE REAL PROPERTY OF THE REAL OF T
64. Chi.Ga R180289742 C11	ATTRACTOR CONTRACTOR ACTIVITIES AND A		A CHIMAN ATTAMAND ADDRESS		TELEVIS MANAGE	Contrast of Annual Contrast	CONTRACTOR DESCRIPTION OF ALL	CRYSER CALVERSING TO THE READ OF THE T. THE TRANSMICS OF THE TRANSMICS OF
140. Children 1740 2467462 Child	ATTRANSI GEFORITOR ACTIVITY AND CONTRACTOR		a cacata arasanana ar ta ta ta ta ta ta ta ta ta ta ta ta ta	CONTRACTOR CARDING COMPANY AND AND AND AND AND AND AND AND AND AND	THE MAKES	CONTRACTOR CA. COLLAR TOTAL CARD	CLEATER AND AND A MARKED AND A DESCRIPTION OF A DESCRIPTI	CATHER CARACITATION TO THE PERSON AND AND AND AND AND AND AND AND AND AN
861. ChuGi R180289742 CH	ATTRIANS OFFICIER ACTORNC ETTRINGTOCHTE-	The second	A CHIMAN AND AND THE	CINERAL STREET, CARTER CARE GIT CARE AND AND AND AND AND AND AND AND AND AND	TUBART MARKED	Contraction of the local data and the local data an	Christian Contraction of the Address	CY290 Charlences I I I I I I I I I I I I I I I I I I I
642. Chi.G5 R180259742 C4	ATTRACT OFFICIES ACCOUNTS		- CHEMICAL AVERAGED AUGUST	CONTRACTOR DESCRIPTION OF A CONTRACT OF A CONT	TE & REFE & BELTER	Contraction of the second second	CONTRACTOR AND A CONTRACT OF A LAR OF CONTRACT	orazio che se della parte della se vi parti profizzione di la constante della
M3. Ch. G4 R140249242RC C5	ATTRACT OFFICIAL ACTIVITY STATISTICS		A CREAK STRAND AD THO-	DISCONTRACTOR DESCRIPTION DIALE - 02 172 COM CANADADA - DIALATA- DIALATA-	THE ADDRESS AND ADDRESS AND ADDRESS ADDRE	and the second s	CLACKERSCHER CONTRACTOR M. INC. MARCENER	Carrow Charles and the second se
864. ChlGe_R180289242RC_C7	ATTEMAN OFFICIER ACCORD TITICACCOCAT-		A CECH ALEANING AGE THE	CONTRACTOR CONTROL CARE - 6112 CONTRACTOR	TEARLY AND AND A		CLEVENCE CONTRACTORS OF ADDITION	CONTRACTOR DESCRIPTION OF THE TRACTOR OF THE TRACTOR A
#4. CH.GF. B1#12#124(18)C C3	ATTRACTOR CONTRACTOR - MANAGEMENT		A CITAL AND AL		TEAJETTE MAR 1	Contraction of the second seco	CLEAR STRATE AND A DATE ALL DATE AND A DATE AND A DESCRIPTION OF A DESCRIP	-CANE THE REPORT AND REAL PROPERTY AND REAL PROPERTY IN THE REAL PROPERTY.
NG. Ch. G4_R180289240RC_C4	ATTRACT OFFICIAL ACTIVITY TRACTOCATE		- A CREAK MARKING ADDRESS	DISCONTRACTOR DATABASE OF THE CANADALANA AND A MARAN	THE MET ALL AND A	Contraction of the second seco	CERCUTYCARY AND ANY ANY AND ANY AND ANY ANY ANY ANY ANY ANY ANY ANY ANY ANY	-OTH CANTALATT TIME TO THE TYPE THAT THAT A CONTRACT A
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559. ChLOM_R180289742_C7	ATTRACT CITCLERINA ACTIVITIES TITTELESADIEATT		A CREATE ATLANTIC ADVID-	CHEVY REDUCTIVE DESTTING CITED OFFICE OFFICE CATENAL AND A DESTRICTA AND A DESTRICTA AN	THE MAKES BALANCE		CERCIT-SCREWERSTRANSFILM OFFICE ADDRESS	COMPAREMENTING THE APPROXIMATION TO THE ATA OTTACH A
10. CH-CG 1. 199309/45 CH0	Transfer Condition Transfer tradectories		a circular sylenistic righting	CONCERNMENT CONTRACTOR CARE GIVE CONCERNMENT AND A SAME	TO A POLY OF THE P	Commendation and and and and and	CONTRACTOR AND ADDRESS OF ADDRESS	Chald Construction Links of Al Links Links - Mary - Mary - Market S
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Prz. unuse jeneralnicz C12	ATTACKS STUDIA ALIGHE TITICLESCOCAT-		A LINE ALLER AND ADDRESS	CARACTERISTIC CONTINUE CARDO - WITZ CONCENTRATION AND - 2 MARA	DEARACED SLARAES.	CALLER OF TRANSPORT	COLUMN STATEMENTS OF ALL OF AL	CULUE CONTRACTOR I THERE IN TILLENT P
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	1 10	20 30	40 50	60	70	80 90	100	110	120	130	140	150	160	170	183
Consensus	AACATTACAAAACCTTCC	TCTA CAACAT ACTA	AAA AATTOG AG TOG T OGOO	-CT TTTIG T TTTCT	T TTTATTA AATTO	GGAATAT AGGACAA	TATT TGAAAA	A TTOG TA TAAA	GCACGCTTTAG	ATTGACCCAT	GOSTCOTTOS	ATTGCATGCA	GCAATIGCC	TTCATTT TIG TAC	CGRG
1. ChLG3_1_R180292928_C2	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAAAAT-GG AG TOG TOGGO	G-CT TTTIG T TTTCT	TTTTATTAAATTO	T GAATAT AGGACAA	TATT-TGAAAA	A TTOG TA TAAA	GCACGGCTTAAG	I <mark>IG</mark> IG ACCCA II	GCATC CTTTOG	A <mark>A</mark> IGCA <mark>G A</mark> CA	GCAA <mark>GG</mark> GC <mark>T</mark>	TI <mark>G</mark> ATTT T-GTA	CGAA
2. ChLG3_1_R180292928_C10	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAA AATTGG AGTCGT CGGC	G-CT TTTTG T TTTCT	TTTTATTA AATTO	GAATAT AGGACAA	TATT TGAAAA	ATTOGTA TAAA	GCACGGCTTAAG	G IGACCCAR	SCATC CTTTOS	AATGCAGACA	GCAAGGCT	TIGATTT T-GTAC	CGAA
3. ChLG3_1_R180292928_C43	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAAAATIGG AGTOGTOGG AAA AATIGG AGTOGTOGG	G-CTTTTTGTTTTCT	TTTTATIAAATIC TTTTATTAAATIC	GAATAT AGGACAA	ATT-TGAAAA	A TTOGTA TAAA	GCAUGGETTAAG	IG IG ACCCA I	CATCOTTOG	ANIGCAG ACE	IGCAA <mark>GG</mark> GC <mark>T</mark>	TIGATTT T-GTA	CGAA
5. ChLG3 1 R180292928 C18	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAA AATTGG AGTCGT OGGO	G-CT TTTIGT TTTCT	TTTTATTAAATTO	T GAATAT AGGACAA	TATT-TGAAAA	ATTOGTATAAA	GCACGGCTTAAG	IG IGACCCAR	CATC CITTOS	AATGCA <mark>G A</mark> CZ	GCAA <mark>GG</mark> GC <mark>T</mark>	TT <mark>G</mark> ATTT T-GTA	CGAA
6. ChLG3_1_R180292928_C13	AACATTACAAAACCTTC	TCTACAACATACTA	AAA AATIGG AG TOG TOGGO	G CT TTTIGT TTTCT	TTTTATTAAATTC	T GAATAT AGGACAA	TATT TGAAAA	ATTOTATAAA	GCACGGCTTAAG	G IGACCCA I	GCATC CTTTOG	AAIGCA <mark>G A</mark> CA	IGCAA <mark>GG</mark> GC <mark>T</mark>	TTGATTT T-GTAC	CGAA
7. ChLG3 1 R180292928 C26 8. ChLG3 1 R180292928 C37	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAAAATIGG AG TOG TOGGO AAA AATIGG AG TOG TOGGO	G-CTTTTTATTTCT 2-CTTTTTATTTCT	TTTTATTAAATCO TTTTATTAAATCO	GAATAT AGGACAA	TATT-TGAAAA	ATTOGCATAAA	-GCACCGCTTAAG	GIGACCCAIR	CATC CITTOS	AAIGCAGACA	GCAAGGGCT	TIGATTT T-G TAC	CGAA
9. ChLG3 1 R180292928 C41	AACATTACAAAACCTTC	TCTACAACATACTA	AAAAATTGG AGTCGT CGGC	G-CTTTTTGTTTTCT	TTTTATTAAATTC	TGAATAA AGGACAA	TT-TGAAAA	ATTGCATAAA	GCACEGCTTAAG	G IGACCCA I	GOSTCOTTOS	ANIGCAGACZ	GCAAGGCT	TIGATTT T-GTA	CGAA
10. ChLG3_1_R180292928_C6	AACATTACAAAACCTT C	TCTA CAACAT ACTA	AAA AATIGG AG TOG TOGGO	G-CT TTTT <mark>A</mark> T TTTCT	TTTATTAAATTO	T GAATAT AGGACAA	TATT-TGAAAA	ATTOGTA TAAA	GCACGGCTTAAG	G <mark>IG</mark> IGACCCAI	GOGTCOTTOG	A A IGCA <mark>G A</mark> CA	GCAA <mark>GG</mark> GC <mark>T</mark>	TIGATTT T-G TAC	CGAA
11. ChLG3_1_R180292928_C9	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAA AATTGG AGTCGT (GGG)	G-CTTTTTGTTTTCT	TTTTATTAAATTO	GAATAT AGGACAA	CATT TGAAAA	ATTOGTA TAAA	GCACGGCTTAAG	GIGACCCAR	GOGTCCTTTCG	AAIGCAG ACZ	GCAAGGGCT	TIGATTT T-GTAC	CGAA
13. ChLG3_1_R180292928_C38	AACATTACAAAACCTTC	TCTACAACAT ACTA	AAA AATTGG AG TOG T OGGO	G-CTITTIGTTITCI	TTTTATCAAATTC	TGAACAT AGGACAA	ATT-TGAAAA	ATTOGTA TAAA	GCACGGCTTAAG	IG IGACCCAR	GGTCCTTTCG	AAIGCAGACA	GCAAGGCI	TIGATTT T-GTA	CGAA
14. ChLG3_1_R180292928_C23	AACATTACAAAACCTTCC	TCTA CAACAT ACTA	AAA AATIGG AG TOG TOGGO	G-CTTTTT <mark>A</mark> TTTTCT	TTTTATTAAAT <mark>O</mark> C	T GAATAT AGGACAA	CATT-TGAAAA	ATTOGTA TAAA	GCACCCTTAAG	IGACCCA I	GOGTCCTTOG	A <mark>A</mark> IGCA <mark>G A</mark> CF	IGCAA <mark>GG</mark> GC <mark>T</mark>	TT <mark>G</mark> ATTT T-G TAC	CGAA
15. ChLG3_1_R180292928_C33	AACATTACAAAACCTTCC	TCTACAACATACTA	AAA AATTGG AG TCG TCGGC	G-CT TTTTAT TTTCT	TTTTATTAAAT	TGAATAT AGGACAA	TATT-TGAAAA	ATTOGTATAAA	GCACCCTTAAG	GIG IG ACCCA IK	GOGTCCTTTOG	AAIGCAG ACA	GCAAGGCT	TIGATTT T-GTAC	CGAA
16. GREG3_1_R180292927_C9 17. Chi G3_1_R180292928_C47	AACATTACAAAADCITTAC	TCTACAACAT ACTA TCTA CA <mark>G</mark> CAT ACTA	AAAAATIGG ASTOSTOGG AAAAATIGG AGTOGTOGG	S-CITIT U STTIT-I S-CUUTTIGUUUUU	TTTLATLAAATU. TTTTATTA AATU	GAATAT AGGACAA	CATT-TGAAAA PATT-TGAAAA	ATIOTATAAA ATIOTATAAA	-GCAUGGUTTAAG	G IGACCCA I	SOSTCOTTOS	ANIGCAS ACA	GCARGGCT	TTGATTTTGTAL	CGAA
18. ChLG3 1 R180292928 C39	AACATTACAAAACCTTCC	TCTA CAACAT ACTA	AAA AATTGG AG <mark>A</mark> CG T CGGC	G-CT TTTIG T TTTCT	TTTTATTAAATTO	GAATAT AGG ACAA	TATT-TGAAAA	ATTOGTATAAA	GCACGGCTTAAG	GIG ACCCA I	GOGTCCTTTCG	AAIGCAGACA	GCAA <mark>GG</mark> GC <mark>I</mark>	TT <mark>G</mark> ATTT T-G TA	CGAA
19. ChLG3_1_R180292928_C44	AACATTACAAAACCTTC	TCTACAACAT ACTA	AAA AATTGG AG TOG T OGGO	G-CT TTTIGT TTTCT	TTTTATTAAATTO	T GAATAT AGGACAA	TATT-TGAAAA	ATTOGTATAAA	GCACGGCTTAAG	IG IGACCCA I	GOSTCOTTOS	A A IGCA <mark>G A</mark> CA	IGCAA <mark>GG</mark> GC <mark>T</mark>	TIGATTT T-GTAC	CGAA
20. ChLG3 1 R180292928 C16	AACATTACAAAACCTTCC BACBTTBCBBBBCCTTCC	ГСТАСААСАТАСТА ЧСТАСААСАТАСТА	AAAAATIGG AGTCGTCGGG AAAAATIGG AGTCGTCGGG	3 - CT TTTIG T TTTCT 2 - CT TTTTG T TTTCT	TTTTATTAAATIC TTTTATTAAATIC	GAATAT AGGACAA	CATT-TGAAAA	ATICITA TAAA 3 TICITA TAAA	-GCAUGGCTTAAG	G IGACCCA I	CARCOTTIG	AAIGCAGACA	GCAAGGGC <mark>U</mark> GCAAGGGCU	TTGATTTTGTAC	CGAA
22. ChLG3 1 R180292928 C27	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAA AATTGG AG TOG T OGGO	G-CT TTTIGT TTTCT	TTTTATTAAATTO	GAATAT AGGACAA	ATT-TGAAAA	- TTOGTA TAAA	GCACGGCTTAAG	IG IGACCCA I	GCATC CTTTOG	ANIGCAGGCA	GCAAGGCT	TIGATTT T-GTA	CGAA
23. ChLG3_1_R180292928_C22	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAA AATIGG AG TOG TOGGO	G-CT TTTTG T TTTCT	TTTTATTAAATTO	T GAATAT AGGACAA	CATT-TGAAAA	A TTOG TA TAAA	GCACGGCTTAAG	G IG ACCCA I	GCATC CITTOG	A <mark>A</mark> IGCA <mark>G</mark> GCA	IGCAA <mark>GC</mark> GCC	TT <mark>G</mark> ATTT TTG TAC	CGAG
24. ChLG3_1_R180292928_C32	AACATTACAAAACCTTC	TCTACAACAT ACTA	AAA AATTIGG AG TOG TOGGO	G-CT TTTTG T TTTCT	TTTTATTAAATTO	GAATAT AGGACAA	TATT-TGAAAA	ATTOGTA TAAA	GCACGGCTTAAG	GIGACCCA I	GCAPC CITTOG	AAIGCAGGCA	GCAA <mark>GC</mark> GCC	TIGATTT TIG TAC	CGAG
26 Chi G3 1 R180292927 C3	AACATTACAAAACCTTCC	TCTA CAACAT ACTA	AAAAATIGG AGTCGTCGGC	-CITTIGITICI	TTTTATAAATIC	GAATAT AGGACAA	LATT-TGA G AA	A TIOG TA TAAA A TIOG TA TAAA	GCAGGCTTAAG	G IGACCCA I	GOTCOTTOS	ANIGCAGGCZ	GCAA <mark>GG</mark> GCC	TIGATTI TIGTA	CGAG
27. ChLG3_1_R180292928_C45	AACATTACAAAACCTTC	TCTACAACATACTA	AAA AATTGG AG TOG TOGGO	G-CT TTTIG T TATCT	TTTTATTAAAT	T GAATAT AGGACAA	fatt-tga <mark>g</mark> aa	ATTOGTATAAA	GCACGGCTTAAG	IG IGACCCA I	GOGTCCTTTCG	AAIGCAGGC2	GCAA <mark>GG</mark> GCC	TIGATTT TIG TA	CGAG
28. ChLG3_1_R180292927_C1-1	AACATTA-AAAATCTTCC	TCTACAACATACTA	AAA AATTGG AG TOG T OGGO	G-CT TTTIGT TTTCT	TTTT <mark>TC</mark> TAAATC	T GAATAT AGGACAA	TTT-TGA-AA	ATTCCCA TAAA	GCACG			ANIGCAGGCA	GCAA <mark>GG</mark> GCC	TIGATTT TIG TAC	CGAA
29. ChLG3 1 R180292928 C50 30. ChLG3 1 R180292928 C4	AACATTACAAAACCTTC	TCTACAACATACTA	AAAAATUG AGTOGTOGG AAAAATUG AGTOGTOGG	-CTTTTGTTTCT -CTTTTTGTTTCT	TTTTATTAAATIC	GAATAT AGGACAA	TT-TGAAAA	A TIXIJTA TAAA	-GCAUGGCTTAAG	GACCCA IC	GGTCCTTTCG	AAIGCAGGCA AAIGCAGGCA	GCAAGGCC	TIGATIT TIGTAC	CGAG
31. ChLG3 1 R180292928 C28	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAA AATTGG AG TOG T OGGO	G-CT TTTTAT TTTCT	TTTTATTAAAT	GAATAT AGGACAA	ATT-TGAAAA	A TTOGCA TAAA	GCACGGCTTAAG	TITGACCCAR	GOGTC CTTTOG	ANIGCAGGCA	GCAAGGCC	TTCATTT TEG TA	CAAG
32. ChLG3_1_R180292927_C7	AACATTACAAAACCTTCC	TCTA CAACAT ACTA	AAA AATTOG AG TOG T OGGO	G-CTTTTT A TTTTCT	TTTTATTAAAT	GAATAT AGGACAA	TATT-TGAAAA	A TTOG <mark>C</mark> A TAAA	GCACGGCTTAAG	TIGACCCA I	BORTCCICIOS	A <mark>A</mark> IGCA <mark>G</mark> GCF	IGCAA <mark>GG</mark> GCC	TTCATTT TIG TAC	.C <mark>A</mark> AG
33. ChLG3_1_R180292927_C10	AACATTACAAAACCTTCC	TCTACAACATACTA	AAA AATTGG AG TOG TOGGO AAA AATTGG AG TOG TOGGO	G-CTTTTTGTTTTCT	TTTTATTAAATTC	CAATAAAGGACAA	TT-TGAAAA	- TTOGCA TAAA	-GCACGGCT-AAG	FIGACC-AR	GOGTC CTTTCG	A-IGCAG-CA	GCAA <mark>GG</mark> GCC	TTTATTT T-GTAC	CAG
35. Chi G3 1 R180292928 C11	AACATTACAAAACCTTCC	TCTACAACATACTA	AAAAATIGG AG TOG TOGGO	G-CTTTTTGTTTTCT	TTTTATTAAATIC	T GAATA <mark>A</mark> AGGACAA	TT-TGAAAA	A TTOG C A TAAA	GCACGGCTTAAG	TI IGACCCA I	GOGTCOTTOS	ANIGCAGGCA	GCAA <mark>GG</mark> GCC	TTCATTT TIGTA	CARG
36. ChLG3_1_R180292928_C40	AACATTACAAAACCTTCC	TCTA CAACAT ACTA	AAA AATTGG AG TOG TOGGO	G-CT TTTIG T TTTCT	TTTTATTAAATTC	T GAATA <mark>A</mark> AGGACAA	TT-TGAAAA	A TTOG CA TAAA	GCACGGCTTAAG	TITIGACCCA IX	GOGTC CTTTOG	A <mark>A</mark> IGCA <mark>G</mark> GCA	IGCAA <mark>GG</mark> GCC	TTCATTT TIG TAC	CAAG
37. ChLG3_1_R180292928_C12	AAC ATTACAAAACCTT C	TCTA CAACAT ACTA	AAA AATTGG AG TOG T OGGO	G-CT TTTTG T TTTCT	TTTTATTAAATTO	TGAATAA AGGACAA	TT-TGAAAA	ATTIGCATAAA	GCACGGCTTAAG	TITGACCCAR	GOGTC CTTTOG	AAIGCAGGCA	GCTAGGCC	TTTATTT TEG TAC	CAAG
39 Chi G3 1 R180292926 C5	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAA AATIGG AG TOG TOGGO	G-CTTTTIGTTTCT	TTTATTAAATTC	TGAATAA AGGACAA	TT-TGAAAA	ATTIGCA TAAA	GCACEGCTTAAG	TTGACCCAR	GGTCCTTTCG	ANIGCAGGCA	GCAA <mark>GG</mark> GCC	TTTATTT TIG TA	CAAG
40. ChLG3_1_R180292928_C8	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAA AATTGG AG TOG T OGGO	-CT TTTIG T TTTCT	TTTATTAAATTO	T GAATA <mark>A</mark> AGGACAA	TT-TGAAAA	attog c ataaa	GCACGGCTTAAG	TIGACCCAR	GOGTC CTTTOG	A <mark>A</mark> IGCA <mark>G</mark> GCA	GCAA <mark>GG</mark> GCC	TTTATTT TEGTA	CAAG
41. ChLG3_1_R180292928_C21	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAA AATTGG AG TOG TOGGG	G CT TTTIG T TTTCT	TTTTATTAAATTC	T GAATA <mark>A</mark> AGGACAA	TTTTGAAAA	A TIXIG CA TAAA	GCACGGCTTAAG	TIGACCCA I	GOGTCCTTTOG	A A IGCA <mark>G</mark> GCA	IGCAA <mark>GG</mark> GCC	TT T ATTT TIG TAC	CARG
42. ChLG3 1 R180292928 C42 43. ChLG3 1 R180292928 C36	AACATTACAAAACCTTC AACATTACAAAACCTTC	TCTA CAACAT ACTA TCTA CAACAT ACTA	AAA AATIGG AG TOG TOGGO AAA AATIGG AG TOG TOGGO	5-CTTTTIGTTTTCT 3-CTTTTTGTTTTCT	TTTTATTAAATTC TTTTATTAAATTC	GAATAAAGGACAA GAATAAAGGACAA	TTTTGAAAA	A TTOG CA TAAA A TTOG C A TAAA	-GCAUGGCTTAAG -GCAUGGCTTAAG	TI IGACCCA IC	SOGTCOTTUS	AAIGCAGGCA AAIGCAGGCA	GCAAGGCC GCAAGGCC	TTTATTTTIGTAC TTTATTTTIGTAC	CAAG
44. ChLG3 1 R180292928 C35	AACATTACAAAACCTTC	TCTACAACATACTA	AAA AATTGG AG TCG T OGGO	G-CTTTTTGTTTTCT	TTTTATTAAATTC	T GAATA <mark>A</mark> AGGACAA	TT TGAAAA	ATICGCATAAA	GCACGGCTTAAG	TIGACCCAR	GAGTCCTTTAG	A <mark>A</mark> IGCA <mark>G</mark> GCA	IGCAA <mark>GG</mark> GCC	TTTATTT TIGTA	CARG
45. ChLG3_1_R180292928_C30	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAA AATIGG AG TOG TOGGO	G-CT TTTIG T TTTCT	TTTTATTAAATTC	T GAATA A AGGACAA	TTT-TGAAAA	A TTOG C A TAAA	GCACGGCTTAAG	TTIGACCCA II	GOTCCTTTOS	A A IGCA <mark>G</mark> GCA	IG CA A <mark>GG</mark> G CC	TTTATTT TIG TAC	.CAAG
46. ChLG3 1 R180292928 C24 47 ChLG3 1 R180292928 C24	CACATTACAAAACCTTC	TCTA CAACAT ACTA	AAAAATIGG AG TOG T OGGG AAA AATIGG AG TOG T OGGG	3 - CTTTTIGTTTCT 2 - CTTTTTGTTTCT	ΤΤΤΤΑΤΤΑΑΑΤΤΟ ΤΤΤΤΑΤΤΑΑΑΤΤΟ	CAATAA AGGACAA	TT-TGAAAA TT-TYLAAAA	ATIXIG CA TAAA ATIXIZ C ATAAA	GCACGGCTTAAG	FIFIGACCCAR	COTC CTTTOS	ANIGCAGGCA ANIGCAGGCA	GCAR <mark>GG</mark> GCC	TTTATTTTTGTAC	CAAG
48. ChLG3 1 R180292928 C7	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAA AATTGG AG TOG TOGGO	G-CTTTTIGTTTTCT	TTTTATTAAATTO	TGAATAA AGGACAA	TTT-TGAAAA	A TTOG CA TAAA	GCACGGCTTAAG	TITACCCAI	GOTCOTTICG	ANIGCAGGCZ	GCAAGGCC	TTCATTT TIG TA	CAAG
49. ChLG3_1_R180292928_C17	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAA AATTGG AG TOG T OGGO	G-CT TTTIG T TTTCT	TTTTATTAAATTO	T GAATAT AGGACAA	TATT-TGAAAA	attog <mark>c</mark> ataaa	GCACGGCTTAAG	T IGACCCA I	GOTC CITTOS	A <mark>A</mark> IGCA <mark>G</mark> GCA	IGCAA <mark>GG</mark> GCC	TTCATTT TEG TAC	CAAG
50. ChLG3_1_R180292928_C48	AACATTACAAAACCTTC	TCTACAACAT ACTA	AAA AATTOG AG TOG TOGGO	G - CT TTTTG T T <mark>A</mark> TCT	TTTTATTAAATTO	GAATAT AGGACAA	TATT TGAAAA	ATTCGCATAAA	GCACCCTTAAG	TIGACCCA I	GAGTCCTCTCG	ARIGCAGGCA	GCAA <mark>GG</mark> GCC	TTCATTT TIG TAC	CAAG
52 Chi G3 1 R180292928 C19	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAAAATIGG AGTCGT CGGC	G-CITTIGITICI	TTTTATTAAATIC	GAATAT AGGACAA	TATT-TGAAAA	ATTOG C ATAAA	GCACGGCTTAAG	TTGACCCAR	GICCITTOS	ANIGCAGGCA	GCAA <mark>GG</mark> GCC	TTTATTT TEGTA	CARG
53. ChLG3 1 R180292927 C8	AACATTACAAAACCTTC	TCTACAACATACTA	AAA AATTGG AG TCG T CGGC	G CT TTTTGT TTTCT	TTTTATTAAAT	T GAATAT AGGACAA	TATT TGAAAA	ATTOGCATAAA	GCACGGCTTAAG	TGGGACCCA T	GAGTCCTTTAG	A <mark>A</mark> IGCA <mark>G</mark> GCA	GCAA <mark>GG</mark> GCC	TTCATTT TIGTA	CARG
54. ChLG3_1_R180292928_C25	AACATTACAAAACCTTC	TCTA CAACAT ACTA	AAA AATIGG AG TOG TOGGO	G-CT TTTIG T TTTCT	TTTTATTAAATTC	TGAATAT AGGACAA	ATT-TGAAAA	ATTOG TA TAAA	GCACGGCTTAAG	IG IG ACCCA I	GCATC CTTTOG	AAIGCAGGCA	GCAA <mark>GG</mark> GCC	TTCATTT TIG TAC	CAAG
55. GILG3 1 R180292927 C5	AACATTACAAAACCITT	TCTACA <mark>G</mark> CATACTA TCTACA <mark>G</mark> CATACTA	AAAAATTAG AGTUGTUGA. AAA AATTIG AGTUGTUGA	3-CTTTTIGTTTTCT 2-CTTTTTGTTTTCT	ΤΤΤΤΡΑΤΤΑΑΑΤΙΟ ΤΤΤΤΡΑΤΤΑΑΑΤΙΟ	GAATAT AGGACAA	TT-TGAAAA	ATIXISTA TAAA ATIXISTA TAAA	-GCAUGGCTTAAG	G REACCCAR	acter correction	ARIGCAGGCA ARIGCAGGCA	IGCALAGGIGCC IGCALAGGIGCC	TTCATTTTRETAC	CGAG
57. ChLG3 1 R180293367 C3	AACATTACAAGACCTTCO	TCTA CAACAT ACTA	AAA AATTGG AG TOG T OGGO	G-CT TTTIGT TTTCT	TTTTATTATAT	GGAATA <mark>C T</mark> GGACAA	ATT-TGAAAA	ATTOGTATAAA	GCACGGCTTAAG	ATGACCCAT	GOTCCTTTOG	ANIGCAGGCA	GCARGGCC	TTCATTT TIG TA	CGAG
58. ChLG3_1_R180293367_C5	AACATTACAAGACCTT	TCTA CAACAT ACTA	AAA AATTGG AG TCG T CG 🖁	G-CTTTTTGTTTTC	rtttatta <mark>T</mark> at <mark>cs</mark>	ggaatat <mark>t</mark> ggacaa	TATT TGAAAA	ATTCGTA TAAA	GCACGGCTTAAG	ATGACCCAR	GOGTCCTTTOG	A <mark>A</mark> IGCA <mark>G</mark> GCA	IGCAA <mark>GG</mark> GCC	TTCATTT TTG TAC	CGAG
59. ChLG3_1_R180293367_C2	AACATTACAAGACCTTCC	TCTA CAATAT ACTA	AAA AATTGG AG TOG T OGGO	G-CTTTTTGTTTTCT	TTTTATTA TATO	GAATACTGGACAA	TATT TGAAAA	ATTOTATAAA	GCACGGCTTAAG	ANGATCCAR	GOGTCCTTTTG	ABIGCAGGCA	GCAAGG TT	TTIG TTT TTG TAC	CGAA
61. Chl G3 1 R180293367 C8	AACATTACAAGACCOFT	TCTACAACATACTA	AAAAATTGG AGT <mark>T</mark> GT CGGC	3-CITTIGITTICI 3-CITTIGITTICI	TTTTATTAAATO.	GGAATAT AGGACAA	LALT-TGAAAA	ATTOTATAAA ATTOGTATAAA	GCACGGCTTAAG	ATGACCCAT	GOTCOTTTO	An IGCAGGCA	GCAR <mark>GG</mark> GCC	TTCATTT TEGTA	CGAG
62. ChLG3_1_R180293367_C4	AACATTAGAAGACCCFT	TCTACAACATACTA	AAA AATTGG AG TOG TOGGO	G-CTTTTTGTTTTCT	TTTTATTAAAT	GGAATAT AGGACAA	CTT-TGAAAA	ATTOGTATAAA	GCACGGCTTAAG	ATGACCCAR	GOGTCCTTTT	AAIGCAGGC2	GCAA <mark>GG</mark> GCC	TTCATTT TIG TA	TGAG
63. ChLG3_1_R180293367_C13	AACATTACAAGACCTT	TCTA CAACAT ATTA	AAAAATTAGAGTOGTOGG	G-CTTTTIGTTTTCT	TTTTATTAAAT	GGAATAT AAGACAA	ATT-TGAAAA	ATTOGTA TAAA	GCACGGCTTAAG	ANTGACCCAR	GOGTCCTTTCG	AAIGCAGGCA	GCAAGGCC	TTCATTT TIG TAC	CGAG
65. ChLG3 1 R180293367 C11	AACATTACAAGACCTT	TCTA CAACAT A <mark>T</mark> TA	AAAAATT A SAGTOGTOG A AAAAATT A SAGTOGTOG A		i i teatta t at <mark>os</mark> TTTTATTA <mark>T</mark> AT <mark>OS</mark>	GGAATAT AGGACAA GGAATAT AGGACAA	ATT-TGAAAT TATT-TGAAAT	antostacata Antostacata	GCAUGGCTTAAG GCAUGGCTTAAG	G IG ACCCT II	GOGTCGTTTCA	atusca <mark>s</mark> gCa Atusca <mark>s</mark> gCa	ig caa <mark>gg</mark> gcc Ig caa <mark>gg</mark> gcc	TTCATTT TIGTAC	LG AG

66. ChLG3 1 R180293367 C7	AAC ATTACA XGACCTTE CICTA CAACAAT ACTAAAA AATTEG ASTE IT CEGTTETE TTTCTTTE TATCAATCEG GAATAT AGG ACAA TATT - TG AAAAA TTCGTA TAAA-G C ACEG CT TAAA TCGTA TAAA-G C ACEG CT TAAA TTCGTA TAAA
67. ChLG3 1 R180293367 C9	AAC ATTACA AGACCORTICTCTA CAACAAT ACTAAAA AATTIGG ASTCG T CGC CA COA CA COTTCATTATATA AATCO CAACAAT ATTATTA AATCO CAACAAT ACTAAAA ATTCG TATAAA COA CAACAAT ACTAAAA ATTCG TATAAAA COA CAACAAT ACTAAAATTCG TATAAAATCO CAACAAT ACTAAAATTCG TATAAATCO CAACAAT ACTAAATTCG TATAAATTCG TATAAATTCG TATAAATCO CAACAATAATTCG TATAAATTCG TATAAATCO CAACAATAATTCG TATAAATCO CAACAATAATTCG TATAAATTCG TATAA
68. ChLG3 1 R180293367 C12	AACATTACAAGACCCTTCTCTACAACAT ACTAAAAAATTIGE ASTCGTCEGG - TITTTIGITTTTGTTTTTTTTTTTTTTTTTTTTTT
69. ChLG3_1_R180292927_C2	AACATTE TAAAACCTE ATTOTA CAACAT ACTAAAA AATTOG ETTOGE CEGG-CETTTEET TETCTETTETATTA, EGGACAA TATE-TGAAAA ETTETATAAA. GCACGCETEAGAATACCCA EGCGCCECAAGGCCE CAAGGCCE CA
70. ChLG3_1_R180292927_C4	AACATTE CAAAACCTE AT TOTACAACAT ACTAAAAAATTEG ESTOGTOGG- CTTETTET TETTET TETTATEG BAATAT AGAACAATATE TEAAAA GCAGGCE TAAGAATGCCCATGGTCGACGGCGCAAGGCCCAAGGCCCTTCATTETTETTATE
71. ChLG3_1_R180292928_C49	AACATTACAAAACCTTCTTCTACAACAT ACTAAAAAATTGG ASTGG TGGG-CTTTTTET TTTCTTTTTTTTTTTTTTTTGGAAAATATT-TGAAAAATTTTGTATAAA GC AGGCTTAACAG GGCGTGTGGATGGATGGACGGCGTGGGCGGCGTGGACGGCCCTTGGATTTTTTTT
72. ChLG3 1 R180292823RC C6	AACATAAAACTT COTOTA CAACAT ACTAAAA AATIGG AGTOG TAAG - CTITTES T TTICTT TTAATAACGEGAATAT AGE CAA TOTT - TG CAAAA TTOGTA TAAA-ACAOS CTITTAAT IS ACCEAT ACTAAAAACTT COTOTA CAACAT ACTAAAAAATIG AGTOG TATAAAAAGCC TITTAATI AATIG AGTOG TATAAAAACTT COTOTA CAACAT ACTAAAAAATIG AGTOG TATAAAAAGCC TITTAATI AATIG AGTOG TATAAAAAATIG AGTOG TATAAAAAAATIG AGTOG TATAAAAAAATIG AGTOG TATAAAAAAATIG AGTOG TATAAAAAAAAAAACTT COTOTA CAACAT ACTAAAAAATIG AGTOG TATAAAAAAATIG AGTOG TATAAAAAATIG AGTOG TATAAAAAAATIG AGTOG TATAAAAAAATIG AGTOG TATAAAAAATIG AGTOG TATAAAAAATIG AGTOG TATAAAAAATIG AGTOG TATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
73. ChLG3_1_R180292823RC_C9	GACAUMACA/GACCITECCTCTACAACAT ACTAAAAAATIIGGAMIGGTAAAAA CTITITGST TTICTTETTAAATAAATGGIGAATAT AXGTCAAAAATIIGGTATAAA ACGACGTTTIGACTGACGATIIGGACGTTIGACATGCAGGAAAATIIGGAAAAATIIGGACGAAAATIIGGACGACGATATAXGTAAAAAATIIGGACGACGAAAATIIGGACGACGATATAXGTAAAAACGAGACATIIGGACGACATATAXGTATAAA
74. ChLG3 1 R180292823RC C8	AACATMACAAAAACTT CCTCTACAACAT ACTAAAAATTIGG AGTIGT GAAG- CT TTGGT T TITTITT TTATTAAATOG GAATAT AGGACAA TATT - TG AAAAATTIGG TA TAAA- AC AUG GCT TTAGAT ISG CCG TTTAG AT ISG CCG TATAG CAG AA ATAG CC TTCGTT TTICATTA AATOG GAATAT AGGACAA TATT - TG AAAAATTIGG TA TAAA- AC AUG GCT TTAGAT ISG CCG TTTAG AT ISG CCG AT AGTAG CCG TTCAGT TTTGGT CAGAAATTIGG TA TAAAAATTIGG TA TAAA- AC AUG GCT TTAGAT ISG CCG TTTAG AT ISG CCG AT AGTAG CCG TTCAGT TTTGGT CAGAAATTIGGT CAGAAATTIGGT CGG TTTAGAT ISG CCT TCGATAGT CGG CCG AT AGTAG CCG TTCAGT TTGGT CAGAATTIGGT CGG TTTAGAT ISG CCG TTCAGT TTGGT CGG AT AGTAG CCG TTCAGT TTGGT CGG CGG TTTAGAT ISG CCG TTCAGT CGG AT AGTAG CCG TTCAGT CGG CGG TTGGT CGG AT AGTAG CCG TTCAGT CGG CGG TTGGT CGG TTGGT CGG CGG CGG C
75. ChLG3_1_R180292823RC_C4	AACATEACATACATCCTCCCCCACACATACTAAAAATTECATCCATC
76. ChLG3_1_R180292823RC_C2	AAC AT BACA JG ACCTT CCITCTA CAACAAT ACTABAA AATTIGG AETIGT TAAC CTITTEGT TITICTT TITATTE TATOG GAALAAT ASCE CAACAAT ACAG CAACAACAAT ACAG CAACAACAAT ACAG CAACAACAACAACAACAACAACAACAACAACAACAACAA
77. ChLG3_1_R180292823RC_C5	AACATTACAYCAACTITECTTACAACATTACTAAAAAATTEG AETICITEATEC TITICETITITATTAAATAGIG GAATAT ASCACAATATTI TE AAAAATTIGTA 100A 6 CAEGOTTITEAT ERACEATEGICE TITIGEATECATIGCAE CAATGOCCTITACTITITE AAG
78. ChLG3_1_R180292823RC_C7	AC ATACCATACCTTC TOTACACCT ACTAAAAATICAACTCI CATECOTTICT TITATAAACCG GAATAT NG ACATATI TIGAAAATICG A CONSCITTICATICAACAT ACTAAAAATICG A CONSCITTICATICAACAATICCC TICATITITIC TITATAAAACCG GAATAT NG ACATATICG A CONSCITTICATICAACAATICCC TICATITITICATAAAAATICG A CONSCITTICATICAACAATICCC TICATITITICATICAACAATICCC TICATITICATICAACAATICCC A CONSCITTICATICAACAATICCC A CONSCITTICATICAACAATICCC A CONSCITTICATICAACAATICCC A CONSCITTICATICAACAATICCC A CONSCITTICATICAACAATICCC A CONSCITTICATICAACAATICCC A CONSCITTICATICACCI A CONSCITTICATICAACAATICCC A CONSCITTICATICAACAATICCC A CONSCITTICATICAACAATICCC A CONSCITTICATICAACAATICCC A CONSCITTICATICAACAATICCC A CONSCITTICATICAACAATICCC A CONSCITTICATICAACAATICCC A CONSCITTICATICAACAATICCC A CONSCITTICAACAATICCC A CONSCITTICAACAATICCCC A CONSCITTICAACAATICCCC A CONSCITTICAACAATICCCCCAACAATICCCCCAACAATICCCCCAACAATICCCCCAACAATICCCCCAACAATICCCCCAACAATICCCCCAACAATICCCCCAACAATICCCCCAACAATICCCCCAACAATICCCCCAACAATICCCCCAACAATICCCCCCAACAATICCCCCAACAATICCCCCAACAATICCCCCAACAATICCCCCCAACAATICCCCCCAACAATICCCCCCAACAATICCCCCCAACAATICCCCCCAACAATICCCCCCAACAATICCCCCCCAACAATICCCCCCAACAATICCCCCCAACAATICCCCCCAACAATICCCCCCAACAATICCCCCCAACAATICCCCCCAACAATICCCCCCAACAATICCCCCAACAATICCCCCCAACAATICCCCCAACAATICCCCCAACAATICCCCCCAACAATICCC
79. ChLG3_1_R180292823RC_C10	GRCATEACCATECTTCCTCTCCATET ACTAAAAATTE XITCITATECTITTCTTTTTTTTTTTTTTTTTTTTTTTTTT
80. ChLG3_1_R180292823RC_C11	ACATACCARACTICUCTOR CACACACACACACACACACACACACACACACACACACA
81. ChLG3_1_R180292823RC_C3	ACTIVATION ACCESSION ACTIVATIONA ACTIVATION ACTIVA
82. GILG3_1_R180292927_G-2	
03. UILGO KIOUZO0323 U3	
64. UNLGO KIOUZO0323 US	ARE ATTRACTOR AND A TRACTART ANTARA ANT BY AS 120 TRACK OF THE ATTRACT AND A TRACTART
65. CHLGO K100200323 CO	
97 CHILGO K100200323 C4	
88 CHICS P180282410 C11	
89 Chi G5 P180282410 C12	
90 Chi G5 R180282410 C10	AA BATTACA ARACAITT CONCTA CARCAA GUTTAGAAA GATTAG ASTRONO GATTACTAGE TTTTCTATTA ARACCATEGAAAAA ATTTTTE GAABAAA ATTTTE GAABAACAICG TTTACA GUTACCATEGATTACAAAAAAAAAAAAAAAAAAAAAAAAAAA
91 Chi G5 R180282410 C1	
92 Chi G5 R180282410 C4	AN BATARCAAAACAIT CONCTA CAACAT GURAAAACAT TIG ACTUC TO TO CONTROL TO TO CONTROL TO TATE AND TA TAKATA AND TO CAADAA AT TO CAADAA AT TO CAADAA AT TO CAADAACAT CONTRACT AT TAKATAAAAAA TO TO CAADAACAT CONTRACT AT TAKATAAAAAAAA TO TO CAADAACAT CONTRACT AT TAKATAAAAAAAAAAAAAAAAAAAAAAAAAAAA
93 Chi G5 R180282410 C5	AA BATACAAAACAIT COTTA CAACAIG TRAAAAGATTEG AGTED TO BE CATGE TITTED TITTETTATA AATTCO TAAGAA ATTTE CAAAAA ATTO CAAGA TITTE CAAAAAA ATTO CAAGA TITTE CAAAAAA ATTO CAAGA TITTE CAAAAAA ATTO CAAGATIC CAATE CAACAACAACAACAACAACAACAACAACAACAACAACAA
94 Chl G5 R180282410 C3	AA BATTACAAAACAITECTICTA CAACATGTTAAAAAGATTAG ASTEETCASG-CFTTTGCTTTTTTTTTTAAAATTCETAAAAAATTCETAAAAAAAT-ING CAATAACATCGTTTAAAAAAATTCETAAAAAAATTCETAAAAAAATTCETAAAAAAATTCETAAAAAAATTCETAAAAAAATTCETAAAAAAATTCETAAAAAAAA
95. ChLG5 R180282410 C6	AA TATA AAAACAT COTTA CAACAT CATTA AAACAT IS SO TO STORE OF THICK TITCH THATAAAN CO CAACAA ATA TATA AAACAT CATTA
96. ChLG5 R180282410 C13	AALATTACAAAALTTCTCTACAAAACTICTTCAAAAACATIGG ASTESTCT3G-CTTTCCTTTTATAAAACTTTTTTAAAACTAAAACATICTTTTTAAAACAAAAA
97. ChLG5 R180282410 C16	aa h aitaca aaa a kutu cuta caacat <mark>gu</mark>taaaa<mark>g</mark>atuge as in ste as cutut (C) tuteet titata aatee (C) gaagaa an tutee aatee (C) aabaa a atee (C) aabaa aatee (C) aa
98. ChLG5 R180282410 C14	AN TATACAAAACAT COTOCA CAACAT GATAAAAGAT IGG AA ING CATTEG AT TO CATTE TO CAACAA AT A TAA AT TO CAAAAAA TO CAACAAC AGG IT TAG AQ ISACCOA ING GATAC AGG IT TAG AQ ISACCOA ING GATA CAACAACAACAACAACAACAACAACAACAACAACAACA
99. ChLG5 R180282410 C15	AN BAITACA AAAMCITTCICCA CAACATGETAAAAAGATIGG ASTEST CITIGG - CITITGET TITATAAAACCCGAAGAT ATAA AACATTE GAAAAAATTE GAAAAAACAGGET ITAGAGIGACCCA IGGGICGAAAGACAGGICA IGGGICGAAAGACAGCAAIGGA ATTACCITICAITT IIG IAGG
100. ChLG5 R180282410 C7	AA TATAACAAAACAIT CCTCTA CAACAT GCTAAAAGATIGG AGTEGT CATTGCT TTTTTTC AATTCCTTATTA AATTCCTTAAAATTCCTTAAAATTCTTTGAAAAAATTCTTTGAAAAAATTCCTTAAATACATGGCCAGGCCCGAATACGCCCGAACAACACCGCCCCCAATTACCTTTATTAAATTCCTTTATTAAATTCCTTTTTT
101. ChLG5 R180282410 C9	ARTATTACAAAACAIT COTOTA CAACAATGC ATIGA STEET CHEG-CTTTIGE T TITOTIT T-ATTAARTIC CTAAARAATTE THE GAAAAAAAT-TIGE GAATAAC A COG TITTAE ACTIGACCCA TE GOG CGAAAAGA ATTACC TTIGATTE TTIE TAGE
102. ChLG5_R180282410_C8	AR TATTACA AAACAIT COTOTA CAACAAT GOGOCITET CAACAA AATIGO CITAGE CITATIC TITUTITITIC CAACAA AATIT CITAGA CAACAA
103. ChLG5_R180282410_C2	AA TATA CA AAACATT COTOTA CAACATC TTAAAACATTC ATTICATT ACTITICATITAT TA AATTIT TO AAAATATATTT TO AAAAATATATTIT TO AAAAATA
104. ChLG3_2_R180295150_C26	AAC ATTACE AAACCTTE CITETACAACAAT ANTAAAAAATTGE AGCEST OUGG-COTTECT TITCATTAAAATTGE AAAATT DAAAAAAAAAATTAGAAAAAC TGAAAAAAC TGAAAAACATE TCTTEGAT IS ACCCACEGOTCCAATACCATE CITCATTACTTCATTATAAATTOG AAAATT TAAAAAAAAAATTAGAAAAAAC TGAAAAAAC TGAAAAACATE TCTTEGAT IS ACCCACEGOTCCAATACCATE ATTACCATCAATACCTTCATTATAAATTAGAAAAAAAATTAGAAAAAAAA
105. ChLG3_2_R180295150_C43	AACATTAGAAAACTTGCTTACAACATATTAAAAAAATTIGG SCTETTOGG TTTICATTTATAAATTIG AAAATTTAAAATTIG AAAAAATTGAAAAAACTTTGCAGAACATTECTTGATTGATGACCCAGGGTCGAATACATTGCTTCATTTATTAAATTIG AAAAAAAACT
106. ChLG3_2_R180295150_C50	AACATTAG AAACCITECTITACAACAT ATTAAAAATTEE SCHETEGG CITTICET TITCAT TITATAAATTE AAATTE AAAAAATTE CAAAAACTEGCAACATE TOTTECAT EAACACE COTCEATTECT TCCTTCCT TTATTAAATTE AATTE AAAAAATTE AAAATTE AAAAAATTE AAAAATTE AAAAATTE AAAAATTE AAAAAATTE AAAAATTE AAAAAATTE AAAAAATTE AAAAAATTE AAAAAATTE AAAAAATTE AAAAATTE AAAAATTE AAAAAATTE AAAAATTE AAAAAATTE AAAAATTE AAAAAATTE AAAAATTE AAAAATTE AAAAATTE AAAAATTE AAAAATTE AAAAATTE AAAAAATTE AAAAATTE AAAAATTE AAAAATTE AAAAATTE AAAAAATTE AAAAATTE AAAAATTE AAAAATTE AAAAAATTE AAAAATTE AAAAAATTE AAAAAATTE AAAAAATTE AAAAAATTE AAAAATTE AAAAAATTE AAAAAATTE AAAAAATTE AAAAAATTE AAAAAATTE AAAAAATTE AAAAAATTE AAAAAATTE AAAAATTE AAAAATTE AAAAATTE AAAAAATTE AAAAATTE AAAAAATTE AAAAAATTE AAAAAATTE AAAAA
107. ChLG3_2_R180295150_C3	AC ATTACE AAACCITE CITIES CALL ATTAAAAATTICE ASCIST CUS - CITIES TITICATITATAATTICE ASAATTI TAAAAAAAACTSCACAACCAT IS CUTTEEATTE ACCACEGI STCEATTE CITIES TITICATTICT THE SCE
108. ChLG3_2_R180295150_C37	ACCITICATION ACCIT
110 ChLC3 Z R100293130 C44	NORTING AND DEVELOPMENT RELATIONS TO DEVELOPMENT RELATIONS TO DEVELOPMENT AND DEVELOPMENT TO DEVELOPMENT TO DEVELOPMENT AND DEVELOPMENT RELATIONS TO DEVELOPMENT AND DEVELOPMENT RELATIONS TO DEVELOPMENT AND DEVEL
111 CH C3 2 R100255150 C25	
112 CHLC3_2_P180205150_C30	
113 Chi G3 2 R180295150 C17	ACCUPTING ADDRESS OF THE CALCULATION AND ADDRESS ADDRES
114 Chi G3 2 R180295150 C40	ARCATTACE ARACCTTECT TACACACAT ANTARAR ANTIG SCHITCONG CONTROL TITCATTA ANTICE RAANTICE RAANTICE RAANTICE TAGAARAR ANTICE TICATTACTACTACACTER CONTROL TO CATACACATER CONTROL TO CATACACATER CONTROL TO CATACACATER CONTROL TO CATACACATER CONTROL TO CATACACATER CONTROL TO CATACACATER CONTROL TO CATACACATER CONTROL TO CATACACATER CONTROL TO CATACACATER CONTROL TO CATACACATER CONTROL TO CATACACATER CONTROL TO CATACACATER CONTROL TO CATACACATER CONTROL TO CATACATER
115 Chi G3 2 R180295150 C7	AACATTAGE AAACCOTECTT TACAACAT ABTAGAA AATTEG ACCOTT CONT CONTTOCT TITCHT THATAAATTEG AAABTE TAAAAAATTEG AAAATTEG AAAATTEG ACATTACTATATAAATTEG ACCOTECTTACATTACAAAATTEG ACCOTECTTACATTECTTACAAATTEG ACCOTECTTACAAATTEG ACCOTECTTACAATTEG
116. Chi G3 2 R180295150 C15	AAC ATTACE AAACCETECTETA CAACAT ARTA-AA AATTGE ACCETTTECTTTECTTTTETA AATTCE AAAATTCE AAAATTCE AAAATTCE AATTACAAAAATTCE AATTACAAAATTCE AATTACAAATTCE AATTACAAATTCE AATTACAAAATTCE AATTACAAAAATTCE AATTACAAAAATTCE AATTACAAAATTCE AATTACAAAAATTCE AATTACAAAATTCE AATTACAAAATTCE AATTACAAATTCE AATTACAAAATTCE AATTACAATTCE AATTACAATTCE AATTACAAATTCE AATTACAAAATTCE AATTACAAAATTCE AATTACAAAAATTCE AATTACAAAATTCE AATTACAAAAATTCE AATTACAAAAATTCE AATTACAAAAAATTCE AATTACAAAAATTCE
117. ChLG3 2 R180295150 C48	AAC ATTACE AAAC ACTE TA CAACAAT AATAAAAAATTIGG ACTTICE TTICE TTICE TTICE TATAAAAATTICE AAAATTICE AAAATTICE TAAAAAA TAAAAA TAAAAAA TAAAAAATTICE AAAATTICE TAAAAAAATTICE TAAAAAA
118. ChLG3 2 R180295150 C53	AACATTAC <mark>S</mark> ARACCE <mark>IS</mark> CTERACAACATAETRAAAAATTIGS ASCELSTOEGS-CETTISCTTATTAAATTIG EASAATTI TAAAATTIG EASAATTI TAAAAAETTIG AAAAAETTISCTISAATAAAAATTIG AAAAAETTISCTISAATAAAAATTIG AAAAAETTISCTISAATAAAAAATTIG AAAAA
119. ChLG3 2 R180295150 C45	AAC ATTACE AAACCETECTETA CAACAAT AETAAAA AAATEG ASCELT CERTCE, TATCE TATTA AAATTAG AAAETTAG AAAAETTAG AAAAAE AATTAG AAAAAATTAG AAAAATTAG AAAATTAG AAAATTAG AAAATTAG AAATTAG AAAATTAG AAAATTAG AAAATTAG AAAATTAG AAAATTAG AAAATTAG AAAATTAG AAAATTAG AAAATTAG AAATTAG
120. ChLG3 2 R180295150 C24	AAC ATTACE ARACCETE TA CAACAAT ANTRAAR AAATIGG ASCHITT CORTAGE T TITCE TATTA ARATTCE ARAATE TAA AAA AAATE TAA AAAA CAATE TO CAACAATE AAAATE CAACAATA AAAATE AAAAAAAAAA
121. ChLG3 2 R180295150 C21	AACATTACE AAACCELECTETA CAACAT AETAAAA AATTES ASCELT CETTES T TITCE T TITCE T TITCE T TITCE T TATA AATTES AAAAETTE TAAAATTES AAAAAE T 16 CASAAACACE TECTAS AT IS ACCCAES OST CO AATAE ATTES CATE CATE CATE ATTES
122. ChLG3 2 R180295150 C20	AAC ATTAG <mark>,</mark> AAACCOT <mark>G</mark> CITTA CAACAAT A <mark>RTAAAA AATTOG AG CI</mark> TT GOTG - C O TTIG <mark>A</mark> T TITCATTAAARTOG AAAAATTOG AAAAA AT I TAAAAAAA A C AATTAG
123. ChLG3_2_R180295150_C6	AAC ATTACE ABACCOLO CABCA TATABAA BATTE AGTATE COTTE CALT CALTER ANTICATE ABTIC ATTABATT CABAABA ANTIC ABAABA A
124. ChLG3_2_R180295150_C8	AACATTAGE AAACCOLSCTETA CAACAAT ANTAAAA AAATEGE ASCEST OF COTTICE T TITCATTA AATTOG AAAATE TAAAAAAAAA — TG AAAAAACT TG CAGAAAC AOES TO THAAT IG ACCCA CS OG TCG AATAS ATTAG CA TTAATA CT TTATTA AATTOG AAAATE TAAAAAAAAA TG AAAAAACT TG CAGAAAC AOES TO THAAT IG ACCCA CS OG TCG AATAS CT CATTOC TT TTATTA AATTOG AAAATE TAAAAAAAAAA
125. ChLG3_2_R180295150_C14	AAC ATTAGE AAACCORSCTTTA CAACAAT AATAAAA AATTGG AGOTGT COTTTGC T TTTCATTAAAATACG AAAATT TAAAAAA AAAAATTGG AAAAATTGG AAAAATTAG AAGAAAAAATTGG AAAAATTAG AAGAAAAATTAG AAGAAAAATTAG AAGAAAAATTAG AAGAAAAAATTAG AAGAAAAATTAG AAGAAAATTAG AAGAAAATTAG AAGAAAAATTAG AAGAAAAATTAG AAGAAAATTAG AAGAAAAATTAG AAGAAAAATTAG AAGAAAATTAG AAGAAAAATTAG AAGAAAATTAG AAGAAAATTAG AAGAAAAATTAG AAGAAAAATTAG AAGAAAAT
126. ChLG3_2_R180295150_C19	AAC ATTAGE AAACCORSCITETA CAACAAT ARVAAAA AATTIGE ASCEDT TO CATTAGE TO THICALITET TAAAATAA AAAAATTIGE AAAAATTIGE AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
127. ChLG3_2_R180295150_C5	AACATTAGAAAACTTGCTETACAACAT ARTAAAAAATTG ASCEDT COG - COTTGCT TTTCATTATAAATTE AAAATTA AATTE AAAAAAAAT TGAAAAACT- IGCAGAACACE COTTGCT IGCAGAACACE CATTACT TTGCACCACGCGACTAC AT A AAAATTACTTCATTATAAATTE AAAATTACTTCATTATAAAATTE AAAAAAAAAA
128. ChLG3_2_R180295150_C42	AAC ATTAGE AAACCTTGCTTTACAACAAT AATAAAAAATTGC AGCTGTCGGG-CCTTTGCTTTACTAAATTTTCAAATTTTCAAAATTTTCAAAATTTCAAAATTTCAAAAATTTCAAAAATTTCAAAAATTTCAAAAATTTCAAAAATTTCAAAAATTTCAAAAATTTCAAAAATTTCAAAAAA
129. ChLG3_2_R180295150_C10	AAC ATTACE MAACCITESCIT TA CAACAT ARTAAA AATTIG ASCHET OUSG - CETTICE TITICATITATAAATTIG AAANTI TA-AAAABAAATT- IG CAGAACATE COTTACAT IS ACCACS CICCATICATIC ATTICATIC TITCATITATAAATTIG AAAAAATTIG AAAAAATTIG AACAAAATTIG AACAAAATTIG AACAAAATTIG AAAAAATTIG AACAAAAATTIG AACAAAAATTIG AACAAAAATTIG AACAAAAATTIG AACAAAAATTIG AACAAAAATTIG AACAAAAAAAAATTIG AACAAAAATTIG AACAAAAATTIG AACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
130. ChLG3_2_R180295150_C12	AGUATTARU ARAULTING UTEL CARLAT ARTAAAA AATTAG SOUBSTUDG CUTTING TITATTAAAAAATTU AAAATTU AAAAAATT - TG CACAACAUD CUTTING ATTAATAAAAATTAG CAAAAATTU TAATAAAAAATTU AAAAAATTU AAAAAAATTU AAAAAAATTU AAAAAATTU AAAAAATTU AAAAAATTU AAAAAATTU AAAAAAATTU
131. UNLG3_2_R180295150_C28	ARE ATTACK TARGET AND A TRADE AND A SOLD TO A TRADE AND A SOLD TO A TRADE AND A SOLD TO A SOLD T
132. GHLG3 Z K180293130 C29	MALE INCOME DESCRIPTION AND ADDRESS OF ADDRE
135. UNLG3 Z R180295150 C30	AALATTAL CAARACTING CINING AND AND AND AND AND AND AND AND AND AND

g) alignment of cluster 8

	1	10	20	30	40	50	60	70	80	90	100	110	120 130	135
Consensus	AAG	AAAG AATCGTCCG	AAAT	-AAG CCGTTTTC	ATCCAAACTAT	AACATAAAT -	<mark>CG TTC</mark> -	TTTTG AG O	CAG AA TAA	-GG CG TTTT CAG TO	TG TT TT ATG A	AAGTTTTCTC	G	AAA
1. ChLG5 R180282547RC C2		AAG AATCGCCAG	AAAT	-AAACCGTTTTC	ATCCAAATTAT	AACATAAATAG	GTTG TTTG	TTTCCCGGC	TAAAATAA-	-GCCGTTTTCAAC	CACTTCTCAAA-	AAGTTTTCTC	G TT TG TAAG CA	
2. ChLG5 R180282547RC C4		AAG AATCG CA	AAAT	-AAG CCGTTTTT	ATCCAAACTAT	-AACATAAAT CC	GTTGTT	TT <mark>C</mark> G C	TA <mark>A</mark> AATAA-	-GG CG TT TT CAG 🖸	C <mark>AC</mark> TT <mark>A</mark> TA <mark>CA</mark> A-	GAATTTTCTC	g <mark>tg</mark> t <mark>c</mark> taaa	
3. ChLG3 1 R180293225 C2		AAG AATCGTT	AAAT	-AAG CCGTTTT	ATCCAAACTAT	AACATAAAT	<mark>- T T</mark> G TT	T <mark>C C</mark> AG C	TAG AA TA A -	-GCTG TTTT CAG C	CAATTCTCAAA	GAATTTTCGC	G <mark>TT</mark> TT T <mark>T</mark> T <mark>G</mark> AG CA	
4. ChLG3_1_R180293225_C6		AAG AATCGTC <mark>T</mark> G	GAAAT	-AAG CCGTTTTC	ATCCAAACTAT	-AACATAAAT 😋	GTTGTT		T AG AA TAA -	-GCTGTTTTCAGC	CAATT CT CAAA	GAATTTTCG C	G TT TT T T T <mark>GG</mark> G CA	
5. ChLG3_1_R180293225_C4		AAGAATTGTCT	AAAT	-AAG CCGTTTTC	ATCCAAACTAT	AACATAAAT	3 T T		T AG AA TAA -	-GCCATTTCCAGC	CAATTACAAAA	GAGTTTTCGC	g <mark>tt</mark> ttt g agga	
6. ChLG4_R180280157_C1		AAAACCGTCTC	AAAT	-AAG CCGTTTTC	ATCCAAACTAT	AACATAATTA	TTTT	- TT T <mark>G</mark> G AG C	TAG AA TAA -	-GTTTTCAG T	TG TT TCACAA-	AAGTT <mark>CA</mark> CTC	C-TTT-TTAAG CA	
7. ChLG4_R180280157_C3		AAAAACCGTCTC	AAAT	-AAG CCGTTTTC	-ATCCAAACTAT	AACATAATTC	CCTTT	- TT T <mark>G</mark> G AG C	TAGAATAA -	-GG CATTTT CAG T	TG TT TCACAA-	-AAGTTTACTC	C-TTC-TTAAG CA	
8. ChLG4_R180280157_C5		AAAAAACGTCTC	TAAAT	-AAG CCGTTTTC	-ATCCAAATTAT	-AACATA	TTTTT	- TTTTG AG C	TAGAATAA-	-GG CG TT TT CAG T	TG TT TTACAA-	-AAGTTTACTC	C-TTT-TTAAG CA	
9. UNLU4 K100200137 U7		AATAAACGTCTC	AAAT	AAG COGTTTTT	ATCCAAACTAT	AACATA						AAGTTTACTC	TT-CTARGCA	
10. CHLGO K100200349KC C3		AGG MATCGTCH:	AAAI	-AAGCCGTTTTC	- AATCAAACTAT	TACACAA TT		TRITACO			- 16 II II AI HAI - 17 TT TT AI HAI	AAAAGIIGACII		
12 CH G3 2 R180200348CC C3		ABGAATCGT	AAAT	-ATGCCGTTTTC	- ATCCAAACTT	-AACAAAAAT						AAGTTTACTC	G-TTT-CTAATTA	
13 Chi G3 2 R180297093RC C13		AAGAATCGTTT	AAAT	-ATG CCGTTTTC	ATGCAAACTT	AACAAAAAT	CTTTC-	TTCTAAG	CAGAATAT	-GG CG TT TT CAG TO	CTG TT TT <mark>G</mark> TG A-	AAGTTTACTC	G-TTT-CTA-TTA	
14 Chi G3 2 R180297093RC C7		AAG AATCGTTT	AAAT	TTGCCGTTTTC	ATCCAAACTT	AACAAAAAT	-CTTTC-	TTCTAAGT	CAGAATAT	-GG CG TT TT CAG TO	CTG TT TT <mark>G</mark> TG A-	AAGTTTACTC	G-TTT-CTAATTA	
15 Chi G3 2 R180297093RC C10		AAG AATCGTTT	AAAT	TTGCCGTTTTC	ATCCAAACTT	AACAAAAT	-CTTTC-	TTCTAAGT	CAGAATAT	-GG CG TTTT CAG TO	TATT TTGTG A	AAGTTTACTC	G- <mark>T</mark> TT-CTAATTA	
16. ChLG3 2 R180297093RC C12		AAG AATCGT <mark>TT</mark>	AAAT	-ATG CCGTTTTC	- AT <mark>G</mark> CAAACT <mark>T</mark> T	AACAAAAT	-CTTTC-	TTCTAAGT	CAGAA TA <mark>T</mark> -	-GG CG TT TT CAG TO	CTG TT TT <mark>G</mark> TG A-	AAGTTT <mark>A</mark> CT	G- <mark>T</mark> TT-CTAAGTA	
17. ChLG3 2 R180297093RC C5		AAGAATCGTC	AAAT	- TT G CC T I TT T	TATCCAAACT <mark>T</mark> T	-aa <mark>t</mark> acagat -	C <mark>T</mark> TT <mark>G</mark>	TTTTAATT	CAGAATA <mark>T</mark>	- AG CG TT TT CAG TO	CAG TT TTATG A	ATGTTTTCT	G – <mark>T</mark> T <mark>C – TG</mark> AAG C <mark>T</mark>	
18. ChLG3 2 R180297093RC C11		AAG AATCGTCT	AAAT	- TT G CC T F TT T	-ATCCAAACT <mark>T</mark> T	-AA <mark>T</mark> ACAGAT	- C <mark>T</mark> TT <mark>G</mark>	TACTAAG T	CAGAA TA <mark>T</mark>	– AG TG TT TT CAG T	TG TT TT ATG A-		G – <mark>T</mark> TT – CTAAG <mark>T</mark> A	
19. ChLG3_2_R180297093RC_C8		AAG AATCGTCT	AAAT	- TT G CC T FTTT T	-ATCCAAACT <mark>T</mark> T	-AA <mark>T</mark> A <mark>C</mark> A <mark>G</mark> AT	-CTTTG	- TTTT A AG <mark>T</mark>	CAGAATA <mark>T</mark> -	-GG CG TT TT CAG TO	CTG TT TT <mark>G</mark> TG A-	AAGTTT <mark>A</mark> CT <mark>I</mark>	G – <mark>T</mark> TT – CTAAG <mark>T</mark> A	
20. ChLG3_2_R180297093RC_C2		GAGAATCGTCT	AAAT	-TTACCGTTTTC	-ATCCAAACCT	-AACACATAT	CTTT	- TT <mark>CIA</mark> AG <mark>T</mark>	CA <mark>T</mark> AATA <mark>T</mark>	- AG CG TT TT CAG T	TG TT TTAAAA-	ACGTTTACTC	G – TTT – CTAAG CA	
21. ChLG3_2_R180297093RC_C3		AAG AATCATCT	AAAT	-AAG CTGTTTTC	-GTTCAAACTAT	-AACATAA <mark>T</mark> I	CG CTA	TTTTG AG O	CAGAATA <mark>T</mark> -	-GG CG TT TT CAG TO	CTG TT TT <mark>G</mark> TG A	AAGG TAAC T	G - TTT-CTAAG TA	
22. ChLG3_2_R180297093RC_C6		AAGAATTGTCCC	AAAT	-AAG CCGTTTTC	-GTTCAAACTAT	-AACATAA <mark>T</mark> T	TGTTA	TTTTG AG C	CAGAATA <mark>T</mark>	-GG CG TT TT CAG TO	CTG TT TT ATG A-	AAGT TAAC T	G- T TT-CTAAGGA	
23. ChLG3_2_R180297093RC_C9		AAG AATCGTTT	AAAT	-ATG CCGTTTTC	-ATGCAAACTAT	AACATAAT	GTTA	- TT TTG AG O	CAGAATAT-	-GG CG TTTTCTG TC	CIG TT TTATG A-	AAGTTAACT	G-TTT-CTAAGGA	
24. ChLG3_2_R180294957_C5		AAGAATUGTIC		AAACCGTTTTC	AT	-AACATAAAT	-CATTC-	APTIGAGO		-GICATTITIGGI	TG TT TAATGA	A		
20. CHLG3 Z K100294907 CO		AASAATCGTTT	MAA A A AT	AAACCGTTTTC	A1	AACATAAAT	CG TTC	APTIGAG C		- GICATTTTIGG 1	TG TT THATGA	A		
20. CHEG3_2_R100294957_C11	A AG	A A A A A C TOGTOT	3 A A AT	-AAACCGTTTTC			-06 TTC-	-T			TGITTIAIGA TC TTTTATGA	AAGTTTTTTTTTTTT		
28 CH GA P180280157 C-2	1113	A A A A A CCCTCTC	A A AT	-AAGCCGTTTTC	- ATCCAAACTAT	-a ac at aa at	-OG TTC-	- T					G TTTTCAGCA	
29 Chi G3 2 R180296303 C7		AAG AG TCGTCCC	AAA	AAGCCGTTTTC	TCCAAACTGT	AACATAAT	G TAT	TTTTAAGC	AGAATAA -	-GG CG TT TT CG G T	TG TT TT AT TA-	AAGTTTTTTT	T-ATTTCCAAGCC	
30. Chi G3 2 R180296303 C9		AAAAG TTGTCCC	AAAT	AAGCTGTTTTC	ATCCAAACTT	AATAACT	G TAA	TTTTAAGO	CAGAATTA-	-GG CATTTT CAG T	TG TT TT AT TA-	AAGTTTTTT	TTATTTCGAAG CA	
31. ChLG3 2 R180296303 C2		AAGAG TCGTCCG	AAAT	-AAGGCGTTTTC	- ATCCAAACT <mark>G</mark> T	AACATAAT	- CG TAC-	TTTTAAGO	CAGAATAA	-GG CG TT TT CAG T	TG TT TT AT TA-	AAGTTTTTT	C-ATTTCGAAGCA	
32. ChLG3 2 R180296303 C3		AAG A <mark>G</mark> TC <mark>ACG</mark> CO	AAAT	-AAG CCGTTTTC	-ATC <mark>A</mark> AAACT <mark>G</mark> T	-AACATAA <mark>T</mark> I	CATAT	TTTTAAGO	CAGAATAA-	-GG CG TT TT CAG T	TG TT TCAT TA-	AAGTTTTCTC	G T <mark>C</mark> TC <mark>A</mark> AAG <mark>T</mark> A	
33. ChLG3 2 R180296303 C8		AAG A <mark>G</mark> TC <mark>AC</mark> CCG	AAAT	- <mark>G</mark> AG <mark>T</mark> CG T T T T C	ATCCAAACTAT	-AACATAA <mark>T</mark> I	CATAC	TTTT A AG O	CAGAATAA-	-GG CG TT T <mark>A</mark> CAG T <mark>C</mark>	IG TT TCAT TA-	AAGTTTTCTC	T	
34. ChLG3_2_R180296303_C10		AAG A <mark>G</mark> TC <mark>TC</mark> CCG	GAAAT	-AAG CCGTTTTC	- ATCCAAAC T <mark>G</mark> T	-ACCATAA <mark>T</mark> I	- CG TAC	TTTTAAGO	CAGAATAA-	-GG CG TT TT CAG 🖸	ATATT TT AT TA-	AAGTTTTCTC	G — TT T <mark>AG</mark> AAG <mark>T</mark> A	
35. ChLG3_2_R180296303_C4		AAG AG TCGTCCG	AAAT	-AAG CCGTTTTC	-ATCCAAACTGT	-AACATAA <mark>T</mark> I	CG T <mark>AT</mark>	TTTTAAGC	AAGAATAA -	-GG CG TT TT CAG I	TATCTTAT CA-	-AAGTTTTCTC	G TT T <mark>AC</mark> AAG CA	
36. ChLG3_2_R180296303_C5		AAAAG TCGT TCG	AAAT	-AAG CCGTTTTC	- ATC <mark>T</mark> AAACT <mark>G</mark> T	-AACATAA <mark>T</mark> I	- CG T <mark>AT</mark>	- TT TT A AG C	A AG AA TA A -	-GG CG TT TT CAG T	TG TCTTAT CA-	AAGT TTTTTTC	G TT T <mark>AC</mark> AAG CA	
37. ChLG3_2_R180296303_C6		AAAAG TCGTTCG	AAAT	-AAG CCGTTTTC	ATCTAAACTGT	AACATAAT		TTTTAAGO	CAGAATAA-	- G G TTTTCAG I	IG TI TI AT A	AGGTTTTCTC	G TTTAGAAG CA	
36. CHLG4_K180280157_C-3		AAAAACGTCCC	A AT	-AAG COGTTTTC	-ATCCAAACTAT		r c - TTr-	- TTTTG AG T	CHCARAAA -	-GG GG TTTT		-ATTTTC		e G
40 CHLG5 R100202191RC C3		A AT AA TCC CTCC			GTCCAAACTAT								- TITCAABCA	
40. CHEG5_R180282191RC_C6		AAGAATCGTTCG	AAT	-AAGCCGTTTTC	-GTCCAAACTAT	-ACCATAATTC	T-TACTT		CICAATAA-	- AATCTTTTCAG TO	THE TT TT ATC T-	AAGTTTTTTTTTT	G TTTCAAAGCA	
42 Chi G5 R180282191RC C5		AATAATCGTTCC	GAAT	-AAGGCGTTTTC	GTCCAAACTAT	AACATAATTC	TTACTT	TTTTG	CTAAATAA-	-AGTATTTCAGT	TG TT TT ATG	AAGATTTCTC	G TT TCAAAG CA	
43 Chi G5 R180282191RC C2		AATAATCGTTC	AAAT	-GAGCTGTTTTC	GTCCAAACAAT	AAAATAAGT	TGTTC	TTTTGTGT	CTGAATAT	- AG AG TT TT CAG T	TG TT TT AT TC	AAGTTTTT	A TTTTAAAG CA	
44. ChLG5_R180282191RC_C6		AAGGATCGTCC	AAAT	-AAG COGTTTTC	GTCCAAACTT	TAACATAAT	- CG TTC-	TTTTG TG O	CTGAATAT	AG CG TT TT CAG T	TG TT TT AT AT	AAGTTTTCTC	G TT T <mark>TG</mark> AAG CA	
45. ChLG5 R180282191RC C10		AAGAATCGTCC	AAAT	-AAG CCGTTTTC	GTCCAAACTT	TAACATAAT		TTTT <mark>TT</mark> G C	C <mark>T</mark> GAATA <mark>T</mark>	- AG CG TT TT CAG T	TG TT TT AAG T	AAGTTTT <mark>G</mark> T	G — TTTC <mark>G</mark> AAG CA	
46. ChLG5 R180282191RC C9		AAG AAT <mark>TC</mark> TCCG	AAAT	-AA <mark>A</mark> C <mark>T</mark> GTTTT <mark>T</mark>	- <mark>G</mark> T <mark>T</mark> CAAACT <mark>T</mark> T	TAACATAA TT	CG TTC	- TTT-G <mark>T</mark> G O	C <mark>T</mark> GAATA <mark>T</mark> -	- AACATTTTAAG T	TG TT TT AT AT	AAGTTTTCTC	G TT TC AAAG CA	
47. ChLG5 R180282191RC C13		AAG AAT <mark>T</mark> GTCCG	AAAT	-AAGC <mark>T</mark> GTTTT <mark>T</mark>	- <mark>G</mark> TCCAAACT <mark>T</mark> T	TAACATAA <mark>T</mark> I	CATTC-	- TTTTG <mark>T</mark> G O	C TGC ATA <mark>T</mark> -	– <mark>A</mark> G CG TT <mark>AAG</mark> AG T	TG TT TT AT <mark>TT</mark> -	AAGTTTTCTC	G — TT T <mark>T A</mark> AAG CA	
48. ChLG5_R180282191RC_C7		AAGAATCGT <mark>T</mark> CG	<mark>G</mark> AAT	-AAGACATTTC	- <mark>G</mark> TCCAAACTAT	-AACATAA <mark>T</mark> I -	TGTTC	TTTT <mark>AT</mark> G O	C <mark>TAC</mark> ATAA-	-GG CG TT TT CAG TC	CIG TI I – – T AI	- A <mark>T</mark> GTTTTCTC	G TT TC <mark>G</mark> AAG CA	
49. ChLG5_R180282191RC_C11		AAG AATCGT <mark>T</mark> CG	<mark>G</mark> AAT	-AAG TCTTTC	- <mark>G</mark> TCCAAACTAT	-AACATAA <mark>T</mark> I	TGTCC	- TT TTG <mark>T</mark> G O	CTGAATAA-	-GG CATTTT CAG T	TG TT TA-T AT	-AAGTTT-CTC	G TT TC <mark>G</mark> AAG CA	
50. ChLG5_R180282191RC_C4		AAGAATCGTCCG	GAAAT	-AAACCGCTTTC	GTCCAAACTAT	-AA <mark>G</mark> ATAA <mark>T</mark> T-	TGTCC	TTTTG T G O	CTGGATAA-	-GG CG TT TT CA <mark>A</mark> TC	CIG TI TTAT <mark>AT</mark>	ACGTTT-CTC	G — TT T <mark>AG</mark> AAG CA	
51. ChLG8_R180288349RC_C2		AGG AATCGTCA	AAAT	-AAG CCGTTTTC	ATCCAAACTGC	-AACTTAGTT	CG TTC-	TTTTTGO	CTAAATGA-	-GG CG TT TT CAG T	TG TT TT AG AT	-AAATTTTCTC	A TT CCAAAG CA	
52. ChLG8_R180288349RC_C6		AAAATCGTCC	AAAT	-AAG CCGTTTTC	ATCCATACTGT	-AACTTAGTT	CG TTC-	TTTTTG	CTAAAIGA-	-GG CATTTTCAG T	TIG TT TT AG AT	-AAATTTTCTC	A TTCCAAAGCA	
53. UNLG8_K180288349KC_C4		AG AATCGTCC	AAAT	-AAG COGTTTTC	-ATCCTTACTGT	AACTIAATI	USTTC-	- TTTT CT G O	Calif AA 1 <mark>G</mark> A -	-GAUG TTTTCAG TO	DIG TOTTAG AT	-AAGTTTTCTC		
54. UNLG4_R180280157_UZ		AAGAATCGTCCG	AG AT	-AAGCAGTTTTC	-GTTCAAACTAT	-AACATAATT	CG TAC-	-TTTTG AG O	CANAATAA-	-GG CG TG T-CAG TG	TG TT TTAT TA-		G TTACAAAACAA	AAA
55. UNLG4 K180280157 U4		AAGAATUGTCCG	AT CAL	-AAGCAGTTTTC	GG TT AT ACTAT	AASATAATI		- TITIT <mark>T</mark> AG O	CAAAATAA-	-GG GS TTTT CAG 1	IG TI TTAT <mark>T</mark> A-	-AA TTTTTTTTT		AA.

56 CH G4 R180280157 C8	AAG AATCGTCTCAGAGAT-	AGCCGTTTTC	-GTTTAA ACTAT-	AACATAAT	-CTTAC-1	TTTTG AG TG AAG A TA A -	- ΑΑ Ως ΤΤΙ ΤΤΙ Α Ας Τ <mark>ς</mark> Τς ΤΤΙ ΤΤΙ ΑΤ <mark>Π</mark> Α		
57 Chi G4 R180280157 C6	AAAATCGTCCGAAAT-	AAGCAGTTTTC	GTTTAAACTAT-	AAGATAATT	-OG TTC-1	ITTTG AG CTAAAA TAA -	-GG CG TT TT TAG TG TG TT TT AT TAT	- AAAG TTTTTCG -	TTCCAAAGCA
58. ChLG8 R180289864 C4	AAG AAT <mark>T</mark> GT <mark>T</mark> CGAAAT -	AAGCCGTTTTC	ACCCAAACTAT	AACATATA	- <mark>T</mark> G T <mark>C</mark> C-1	ITTTG AG CCA <mark>A</mark> AATAA -	-GG CG TT TT CAG T <mark>G</mark> TG TT TT AT <mark>T</mark> A	AAGTTTTCTCA	TTTCTAAGCA
59. ChLG8 R180289864 C5	AAG AAT <mark>T</mark> GT <mark>T</mark> CGAAAT -	AAGCCGTTTTC	- ACCCAAACTAT -	AACATA <mark>T</mark> A <mark>G TT</mark>	- <mark>T</mark> G T <mark>C</mark> C-7	ITTTG AG CCA <mark>A</mark> AA TAA -	-GG CG TT TT CAG T <mark>G</mark> TG TT TT AT <mark>T</mark> A	-AAGTTTTCTCA	- TT TC TAAG CA
60. ChLG8 R180289864 C6	AAG AAT <mark>T</mark> GT <mark>T</mark> CGAAAT -	AAGCCGTTTTC	- A <mark>C</mark> CCAAACTAT -	AACATA <mark>T</mark> A <mark>G T'T</mark>	- <mark>T</mark> G T <mark>C</mark> C-1	ITTTG AG CCA <mark>A</mark> AA TAA -	-GG CG TT TT CAG T <mark>G</mark> TG TT TT AT <mark>T</mark> A	AAGTTTTCTCA-	- TT TC TAAG CA
61. ChLG8 R180289864 C3	AAG AAT <mark>T</mark> GT <mark>T</mark> CGAAAT -	AAG CCGTTTTC-	- ACCCAAACTAT -	AACA <mark>C</mark> A <mark>T</mark> A <mark>G TT</mark>	- <mark>T</mark> G T <mark>C</mark> C-1	ITTTG AG <mark>G</mark> CA <mark>A</mark> AATAA -	–GG CG TT TT CAG T <mark>G</mark> TG TT TT AT <mark>T</mark> A–-	AAGTTTTCTCA-	– TT TC <mark>G</mark> AAG CA
62. ChLG8 R180289864 C2	AA <mark>A</mark> AATCGTC <mark>T</mark> GA <mark>G</mark> AT -	AAGCCGTTTTC	-ACCCAAACTAT-	AACATA <mark>T</mark> A <mark>G TT</mark>	- T G T <mark>C</mark> C-1	ITTTG AG <mark>G</mark> CA <mark>A</mark> AA TAA -	–GG CG TT TT CAG T <mark>G</mark> TG TT TT AT <mark>T</mark> A–-	AAGTTTTCTCA	TTTCTAAG CA
63. ChLG3_2_R180294957_C6	AAG AAT <mark>G</mark> GTCC <mark>C</mark> AAAT-	GAGCTGTTTT	- A <mark>C</mark> CC <mark>G</mark> AAC T <mark>G</mark> T -	AACATAAATCG	TTC-1	FTTTG AG <mark>G</mark> CAG AA TAA -	-GG CG TT TT CAG T <mark>A</mark> TG TT TT ATG A	AAGTTTT <mark>T</mark> T <mark>T</mark> -	<mark>g</mark> tt t <mark>g</mark> taag ca
64. ChLG3_2_R180294957_C9	AAG AAT <mark>G</mark> GTCC <mark>C</mark> AAAT-	GAGCTGTTTT	- ACCCAAACTGT -	AACATAAATCG		ITTTG AG <mark>G</mark> CAG AA TAA -	-GG CG TT TT TAG TATG TT TT ATG A-	-AAGTTTTTTTTT	G TT TG TAAG CA
65. ChLG3_2_R180294957_C3	AAGAATCGTCCTAAAT-	TAG CTTTTTT	- A <mark>C</mark> OG AAAC T <mark>G</mark> T -	AACATAAATCG	TTC-1	ITTTG AG <mark>G</mark> CAG AATAA -	-GG CG TT TT CAG TA IG TT TT ATG A-	AAGT TTTC <mark>CG</mark>	G TT T <mark>TG</mark> AAG CA
66. ChLG3_2_R180294957_C2	AAGAATCGT <mark>G</mark> CGAAAT-	AAGGT-TTTTT	-ATACAAACTGT-	AA-ATAAAT CGC	TTTTT-1	ITTTG AG <mark>G</mark> CA A AATAA -	-GG CG TT TT CAG TC TG TT TT AT A A-	AAGTTTTCT	GTTTCGAAGCA
67. ChLG3_2_R180294957_C7	AAGAATTGTCCTAAAT-	GAGCCGCTTTT	-ATCTAAAG TAT-	AACATAGATCG	1 <mark>G</mark> C-1	TT <mark>C</mark> IG AGGCGG AA T <mark>T</mark> A -	-GACATTTA-AGTCTGTTGTATAA	-AAGTTT-ACTC	G TTGTGAAG CC
68. ChLG3_2_R180294957_C10	AAGAATTGTCCTAAAT-		-ATCTAAAG TAT-	AACACAAATCA	16C-1	FTCFG AGGCGG AA TAA -		-AAGTTT-ACTC	G TTGTGAAG CCA
69. ChLG3_2_R180294957_C4	AAGAATCGTCATAAAT-		-ATTTAAACTGT-	AACATAGATUG		FTCTG AGGOGS AA TAA -		AAGTTT-ACTC	GTTGTGAAGCC
70. CHLG3 Z K100294937 C1Z				AACATACATO				-AAGITTTTACIC	
				TOCATAAAC		TT IG AGC TAGAATAA		ACACHTTTTTTG	
72. CHLC3 R 100202047 RC C3	ACA ANTACTCC AA ANTA		CCCCCAAATAA	TCCATACAC				ABAGTTTTCTCG	
74 Chi G3 1 R180293225 C7	ACAAATAGTCCAAAATA		GCCCGA AATAA	TGCATAAAC		TTT <mark>CACC-T</mark> ATAATAA-	-GAG TTOTCAG TOTG -TTOTCTA-	AAAGTTTTCTCG-	-TTTTTTTAGCA
75 Chi G3 1 R180203225 C5	ACAAATTGTGCAAAATA	A A T C C T T TC	GTCCGAAATAG	TGCATAAAC		TTT <mark>GAGC-T</mark> AGAATAA-	-GAGE TTOT CAG TOTS -TTOTATC-	GAAGTTATCTCA	TTTTTTAAGCA
76 Chi G6 R180283824 C2	AAAAATTTTTCAAAATC	AATTGATTI	AACAGAACTGG	AAAATAAAT	- CG TT <mark>GT</mark>	ITTCG AC-TAAGC TAA-	- AG OG AT TT CACCT TT TC TACAG C-	GAGATTTTG TTG	TTTTCAGCA
77 Chl G6 R180283824 C9	AAAATTCTTCAAACTT	AA <mark>T TG T</mark> T TT <mark>1</mark>	AACAGAACTGG	AAAATAAAT	- CG TT <mark>GT</mark>	ITT <mark>C</mark> G AC-TAAGC TAA-	- AG CAATTT CACCTTTTC TACAG C-	GAG-TTTTGTTG	TTTTTGAGCA
78. Chl G6 R180283824 C5	AA <mark>AG</mark> AT <mark>TC</mark> T <mark>TC</mark> AAAAT T	AA <mark>T TG T</mark> F TT <mark>1</mark>	AACAGAACTGG	AAAATAAAT	- cg tt <mark>gt</mark> :	ITT <mark>C</mark> G A <mark>C - T</mark> A <mark>AGC</mark> TAA -	- AG CAATTT CACCT TTTC TACAG C-	GAG - TTTTG TTG -	- TT T <mark>T</mark> T <mark>G</mark> AG CA
79. ChLG6 R180283824 C7	AA <mark>AG</mark> AT <mark>TC</mark> T <mark>TC</mark> AAAAT T	AA <mark>T TG T</mark> T TT <mark>1</mark>	AACAGAACTGG	AAAATAAAT	- CG TT <mark>GT</mark> 1	FTT <mark>C</mark> G A <mark>C – T</mark> A <mark>AGC</mark> TAA –	- AG CAATTTCACCTTTCTACAAA-	CGGGTTTTGTG	– TT T <mark>T</mark> T <mark>G</mark> AG CA
80. ChLG6 R180283824 C6	AA <mark>A</mark> AATCGTC <mark>TA</mark> AAAT	TAG T <mark>G T</mark> F TT <mark>7</mark>	TA <mark>CTA</mark> -AAC <mark>CGG</mark>	TTCTIAAAC	-œ <mark>g</mark> tc <mark>t</mark> t	ITTTG A <mark>CA</mark> C <mark>CAG</mark> ATAA -	- AG CG ATTT <mark>T</mark> AAG CT <mark>T</mark> TA TATAG <mark>C</mark>	AAG - TTTCTTG -	– TT T <mark>T</mark> T <mark>G</mark> AG CA
81. ChLG6 R180283824 C8	AAAATCGTCCAAAAT	TAG T <mark>G T</mark> T TT – – <mark>1</mark>	IACTA – AGCTGG	TTCTIAAAC	-CG <mark>G</mark> TC <mark>T</mark>	ITTTG A <mark>CA</mark> C <mark>CAG</mark> A TAA -	- AG CG ATTT TAAG CT <mark>T</mark> TA TATAG C	AAG - TTT <mark>CT</mark> TG -	– TT T <mark>T</mark> T <mark>G</mark> AG CA
82. ChLG6 R180283824 C4	AA <mark>AC</mark> ATCGTCC <mark>A</mark> AAAT	TA <mark>C TG T</mark> T TT <mark>1</mark>	TA <mark>CTA</mark> -AA <mark>T</mark> T <mark>GG</mark> -	TTCTTAAAC	-CG <mark>G</mark> TC <mark>T</mark> T	ITTTG A <mark>TG</mark> C <mark>CAGG</mark> TAA -	- AG CG ATTT CA <mark>AG</mark> CT <mark>T</mark> TA TATAG C	- AAG - TTT <mark>CT</mark> TG -	– TT T <mark>T</mark> I <mark>G</mark> AG CA
83. ChLG6_R180283824_C3	AAAATCGTCCAAAAT	TAG TG T TT 1	TA <mark>CTA</mark> -AACT <mark>GG</mark> -	TTCTIAAAC	- CG TT C <mark>T</mark> I	ITTTG A <mark>CG</mark> C <mark>CAG</mark> ATAA -	– AG TAAT TT CAAGT T <mark>T</mark> TA TT CAG C – -	AAG - TTTT <mark>T</mark> T <mark>T</mark> G -	– TT T <mark>T</mark> T <mark>G</mark> AG CA

h) alignment of cluster 9

	1 10 TGOG CRAACTT TR	20 TTTTTTT -	30 CACCCACTTT	40 ATATCCTGCAATTT	50 TCTTTATT	60	70 I <mark>ARGCC</mark>	80 CCTTOGAT AGG	90 GCCT TOGACTG	100 <u>Taaaa-aaat</u> -	110 - <mark>Catgttosc</mark>	120	130 - <mark>TIGGGI</mark>	140 CCTTAATGAA	150 • • • • • •	160 AAAGATTCTT	TAXGAT	170 TCCCGAT	178 TTC
	T S CAAACI <mark>G</mark> - A G CAAACITTA	TTTTT TTT- JERTJER WRW-	CACCOCCTTT.	ATATCC CCAATTT	TCTTTATT	TTGCAGGAGAT	I-AAGCO	CCTTOGAT GG	GCCT TOGACTG	TA-AA <mark>A</mark> A AAT-	-CAIGTICGO -CAIGTITA	A CAAACAC CCC	TTAGG	CCTTAATAAA	TTTT-	AAAGATTCT I AAAGATTCAI	TAAGATI	FTCCCGAT	TT TT
	CAAACTT TA	TTTTTTTT	CACCCACTTT	ATATCTIGCAATTT	T-TTTATT	TTIGCA CACAGAT	r AAGCC	CCTTOGATAGG	GCCT TOGACIG	TA-AGAAAAT	CATGTT	ACAAAGACCCC	TIGGG/	CCTTAATGAA	TTTTT-	AAAGATTCTT	TAAGAT	FICCOGAT	TT
	T CAAACTT TA	TTTTT TTT-	CACCCACTTT	ATATC T IGCAATTT	T-TTTATT	TTIGCA <mark>CA</mark> AGAT	I-AAGCC	CCTTOGATAGG	GCCTTCGACTG	TA-AGAAAAT-	CAIGTT	acaaa <mark>g</mark> accco	TIGGG	ACCTTAAIGAA:	TTTT	AAAGATTCTI	TAAGATI	ft <mark>t</mark> cogat	ΓT
	OG CAAACATAA		CACCOCCTTT.	ATATOCOGCAATTT	TCTTTATT	FTIGAAAGAGAT!	I-AAGCO	CCTTOGATAGG	GCCT TOGACTG	TA-AGAAAAT	-CAIGTTICO	ACAAACAC CCC	TIGGG	ACCTTAAIGAA	PTTTT-	AAAGATTCTT	TAAAATI	FICCOGAT	fT
	C CAABCTTTA			ATACLU IGLAATTT ATACLU IGLAATTT	-TUTTPATT: -TUTTPATT:	PTRCARGAGAT		CITERAT AGO	GOUTTUGACIG	TA-AAAAAAAT	-CAIGTING -CAIGTING	AUGAACACOCC	TIGGGA	CUTTAAIGAA	6.1.1.1.1. 1.1.1.1.1	CAASATTTTTT	TAASATI TAASATI	FICLUSAT FICCOCS & F	TT TTC
	GCAAACTTTA	TTTTTTT-	CACCONGITT	ATATCCTTCATITT	TTTATT	TIGCARGAGAT	I-AAGCO	CTTTGATAGG	GCCTTOGACTG	TAAAA AAAT	-CA IGTICGO	ACAAACACCCC	TIGGG	TCTTTATGAA	TTTT-	GAAGATTTTT	TAAGATI	FICCOGAT	TTC
	OG CAAACTT TA	TTTTTTTT	CACCC	ATAT <mark>A</mark> CT <mark>T</mark> CA <mark>T</mark> ITT	TTTATT	TTIGCA <mark>R</mark> GAGAT	r-AAGCC	CCTTTGATAGG	GOCT TOGACIG	TAAAA AAAT	CATGTTOGO	IA CAAACAC CCC	TIGGGZ	TCTT TATGAA	TTTT-	GAAGATT	TAAGATT	FICCOGAT	TT
3	G CAAACTT	-TTTT TTT-	CACCC IG ITI	ATATCC T <mark>T</mark> CAATT T	TTTATT.	TIGCAGGAGAT	I-AAGCC	CTTOGATAGG	GCCTTCGACTG	TAAAA AAAT	CATGTTCGC	ACAAACAC CCC	TIGGGZ	ACCTTAATGAA	TTTT	aaagatt <mark>t</mark> t i	TAAGATT	ft <mark>t</mark> cogat	ITC
ţ	ACAAACTTAA	TTTTTTTT-	CACCOTCTTT.	ATATCC TTCAACT T	TTTTATT	PTEGCARGAGAT:	I-AAGCC	CTTOGATAGG	GCCTTOGACIG	TAAAA AAAT	-CATGTTOGO	ACAAACAC CCC		ACCTTAAIGAA:	PTTT-	AAAGATTUTI	TANGATI	FICCOGAT	FTC
;	G CAAACIT TA	TTTTTTTTT	-CACCOLCITI	ATATCC T CAATT T	-TTTTATT	TTIGC AGG AGAT	Г- <u>АА</u>				-CAIGIICGO	ACAAACACCCC	TIGGG	ACCTTAATGAA	CTTTT-	AAAGATTTTT	TAAGATI	FTCCOGAT	TTC
6	OG CAAACTT TA	TTTTTTT	CACCOTTT	ATATCC TTCAATT T	TTTTATT	TIGCAGGAGAT	г- <u>аа</u>			AAT	CATGTTOGO	ACAAACACCCC	TIGGG	ACCTTAATGAA	PTTTT-	AAAGATT <mark>T</mark> FI	TAAGAT	FICCOGAT	TTC
	CG CAAACTT TA	TTTTTTTT-	-CAC <mark>TTT</mark> CTTT	ATATCC T <mark>T</mark> CA <mark>T</mark> FT T	-T <mark>T</mark> ITTATT	TTIGCA <mark>A</mark> GAGAT	r-a <mark>t</mark> sc <mark>i</mark>	I CTT <mark>T</mark> GAT AGG	GCCT T <mark>T</mark> GA T IG	TAAAA-AAAT-	-CAIGTIC <mark>I</mark>	A CAAACAC CC	-TIGGG#	ACCTTAATGAA	TTTT-	AAAG <mark>G</mark> TTCT I	TAAGATT	FICCOGAT	TT
	TG CTAACTT TA	TTTTT TTT-	-CACCITCTT .	ATATCC CT CAATT T	TTTTATT	TTIGCATA AGAT	I-AAGCO	CCTTTGGTAGG	GCCT TTCATIG	TAAAA AAAT	CATGTTTG	G CAAACAC CCC	TIGGG	TCTT CATGAA	TTTT-	AAAGATTCTI	TAAGATI	TTCTOGAT	fT
	CTCAAACTTTA CTCAAACTTTA	debuideb data — - Tata Tata Tata — -	CACTOTCTTT.	ATATOCT TA AATTT ATATOCT TA AATTT	-T TC FTATT. -T TC FTATT.	PTIGC <i>AG<mark>A</mark>AGA<mark>G</mark> PTIGC 200 20 20</i>	I-AAGCO I-AAGCO	CTT UGATAT G CTT UGATAT G	GCTITUGACIG	TAAAACAAAT-	-CATTTUGG -CATTTUGG	ACAAACACCCC	TIGGGA	ACTITAAIGAA.	ն մոն մոն։ Ը. Դ.Դ.Դ.Դ.Դ.–	AAATTTTTTTT	"-AUGATI TAUCATI	PICCOGAT	TT որդ
	CG CAAATTAAT	TTTTTTT-	CACGTTTITT	ATAICCITCAATTT	TCFTATT	TTIGCAGGASAT	I-AAGCO	CTTTGATAGG	GCTICICACIG	TACAA AAAT	-CAIGTICO	ACAAACACCCC	TIGGG	ACCTTAATGAA	TTTT-	AAATATTCTI	TAAGATI	FTCCOGAT	TT
	OG CAAA <mark>G</mark> IT TA	TTTTTTT-	CATCOTTRAC	ATATCC T <mark>T</mark> CAATT T	TTTTATT	GIGCAGGAGAT	I-AAGCC	CCTT <mark>T</mark> GATAGG	GOCT TOGACIG	TAAAA-AAAT-	CATTTCC	ACABACATCCC	TIGGGZ	CTTANGAN	PPTT	TAAATTCTI	TANGAT	FICCOGAT	TT
	CG CAAACTTAA	TTTTTTTT-	-CACTTTCTTT	ATACCCTTCAATAT	-TTTATT	TTIGC AGG AGAT	F-AAGCC	CCTT <mark>T</mark> GAT AG <mark>A</mark>	GCCT TCGACIG	TAAAA AAAT	-CATGTTCC	ACAATCACCC	-TIGGG⊉	CTTTAATGAA	TTTT-	AAAGATTCTI	TAAGATT	PT <mark>T</mark> COGAT	ΓT
•	CG CAAACTTAA	TTTTT TTT-	CACCOCTT T	TACCCTTCAATAT	TTTTATT	TTIGC AGG AGAT	I-AAGCO	CCTTTGATAGA	GCCT TCGACTG	TGAAA-AAAT-	-CATGTTCGO	ACAAATAC TCC	TIGGGZ	ACCTTTATGAA	TTTT	GAAAATTCTT	TAAGATI	TTTCOGAT	fT
3	CC CABACTETA	մահանահանգրություն <mark>։</mark> ԴեՇԴԴԵՇԴՇԴ — –	CAUCUACITY.	APATCC BCARTET	-TTTTTATT - TTTTTATT	PTIGC IGGHGAT		CTTERATING	GOUTTUGACIG	TGAAA AAAT	-CAIGTIGG -CAIGTIGG	ACAAACACCCC	-TIGGG	CTTAAUGAA	ս մահանգե	AAATATICTI AAATATICTI	TAASATI TABCATI	FICULIAT	որդ ՄՄ
6	CG AAAACTT TA	TTTTTTTT-	CACCCACTT	ATATCC TGCAATT T	TTT-ATT	TIGCIGGAGAT	I-AAGC	CTTTGATAGG	GCCT TCGACTG	TGAAA AAAT	-CAIGTICGO	ACAAACACCCC	TIGGG	CCTTAATGAA	TTTT-	AAATATTCTT	TAAGATI	TCCOGAT	TT
7	OG AAAACTT TA	TTTTTTTT	CACCCACTTT	ATATCC TG CAATT T	TTTATT	TTIGC TGGAGAT	I-AAGC	CTT <mark>T</mark> GATAGG	GOCT TOGACIG	TGAAA-AAAT-	CATGTTOGO	A CAAACAC CCC	TIGGG	CTTAAIGAA	TTTT-	aaa <mark>t</mark> attCt 1	TAAGATT	FICCOGAT	TT
9	CG CAAACTT TA	TTTTTTTTT	CACCCACTTT	ATATCCTGCAATTT	-TTTATT	PTIGC TGGAGAT :	F-AAGC	CTTTGAT AGG	GCCT TCG ACTG	TGAAA-AAAT-	CATGTTCGC	A CAAACAC CCC	-TIGGG #	CCTTAAIGAA	TTTT-	AAA <mark>T</mark> ATTCT I	TAAGATT	FICCOGAT	ΓT
2	CG CAAACTTTA	TTTTT TTT-	CACCCACTTT.	ATATCC TGCAATT T	TTTTATT	TTIGC TGGAGAT	I-AAGCO	CCTTEATAGG	GCCT AAGACIG	TGAAA AAAT	-CAIGTICGO	ACAAACAC CCC	TIGGGA	ACCTTAATGAA	TTTT-	AAATATTCTT	TAAGATI	FTCCOGAT	fT
12	CC CARACTETA	ահանահանանան առուղություն։	CACCEACTET	ATATOC ITCAATT T	-TTTTTATT -TTTTATT	PTICC CGAGAT	P-AAGCC	CTTURATAG	GOUTTURACIG	TGAAA AAAT	-CAIGTTOR -CAIGTTOR	ACAAATACOOO	TIGGGA	CCTTANGAR.	սատարարը	AAATATICII AAATATICII	TARSATI	FICEUGAT	diale diale
13	OG CAAACTT TA	TTTTT TTT-	CACCCACTTT	ATATOC TG CAATT T	TTTTATT	TIGC GGAGAT	I-AAGCO	CTTTGATAGG	GCCT TOGACTG	TGAAA-AAAT-	-CAIGTICGO	ACAAATACCCC	TIGGG	ACCTTAATGAA	TTTT-	AAATATTCTI	TAAGATI	TCCOGAT	TT
5	OG CAAACIT TA	TTTTTTTT	CACCCACTTT	ATATCC TTCAATT T	TTTATT	TTIGC TGGAGAT	I-AAGTI	CTT <mark>T</mark> GATAGG	GOCT TOGACIG	TGAAA AAAT	CAIGTI	ACAAACACCCC	TIGGGZ	CTTAAIGAA	TTTT-	aaa <mark>t</mark> attCt 1	TAAGAT	FICCOGAT	TT
8	CG CAAACTT TA	TTTTTTTT	CACCCACTTT	ATATCCTGCAATTT	-TTTATT	FTIGC TGGAGAT	r-AAGCC	CCTT <mark>T</mark> GAT AGG	GCCT TCG ACTG	TGAAA-AAAT-	-CAIGTTIC	A CAAACAC CCC	-TIGGG #	CCTTAAIGAA	PTTTT-	AAA <mark>T</mark> ATTCT I	TAAGATT	FICCOGAT	ΓT
10	CG CAAACTTTA	TTTTT TTT	TCACTCACTTT.	ATATOCTCAATTT	TTTAATT	TTIGC TGGAGAT	I-AAGCO	CCTTTGATAGG	GCCT TCGACTG	TGAAA AAAT	-CAIGTTON	ACAAACAC CCC	TIGGGA	ACCTTAATGAA	TTTT-	AAATATTCTT	TAAGATI	FTCCOGAT	fT
14	US CANACTT TR			ATATOCITCAATTI ATATOCITCAATTI	-TTTTAATT -TTTTAATT	PTICC CCAGAGAT	P-AAGCC	CTTRATAGG	GOUTTUGACI	TGAAA AAAT	-CAIGTTER	ACAAACACCCC	TIGGGA	CCTTAAUGAA CCTTAAUGAA	ս մահահահա- ու քեք ենք ա	AAATATICTI AAATATICTI	TARSATT	FICILISAT	diale diale
•	OG CAAACTT TA	TTTTTT-	CACTCTT	ATATCC TTCAATT T	TT-ATT	TIGCAGGAGAT	I-AAGCO	CTTUGATAGG	GCCTTGACTG	TGAAA-AAAT-	CATGTTOGO	ACAAACACCC	TIGGG	CCTTAATGAA	TTTT-	AAAGATTCTI	TAAGAT	FTCCOGAT	TT
	OG CAAACTT TA	TTTTTTTTT	CACCOTCTT	ATATOC T <mark>T</mark> CAATT T	TTTTART.	TTIGCA <mark>R</mark> GAGAT	r-AAGCC	CCTTOGATAGG	GCCT TOGACTG	TAAAA AAAT	CAIGTI	A CAAACAC CCC	TIGGG	AC <mark>T</mark> ITA <mark>G</mark> IGAA:	TTTT-	AAAGATTCTT	TAAGATT	PICCOGAT	TT
	OG CAAACTT TA	TTTTT TTT	CACCCTCTT	ATATCC T <mark>T</mark> CAATT T	TTTTATT	TTIGCA <mark>A</mark> GAGAT	I-AAGCC	CTTOGATAGG	GCCTTCGACTG	TAAAA-AAAT-	CAIGTT	A CAAACAC CCC	TIGGG	AC <mark>T</mark> ITA <mark>G</mark> IGAA:	TTTTT-	AAAGATTCTI	TAAGAT	FTCCCGAT	IT.
5	G CAAACTT TA	TTTTTTTTT	CACCOTCTTT.	ATATCC TTCAATT T	TTTTART.	PTIGCARGAGAT:	I-AAGCO	CCTTOGAT AGG	GCCT TOGACIG	TAAAA AAAT	CATGTT TA	A CAAACAC CCC	TIGGGI		PTTT-	AAAGATTCTT	TAAGATI	FTCCOGAT	FTC
	CG CAAACTT TA	TTTTT TTT	-CACCOTCTT T	ATATCC T CAATT T	TTTTATT	TTIGCARGARAT'	I-AAGCC	COTTOGAT AGG	GCCT TOGACIG	TAAAA AAAT	-CAIGITI	ACCARCACCCC	TIGGG	ACCTTA <mark>G</mark> IGAA	TTTTT-	AAAGATTCTT	TAAGATI	TCCCGAT	TT
	OG CAAACTT TA	TTTTT TTT	CACCOTTT	ATATCCTCAATTT	TTT-ATT	TTIGCA AGAAAT	-AAGCO	CTTOGATAGG	GCCTTCGACTG	TAAAA-AAAT-	CAIGTI	ACGAACACCCC	TIGGG	ACCTTA <mark>G</mark> TGAA	PTTTT-	AAAGATTCTT	TAAGAT	FICCOGAT	TT
	OG CAAACTT TA	TTTTTTTT	- CACCO <mark>T</mark> CTT T	ATATCC T <mark>T</mark> CAATT T	TTT-ATT	TTIGCA <mark>A</mark> GAAAT	r-AAGCC	CCTTOGATAGG	GCCT TOGACTG	TAAAA-AAAT-	CATGTT	A OG AACAC CCC	TIGGGI	ACCTTA <mark>G</mark> IGAA:	TTTT	AAAGATTCTT	TAAGATT	FICCOGAT	ŦΤ
	CG CAAACTTTA	TTTTT TTT-	CACCCTCTTT.	ATATCCTCAATTT	TTTTATT	TTIGCARGAAAT	I-AAGCC	CCTTOGATAGG	ACCT TOGACTG	TAAAA AAAT	-CACGTTTC	ACCAACAC CCC	TIGGGA	ACCTTAG IGAA:	TTTT-	AAAGATTCTT	TAAGATI	FTCCCGAT	fT
5	G CARACITITA OG CARACITITA	debuicheb deub	-ACCOUNTER	ATATOCITCAATTT ATATOCITCAATTT	-TTTTT-ATT	PTRCARGANAT	r-AAGCC	CTTOSATAGG	GOCT TOGACIG	TAAAA AAAT	-CATGTTE	ACCARCACCCC	CTIGGG2	COTTAC IGAA	b debub de	AAAGATICTI	TARSATT	PRODUCT	TTC 4PT
4	CG CAAACTT TA	TTTTT TTT-	-CACCOTG TT T	ACATCCTTCAATTT	TTTTATT	TIGCAGGAAAT	I-AAGCO	CTTOGATAGG	GCCT TCGACTG	TAAAA AAAT	CAIGTICGO	ACAAACACCCC	TIGGG	CCTTAATGAA	TTTT-	AAAGATTCTT	TAAGATT	TCCCGAT	TT
o i	OG CAAACTT TA	TTTTTTTT	CACCOTCTT	ATAT <mark>A</mark> CT <mark>T</mark> CAATTT	TT-ATT	TTGCAGGAGAT	I-AAGCC	CCTTOGATAGG	GCCT TOGACTG	TAAAA-AAAT-	CATGTTOGO	ACAAACACCCC	TIGGG	CCTTAATGAA	TTTT	AAAGATTCTT	TAAGAT	FICCAGAT	TT
2	OG CAAACTT TA	TTTTTTTTT	-CACCC <mark>T</mark> CTTT	ATAT <mark>A</mark> CT <mark>T</mark> CAATTT	TTTATT	TTIGC AGG AGAT	r-AAGCC	CCTTOGATAGG	GCCT TOGACIG	TAAAA AAAT	CATGTTOGO	IA CAAACAC CCC	TIGGG	CCTTAATGAA	TTTT	AAAGATTCTT	TAAGATT	FICCAGAT	\mathbf{T}
1	CG CAAACTT TA	TTTTT TTT-	-CACCOTCTTT.	ATATCC TTCAATT T	TTTTATT	FTIGCAGAAAGAT	I-AAGCC	CCTTOGAT AGG	GCCT TCGACTG	TAAAA AAAT	-CAIGTICGO	ACAAACAC CCC		ACCTTAATGAA	TTTT-	AAAGATTCTT	TAAGATI	FTCCTGAT	fT.
3	CTTTA		-CACCOLCITY.	ATATOO <mark>GTOC</mark> ATTT	-TTTTATT -TTTTATT	PTIGCAGAAAT	P-AAGCC	CTTORATAG	-TCT TOGACTO	TAAAA AAAT	-CAIGITUSC -CACATTEX	ACAAACACCCC	-TTG C SZ -TTG R GZ	CCTTAATGAA	ի մահեմ եր	AAAGOTTCTT	TARGATI	FICCOGAT	արդը Մար
	CACAAACTTTA	TTTTTTT-	CAATCTCTTT	ATATTCCCCAATTT	TTTTATE	TIGAAGGAGAT	I-AAGCC	ATTOGAT AGG	ACCT TOGACTG	TAAAA AAAT	CATGTTOGO	ACAAACACCCC	TIG AG #	ACCTTAATGAA	TTTT-	AAAGATTCTI	TAAGATT	ACCAGAT	TT
	OG CAAACTTT-	TT TTT	TCACCCACTT T.	ATAT <mark>A</mark> C TG O <mark>G</mark> ATT T	TCTTTATT	TIGCAGGAGAT	I-AAGCC	CCT <mark>CG</mark> GAT AGG	g cct tc <mark>a</mark> ac <mark>c</mark> g	TAAAA AAAT	-CATATTOGO	A CAAACAC CCC	TIGGG	ACCTTAA <mark>C</mark> GAA:	PTTTT-	TTAATTT T -A	CAAGTI	FTC <mark>T</mark> C T AT	TT
	OG CAAACTT T-	TTTTT	CACCCACTTT	ATATAC TGOGATT T	TCTTTATT	TTGCAGGAGAT	r-AAGCC	CCT <mark>OG</mark> GAT AGG	GCCT TCAACCG	TAAAA AAAT	CATGTTOGO	ACAAACACCCC	TIGGGZ	ACCTTAACGAA	PTTTT-	TTAATTTT-A	CAAGTI	FICTCTAT	$\mathbf{r}\mathbf{r}$
	CG CAAACTTTA	T-TTTTT	TCACCCACTTT.	ATATAC IGCGATT T	TCTTTATT	TTIGCAGGACAT:	I-AAGCO	CCTCCCATAGG	GCCT TCAACOG	TAAAA AAAT	-CAIGTICGO	ACAAACAC CCC	TIGGG	ACCTTAACGAA:	CTTTT-	TTAATTTT-A	CAAAGTI	FTCTCTAT	FT
	CG CAAACTETA	.ը_դգրթերը ը	CACCEACTET.	ATATAC IGCOATTT ATATAC IGCOATTT	-TCTTTATT	PTECASGANAT:	T-ARGCC	CTCGAATAGG	GOCT TO ACOS	TAAAA AAAT	-CAIGTTUG	ACAAACACCCC	TIGGGA	CCTTAACAAA	սահանահեր- հերուրդերություն	TRATTER	TAACT	PICECEAT PICECEAT	արդը Մեր
	CG CAAACTT TA	TTTTTTTTT	TCACCCACTTT	ATATACTEC	TCTTTATT	TIGCAGGAGAT	I-AAGCO	CCTOGGATAGG	GCCT TCAACCG	TAAAA AAAT	CAIGTICGO	ACAAACACCCC	TIGGG	ACCTTAACAAA	TTTT-	TTAATTTTT	TAAAGTI	TTCTCCAT	TT
	OG CAAACTTT-		TCACCCACTTT.	ATAT <mark>A</mark> CTGO <mark>G</mark> ATTT	TCTTTATT	TIGCAGGAGAT	r-AAGCC	CCT <mark>CG</mark> GAT AGG	GCCT TC <mark>A</mark> AC <mark>C</mark> G	TAAAA-AAAT-	CATATTOGO	ACAAACACCCC	TIGGG	CCTTAACAAA	TTTT	TT A <mark>AT</mark> TTTT	TAAAGT	FTC <mark>T</mark> CCAT	TT
	CG CAAACTTTA	TTTTTT	TCACCCACTTT.	ATATAC TGOGATT T	TCTTTATT	TTIGC AGG AAAT	I-AAGCC	CCTCCGAT AAG	GCCTTCGACIG	TAAAA-AAAT-	CATATICGO	ACAAAAACCCC	TIGGG	CCTAAAGAA	TTTTT-	TTAATTTT-A	CAAAG TI	FTCTCTAT	ΓT
	CG CAAACTTT-	TT	TATA CCCACTT T.	AIGTCCIGCT	TTTTATT	FTIGCAGAGAT	I-AAGCO	CCTCTGAT AGG	GCCT TCGACTG	TAAAA AAAT	-CATGTTCGC	ACAAACAC CTC	TIGGG	ACCTTAACGAA	TTTTT-	TATTTTTC	TATAG T	FTCTCTAT	r c
	CG CDAACTTTA		CACCEACTER	MEATOURGC-ATTT	TTTTATT.	PTRCAG <mark>A</mark> HJAT	-ARGCC	CULCUSAT AGG	GOUT TUGACIG	TAAAA AAAT	-CAIGTING	ALAAACAC CCC	-TIGGGA	ALL TTARESAR	o dedectedo	T PARTTY PA	TAAA TI	FICEUSAT	1717 1717

Consensus 1. ChLG10 R180276724 C1 2. ChLG9 R180290885RC C9 3. ChLG9 R180290885RC C7 5. ChLG9 R180290885RC C7 5. ChLG9 R180290885RC C7 5. ChLG10 R180278352RC c1 7. ChLG10 R180278352RC c21 9. ChLG10 R180278352RC c23 11. ChLG10 R180278352RC c23 11. ChLG10 R180278352RC c23 11. ChLG10 R180278352RC c24 12. ChLG10 R180278352RC c22 13. ChLG10 R180278352RC c22 14. ChLG10 R180278352RC c22 14. ChLG10 R180278352RC c22 15. ChLG6 R180284753RC C2 16. ChLG6 R180284753RC C2 16. ChLG6 R180284753RC C3 20. ChLG6 R180284753RC C3 20. ChLG6 R180284753RC C3 20. ChLG6 R180284753RC C3 20. ChLG6 R180284753RC C3 20. ChLG6 R180284753RC C3 20. ChLG3 2 R180296940RC C7 22. ChLG3 2 R180296940RC C7 23. ChLG3 2 R180296940RC C2 24. ChLG3 2 R180296940RC C2 25. ChLG3 2 R180296940RC C2 26. ChLG3 2 R180296940RC C3 27. ChLG3 2 R180296940RC C3 28. ChLG3 2 R180296940RC C3 29. ChLG3 2 R180296940RC C4 29. ChLG3 2 R180296940RC C3 30. ChLG3 2 R180296940RC C4 30. ChLG3 2 R180296940RC C6 31. ChLG3 2 R180296940RC C6 32. ChLG3 2 R180296940RC C6 33. ChLG3 2 R180296940RC C1 30. ChLG3 2 R180296940RC C1 30. ChLG3 2 R180296940RC C1 31. ChLG3 2 R180296940RC C1 32. ChLG3 2 R180296940RC C1 33. ChLG3 2 R180296940RC C1 34. ChLG3 2 R180296940RC C1 35. ChLG3 2 R180296940RC C1 36. ChLG3 2 R180296940RC C1 37. ChLG3 2 R180296940RC C1 36. ChLG3 2 R180296940RC C1 37. ChLG3 2 R180296940RC C1 36. ChLG3 2 R180296940RC C1 37. ChLG3 2 R180296940RC C1 36. ChLG3 2 R180296940RC C1 37. ChLG3 2 R180296940RC C1 36. ChLG3 2 R180296940RC C1 37. ChLG3 2 R180296940RC C1 36. ChLG3 2 R180296940RC C1 37. ChLG3 2 R180296940RC C1 36. ChLG3 2 R180296940RC C1 37. ChLG3 2 R180296940RC C1 36. ChLG3 R180278352RC C1 36. ChLG3 R180278352RC C1 36. ChLG9 R180278352RC C1 36. ChLG9 R180278352RC C1 37. ChLG9 R180290631RC C4 49. ChLG10 R180278352RC C1 35. ChLG9 R180290631RC C4 56. ChLG9 R180290631RC C4 56. ChLG9 R180290631RC C4 56. ChLG9 R180290631RC C4 56. ChLG9 R180290631RC C4 56. ChLG9 R180290631RC C1 56. ChLG9 R180290631RC C1 56. ChLG9 R18029063

00. UNLG6_R100209237RU_U3	B CARACITATETITTT CACCOLITITATE SCANTT CONTAINED AND AND AND AND AND AND AND AND AND AN
67. ChLG8_R180289237RC_C7	E CAAACHTAT-THTTTTT CACCOCCTTATATATCGCGAATTT-TCTTTATATTTGCASAGAATTT-AGCCTTCGGCGTCGGAACAACACCGCCTC TIG GACCATAGGAATTTTTTGCCASAGATTTCGCCATTTCGCCATTTGCCGGACCAACACCGCCCTCGGGACCAACACCGCCCTCGGGACCAACACCGCCCCCGGACCAACACCGCCCCCGGGACCAACACCGCCCCCGGGACCAACACCGCCCCCGGACCAACACCGCCCCCGGGACCAACACCGCCCCCGGGACCAACACCGCCCCCC
68. ChLG8_R180289237RC_C15	IS CAAACIT TAT-TITTITICACICOCCTTTATATCOCCCAATTT-TCITTATATTTECREGREGIT-AAGCCIIICGCATASGGCCTTGACIG TAAAA-AAATCAIGIGCCIACCOIC-TIGGGACCTTAAGAATTATT-IITATATTTECREATTTT
69. ChLG8_R180289237RC_C11	G CAAACIT TAT-TITTITITTITTITTITTITATACCCCCTTTATATATATA
70. ChLG8 R180289237RC C13	OG CAAACTETAT-TETTETTETTECACCCCCTETATACTAACCAATETT-TCTTETTECACGAGAGATT-AAGCCTTOGACCETTOGACCETAAAA-AAAT-CATGEGGACCTTAACGAACACCTC-TEGGGACCTTAACGAATETTT-TETATAAAATETTCTCTAACGAATETTT-
71. ChLG8 R180289237RC C9	G CAAACIT TAT-TIT TITE CACCCOCTT TATACTAA CAATIT -TCTTT ATTTTE CAGAGAT T-AAGOCTTQGACTA GEGOCT TGGACTG TAAAA-AAATCATGTQG ACCAACACCTC -TIGGGACCTTAAQAATTTTT TTAACAATTTCTCTAAAATTTCTCTAA
72. Chi G8 R180289237RC C17	G CAAACITEAT-TITTTT CACCCCCTTTATATEC C CAATTT-TCTTTTEC AGAGATT-ANGCCCTCCGATAGGCCTTGACIE TAAA-AAAT CATGTCGAAACACCCC-TIGGGACCTTAAAGAATTTT-TTAAAAAAAAAATTTCCC
73 Chi G8 R180289237RC C19	GE CARACITERAT-TITTTT CACCOCITTATATE COGCARTT TOTTTATTTTEC AGGAGATT AGGCCTTGGACIG TAAAA ARAT CATGTTGGARAACACCOC TTRACACCTTAACAATTTTT TAAAATTTUTE AGGACTTAACAATTTU
74 Chi G9 R180290885RC C6	G CANEDITTAT-TTTTT-CACCEDUCTTATATCO GCAATT-TETTTATTTTECACACACACACACACACACACACACACAC
75 Chi G9 R180290885RC C8	
76 Chi G8 R180289237RC C14	
77 Chi C8 P180289237PC C20	
79 CH CO P18020025710 020	
70. CHICGS KT00230000KC 04	
90 CHICOTO 100270724 03	
00. GILGIU RICUZIO/24 GO	
82. ChLG8_R180289237RC_C16	B CAPITITAT - ITTITI GUCACITTATATU BUCATTT-ULTTATTTIC CRUESATT-AAAL CUTTERTRAGULTUGATIG TAAA-AAA- LATGTUGGAUAALAUUL TIGGGAULTAAISAATTTIT AAASATUUTIGAA ATTUUGATT
63. GILG6 R100269237RC C18	B CARACITIAT HITHT GUCALITIATATU IS CARITI- RITHATITI SCHERARAT FARACUTIARI AGGUT IGAND TARA AAA- TAN DATUGACARACACUC TIJGGACTITARI AATATITI-RITHAATATITI GARAFITI CUGATITI
84. ChLG8_R180289237RC_C8	G CAACIFTAN - FITTING COLOCITATING CAGANITT - FOTTALATTIC CHEMINAL T- AAAC CITTATING CAGANITT - AAAC CITTATING CAGANITT - AAASINTC FITTING CAGANITT
85. ChLG8_R180289237RC_C10	E CARA CETTA - TETTET CCCACETTATATCCCGCAATTT - CATTATETTCCGCAGAGATT - AAAACCCCTTGATHS TAAAA - AAA- TCATGATCGGACAACCCCCC- TTCCGACGTAATGAATTTTT - AAAAATCCTTTAAGATTCCCGCATTT
86. ChLG8_R180289237RC_C12	E CRAACTIN - TITUTI C CCCACTTATATCCTGCARTT TOTTATTTTGC REGREAT T - AAACCCCTTTAT REGEOCT TGA BIS TAAA A AA- TEA TGATGGA CAACCACCCC TTGC RACCATTATATTCT TAAAATTCTTTARGATTTCCCGACTT
87. ChLG8_R180289237RC_C2	TE CARACIT TATITITITA COCACIT TATATOCIE CARIT T-CTITI ATTITIE CAGAAAT T-AAACCCITITAATATOGACIT TGATIC AAAA-AAA-
88. ChLG8_R180289237RC_C4	E CARACITERAT - TTITTE GCCCACITERATATCI GCARTT - TCTTERTTIC AGGAGA - AAGCCCTTEGATE GGCCCTCGATE GAAAA - AAA- TCA IIIIIIIIII GCCCACITERATAA GAATTTTT - AAGATTTTT - AAGATTTTT - AAGATTTTT - AAGATTTTT - AAGATTTTT - AAGATTTTT
89. ChLG8 R180289237RC C6	T. CAAACITTATITTITITIC CCCACITTATATCCIG CAAITT-ICTITATITTIG CAGAGATT-ANGCCCICTGATAIGACGCCTTGATAIG TAAAA AAA-AAA-AAA-ACACCCC-TIGGG TCTTAAIGAATTITT-AAAGATTCTCTAAGATTCCCAAITT
90. ChLG9 R180290631RC C3	T CA <mark>G</mark> ACTT TATTTTTT - CATTCACTT TATATAC TE CAATT T TCTTT ATTTTIE CAEGAS AT T ARGCCCTTCAAT REGECT TO BOIL TARAA A BAT CA TETTOE CAEGACCTT TATATAC TETT A A BATTCTT TAA A BATTCACTT A BATTCACTT A BATTCACTT A BATTCACTT A BATTCACTT A BATTCACTT A BATTCACTT A BATTCACTT A BATTCACTT A BATTCACTT A BATTCACTT A BATTCACTTACTACTACTTACTTACTT A BATTCACTTACTTACTTACTTACTTACTTACTTACTTACT
91. ChLG9 R180290631RC C14	T: CA <mark>G</mark> ACTITATITTTTTT - CATTCACTITATATATCICGCAATITT-TCTITTATITTIGCAGGAGATT-AAGCCCTICAATAGGGCCTTGGACGTAAAA-AAAT-CATGTTGGGACCCTTAATGAATATATCAGAATITTT-AAAGATTTTTAAGATTTT
92. ChLG9 R180290631RC C7	TE CAGACITTATITITTT - CATTCACITTATATA CIG CAGITT - TOTTI ATTITIC CAGAGAT T- ANGOC CITCAAT AGGC CITCAACIG TAAAA - AAAT - CA IGTICGGA CAAGCAC COC - TIG GAACCITTAATATA CIG CAGITT - AAACATTCIT TAAGAT TICCOGATTT
93. ChLG9 R180290631RC C9	T: CA <mark>G</mark> ACTT TATTTTT TT - CATTCACTT TATATCC TO CAATTT - TOTTT ATTTTTC CAG <mark>A</mark> GAT T - AAGC COTTGAA AGGO COTTGA AGGO COTTGA AAA - AAAT - CA TG TOGG A CAA <mark>G</mark> CAC COC - TIG AAACATT TTT - AAAGATCT TTATGACT TTATGACT TA COG A TTT
94. ChLG9 R180290631RC C5	TE CARACTITTTTTTTCACCCACACAC TATATATACTECCAATTT-TCTTTATTTTE DAGAGATT-AAACCCAACGATAGGGCCTTGACIE TAAAA-AAATCATGTTCGACAAACAC CCC-TTAAAGAATTTCT-AAAAATTCTTTAAGATTTT
95. ChLG9 R180290631RC C16	E-CARACITITITITITICACCACECECECECECECECECECECECECECECECECE
96. Chi G9 R180290631RC C12	TO CARACET TO TETTET TO ACCORDING TO CARACET TO CARACET TO TETTET TO TETTETTE TO TETTETTE TO ACCORDING TO A CARACET
97 Chi G9 R180290631RC C18	CARACTENTITETTET CACCER CACAGUA TATATAC TE CARTETT TOTTET ATTETTE AGGEGAT T- ARACCERTAGE ACCERTER AGGECET TO ACCERTE A CALE OF THE
98 Chl G9 R180290631RC C10	G CANACIT TATTITITIT - TRACCCACITI TATATA CIGC ATTIT - TATATTITIC CACAGAT T- AGOC CITIGAT REGOCT TGACES TANAA - AAAT CA IGTIGGA CAACAC CCC - TIG ADACAT TATATA CATTITIT - AAACATTITIT T - AAACATTITITIT - AAACATTITITIT - AAACATTITITIT - AAACATTITITITITITITIC CACATTITITITIC CACATTITITITITIC CACATTITITIC CACATTITITIC CACATTITITIC CACATTITITIC CACATTITITIC CACATTIC CACATTITITITIC CACATTITITIC CATTITITIC CACATTITIC CACATTITIC CACATTITIC CACATTITITIC CACATTITITIC CACATTITIC CACATTIC CACATTIC CACATTIC CACATTIC CACATTIC CACATTIC CACATTIC CACATTIC CACATTIC CACATTIC CACATTIC
99 Chi G3 2 R180296745 C3	
100 Chi G3 2 R180296745 C5	
101 CH G3 2 P180296745 C6	
102 CH C3 2 P180296745 C1	
102. CHLC3_2_R100280745_C1	
103. CHEC3 2 R 100280745 C2	
104. CHLO3 Z K100230/43 C4	
100. CHLC0 Z R100280740 C7	
100. GILG9 R 100291449 GZ	
107. CHLG9 K 100291449 CO	
108. ChLG9_R180291449_C3	TCAACHTATTICAUACHTTUAAAAACACACHT TEIGTTTTUGGAGAATT AAGUCHTURITAAGUTTUGOISTAAAAAAUTGITTTTUGAAAAAACACUT TERGAGUTTAAAAATTTTUTAAAATTTUUTAAA
109. ChLG9_R180291449_C4	TACAAACITTTTATTCACACITTTCGAAACASCACCACITTTGCGCACACAACTTCAAACATTTTCCCCACATT-AASCCCTTCGCTCGACTTCAAACATCTTTGCACACCACCCC-TECAACCACCCCC-TECAACCACCACCTTAATTTTTCCTAACTTTTCCCCACTTT
110. ChLG9_R180291449_C8	TACAAACITTTITTTCACACITTTCGAACHCCCCTTTTCGCHCHARGTTCCCTATTTTCCCAACITTTCCCTATTTTCCCAACITTTCCCTATTTTCCCTATTTTCCCAACITTTCCCTATTTTTCCCTATTTTTCCCTATTTTCCCTATTTTCCCTATTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTCCCTATTTTTT
111. ChLG9_R180291449_C7	TACAAACTTTTTTTTCACCACCTTTCCAACAGCAGTTT IGIGTTTTTCGCCAGAGATT ARGCCCTTCATT REGCCTTGACIG TAAAAAAT T-CGITTTGGCCAAACACCCCC TAGGGACCTTAATACATATTTITCCTAAAGTTTTCCCTAAGGTTCCCGGAGAAAAA
112. ChLG9_R180291449_C5	E CAAACTTTTTTTTCACCACCTTCCCAAACAGCACTTT-IGTTTGGTAGGAGATT-AAGCCCTGCAATAGGGCTTGGACGGTAAAAAAT-T-CGIGTTCAGACAAACACCCC-TAGGGACCTTAATACATATTT-AAAATTTCCCTAATAC
113. ChLG9_R180291449_C9	TE CAAACITTTITTTCACCACCITCCCAAACAE CACITT-ICOTTATITTIGC AGGAGATT-AAGOC CICCAAAGGGGCCTIGGACIG TAAAAAAT-TCGIGTIGGACAAACACOCC-TAE AGACUTTAATACATATTT-AAAAATITTCCCTAAAGACUTC-CTA
114. ChLG9_R180291449_C1	TTTTTTT CACCCCCTTCCCAACACACCACCACCTT TAL-TATTTTACACAGAGATT ABSOCCTCCAATAGGGCCTTTGGACGACAGACACCCCC TAGGGACCTTAATACATACATACTT TAAAAGTTTCCCTAAGGCCTTAGGGACCAGACACCCCC TAGGGACCTTAATACATACTT TACATACTTTACCACAGAGACACCCCC
115. ChLG9_R180291450RC_C4	T: TAAADITTAT-TTTT- — TAGCOTCTT COCAAACASCACTT - TCTTTATTAAAGGAGAT C TT-CCCCTTCAATAGGGACT TT-ATDIC CCAAAAAAAAA — CA IGTTTAAACCAAACACDCC-TAFGGACCTTAAGGTATTTTTAAAA
116. ChLG9 R180291450RC C7	TACAANGITTTITTTTACCTOCITICCCAAACHECAGUITT-TCTTTATITTIGARAAGATC-ADAGCCITTTGACAGACCTTTGACGACCITAGCAGACCCC-TAGGGACCITAAGSTATTTIGARAAAGACTCC-TAGGGACCITAAGSTATTTIGARAAAGACTCC
117. ChLG9 R180291450RC C2	TTITAT CACCTTTIT CCCAAACAACACCACCACCACACAACAACAACACACAC
118. ChLG9 R180291450RC C6	TE CANCET ANTITUTE - CACTOCCUT COCARACARTT - TOTTANTITE CACAGATA CAACUUT CACAGATA ACTOR CACAACACUT - TA ISTITE SACAACUUC - TRESSACUUT AAGAATT - COTTANTANT - TOTTE CACAACUUC - TRESSACUUT AAGAATT - COTTANTANT - TOTTE CACAACUUC - TRESSACUUT AAGAAU
119. ChLG9 R180291450RC C3	T: CANGITANGTITTT- CACTOCITICEANCH:C-TT-TTTTTANGA-FOTOTANAGATE AD: ACCTOCAN AGGCCTTT: ACGCCTTT: ACGCACCAAAACCCCC TR: GGACCTTAACAACTTTANGA-FOTOTANAGATTTTTCAAAAGATE
120. ChLG9_R180291450RC_C5	CONVENTION AND A CONCEPTION AND A CARCA-CONT THE TABLE AND A CARCA-CONT AND A CARCA-CONTACT AND A CARCACON A CARC

i) alignment of cluster 10



Supplementary Figure 4.2.3. Alignments of all cloned fragments obtained by PCR. **a)** Clones obtained with primers kl1_F and kl1_R; **b)** Clones obtained with primers kl2_F and kl2_R; **c)** Clones obtained with primers kl3_F and kl3_R; **d)** Clones obtained with primers kl4_F and kl4_R; **e)** Clones obtained with primers kl5_F and kl5_R; **f)** Clones obtained with primers kl7_F and kl7_R; **g)** Clones obtained with primers kl8_F and kl8_R; **h)** Clones obtained with primers kl9_F and kl9_R; **i)** Clones obtained with primers kl10_F and kl10_R

a) Clones obtained with primers kl1_F and kl1_R

Consensus	1 10	20 TGGATTCCGC kl1_R	30 CCGGTCATTC	40 TACGTTAGAA	50 ACACTCAATT	CTAAGGACAT	70 GACCCCGAAT	80 AGAAAGAAAA	90 TAATGAAGAC	100 TATTTGGTTT	110 CGATAAATTT	120 TGACAAGGCT
1. CI1_3 2. CI1_5 3. CI1_4 4. CI1_7 5. CI1_2 Consensus	TTTGCAAATT TTTGCAAATT TTGCAAATT TTGCAAATT TTTGCAAATT 130 AAATTTTTGC	TGGATTCCGC TGGATTCCGC TGGATTCCGC TGGATTCCGC TGGATTCCGC GGATATTTC	CCGGTCATTC CCGGTCATTC CCGGTCGTTT CCGGTCATTC CCGGTCATTC CGAACGGTTA	TACGTCAGAA TACGTCGAA TACGTCAGAA TACGTTAGAA TACGTTGGAA 160 GTCGTAGCCG	ACACTTAATT ACACTCAATT ACACTCAATT ACACTCAATT CACTCAATT 166 ACTTAA	CTTAGGACAT CTAAGGACAT CTAAGGACAT CTAAGGACAT CTAAAGACAA	ACCCAGAAT ACCCCGAAT GACCCCGAAT GACCCCGAAT GACCCCGAAT	AGAAAGAAAA AGAAGGAAAA AGAAAGAAAA AGIIIIGGAAAA AGIIIIAAAAA	TAATGAAGAC TAATGAAGA TAATGAACAC TAATGAAGAC TAATGA <mark>G</mark> GA <mark>A</mark>	TATTTGGTGT TATTTGGTTC TATTTGGTTT TATTTGGTTT GATTTAATGT	ССАТАААТТТ САТАААТТТ ССАТАААТТТ ССАТАААТТТ ССАТАААТТТ ССАТАААТТТ	TGAC G AGGCT TGAC G AGGCT T <mark>AG</mark> CAA AT CT TGACAAGGCT TGACAAGGCT
1. Cl1_3 2. Cl1_5 3. Cl1_4 4. Cl1_7 5. Cl1_2	AAATTTTTGC AAATTTTTGC AAATTTTTGC AAATTTTTGC AAATTTTTGC	CGATATTTTC CGATATTTTC CGATATTTTC CGATATTTTC CGATATTTT	CGAACGGTTA CGAACGGTTA CGAACGGTTA CGAACGGTTA AGAACGGTT	GTCGTAGCCG GTCGTAGCCG GTCGTAGCCG GTCGTAGCCG	ACTTA ACTTA ACTTA ACTTA							

b) Clones obtained with primers kl2_F and kl2_R



c) Clones obtained with primers kl3_F and kl3_R



d) Clones obtained with primers kl4_F and kl4_R

Consensus	1 10 20 TGTTTGTTCCAGEGAATTCT kl4_F	30 40 GCGGCTCATTTTCTGTATTA	50 60 CACCGTCATTTTTACARCAC	70 80 TACCTCACTCGANGACTTAG	90 100 TTAAAAATTTATTTATTAAC	110 120 TTGAAAAATGGTGGATGCGC
1. Cl4 1 2. Cl4 4 3. Cl4 5 4. Cl4 6 5. Cl4 7 6. Cl4 8 Consensus	TGTTTGTTCCAGTGAATTCT GTTTGTTCCAGTGAATTCT TGTTTGTTCCAGTGAATTCT TGTTTGTTCCAGTGAATTCT CAGTGAATTCT TGTTTGTTCCAGTGAATTCT 130 140 CAAATTAWTWATTAAAAAAT	GCGGCTCACTTTCTGTATTA GCGGCTCATTTTCTGTATTA GCGGCTCATTTTCTGTATTA GCGGCTCATTTTCTGTATTA GCGGCTCATTTTCTGTATTA GCGGCTCATTTTCTGTATTA GCGGCTCATTTTACATATA	CACCGCCATTTTTGCAACAC CACCGCCATTTTTGCAACAC CAACGTCTTTTTACAGCAC CAACGTCTTTTTACAGCAC IACCATTTTTACAGCAC IACCATTTTTACAGGAA 170 178 GICGIAGAGCAAAAACGGA kl4_R	ACCTCACTCGACGACTTG ACCTCACTCGACGACTTAG TACGTCACTCCAGGACTTAG TACGTCACTCCAGGACTTAG TGCCTCACTCCAGGACTTAG TGCCTCACTCGAAGACTTAG TAAAAGTTTAAAATTTTTCG	TCAGCAATTTATTATTATTAAC TAGGAAATTTATTTATTAAC TTAAAAAATTATTTATTAAAC TTAAAAAATTATTATTAAAC CTAA-AATTTATGTATTAAC CCTAAAATTTATGGGTAGTCAT	TTGAAAAATGGTGGATGCGC TTGAAAAATGGTGGATGCGC TTGAAAAATGGTGGATGCGC TTGAAAAATGGTGGATGCGC TTGAAAAATGGTGGATGCGI TTG TC- -ATAGTGGA <mark>AAATT</mark>
1. Cl4 1 2. Cl4 4 3. Cl4_5 4. Cl4_6 5. Cl4_7 6. Cl4_8	CGAAMTAATAATTWAAAAAA CGAAMTAATAAATTWAAAAAA CAAATTAWTWATTAAAAAMT CAAATTAWTWATTAAAAAMT CAAATTAWTWATTAAAAAAT TWAWTWAATAAAAAAAT	ТТАТААСТСАААААСТАААА ТТАТААСТСАААААСТАААА ТТАТААСТСАААААСТАААА ТТАТААСТСАААААСТАААА ТТАТААСТСАААААСТАААА ТСАТААСТССАААААСТАААА	GTCGTAGAGCAA GTCGTAGAGCAAAACGGA GTCGTAGAGCAAAACGG GTCGTAGAGCAAAACGG GTCGTAGAGCAAAACGGA GTCGTAGAGCAAAACGG			

e) Clones obtained with primers kl5_F and kl5_R



f) Clones obtained with primers kl7_F and kl7_R

Consensus	1 10 GAGGCCGICC GGCCTTTG	30 ST TTCATTTTA TTATATTC	GA AACITITICAA AAAAATT kl7_R	60 70 GGA AAATTTGCAT AA	AACATTGTC TTAGATTGAC ki7_F	CCATGCGTCG AATAGATTC	110 120 GO ATGCAGCAAT
1. CL7_AC2a 2. Cl7_AC1 3. Cl7_AC2 4. Cl7_AC5b 5. Cl7_AC5c 6. Cl7_AC10a 7. Cl7_AC4a 8. Cl7_AC12b 9. Cl7_AC12b 9. Cl7_AC12a 10. Cl7_AC12a 10. Cl7_AC16 13. CL7_AC4 14. Cl7_AC12 15. Cl7_AC5a 16. Cl7_AC12 17. Cl7_AC1a	GAGGCCGTCC GGCCTTTG GAGGCCGTCC GGCCTTTG GGGGCCGTCC GGCCTTTG GAGGCCGTCC GGCCTTTG GAGGCCGTCC GGCCTTTG GAGGCCGTCC GGCCTTTG GAGGCCGTCC GGCCTTTG GAGGCCGTCC GGCCTTG GAGGCCGTCC GGCCTTG GAAGCCGTCC GGCCTTG GAAGCCGTCC GGCCTTG GAAGCCGTCC GGCCTTG GAAGCCGTCC GGCCTTG GAAGCCGTCC GGCCTTG GAAGCCGTCC GGCCTTG GAAGCCGTCC GGCCTTG GAAGCCGTCC GGCCTTG GAAGCCGTCC GGCCTTG	GT TTTCATTTA TTATATTC GT TTTCATTTA TTATATTC GT TTTCATTTA TTATATTC GT TTTCATTTA TTATATTC GT TTTCATTTA TTATATTC GT TTTCATTTA TTATATTC GT TTTCATTTA TTAATTC GT TTTCATTTA TTAATTC GT TTTCATTTA TTATATTC GT TTTCATTTA TTATATTC GT TTTCATTTA TTATATTC GT TTTCATTTA TTATATTC GT TTTCATTTA TTATATTC GT TTTCATTTA TTATATTC GT TTTCATTTA TTATATC GT TTTCATTTA TTATATC GT TTTCATTTA TTATATC GT TTTCATTTA TTATATC GT TTTCATTTA TTATATC GT TTTCATTTA TTATATC GT TTTCATTTA TTATATC	GA AACTTTTCAA AAAAAT GA AACTTTTCAA AAAAATT GA AACTTTTCAA AAAAATT	GGA AAACTTGCAT AA GGA AAACTTGCAT AA GGA AAATTTGCAT AA	AACATTGTC TTAGATTGAC AACATTGTC TTAGATTGAC	CCATGCGTCG GATAGAIN CATGCGTCG AATAGAIN CCATGCGTCG AATAGAIN	GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT GC ATGCAGCAAT
Consensus	TACCTTCATT TTTGCAGG	AG AACATTACGA AACCTTGC	TT TACAACATAA TAAAAAA				
1. CL7_AC2a 2. CI7_AC1 3. CI7_AC2 4. CI7_AC5b 5. CI7_AC5c 6. CI7_AC10a 7. CI7_AC10a 7. CI7_AC10a 8. CI7_AC12b 9. CI7_AC12b 9. CI7_AC12a 10. CI7_AC12 11. CL7_AC16 13. CL7_AC16 13. CL7_AC12 15. CI7_AC5a 16. CI7_AC17 17. CI7_AC1a	TACCTTCATT TTTGAAGG TACCTTCATT TTTGAGG GACCTTCATT TTTGCAGG TACCTTCATT TTTGCAGG	AG AACATTACGA AACCTTGC AG AACATTACGA AACCTTGC AG AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGG AACCTTGC AACATTACGA AACCTTGC G AACATTACGG AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC G AACATTACGA AACCTTGC	ТТ -АСААСАТАА ТАААААА ТТ ТАСААСАТАА ТАААААА ТТ ТАСААСАСАА ТАААААА ТТ ТАСААСАСАА ТАААААА ТТ ТАСААСАСАА ТАААААА ТТ ТАСААСАСАА ТАААААА ТТ ТАСААСАСАА ТАААААА	TT TT TT TT TT TT TT TT TT TT TT TT TT			

g) Clones obtained with primers kl8_F and kl8_R

Consensus	1 10 TGAATCGTCC	GAAATIAAGCC kl8_R	30 GTTTTCAATC	40 AAACTATTAC	50 ATTATTTGTT	6 TTTT <mark>-GAGCC</mark>	70 TGAATAAGAA	80 GTTTTCAGTG	90 TGTTTTATAC	100 AAATTTACTC	110 GTTTCTAAAA	AAGGAATCGT
1. CI8_6 2. CI8_8 3. CI8_4 4. CI8_3 5. CI8_1 6. CI8_2 7. CI8_5 8. CI8_7 Consensus	GAATCGTCC GAATCGTCC GAATCGTCC TGAATCGTCC TGAATCGTCC TGAATCGTCC GAATCGTCC GAATCGTCC CCGAATTAGG kl8_F	GAAATAAGCC GAAATAAGCC GAAATAAGCC GAAATAAGCC GAAATAAGCC GAAATAAGCC GAAATAAGCC GAAATAAGCC GAAATAAGCC GAAATAAGCC GAAATAAGCC	GTTTTCAATC GTTTTCAATC GTTTTCAATC GTTTTCAATC GTTTTCAATC GTTTTCAATC GTTTTCAATC GTTTTCAATC GTTTTCAATC 150 -AAAGTATA	АААСТАТТАС АААСТАТТАС АААСТАТТАС АААСТАТТАС АААСТАТТАС АААСТАТТАС АААСТАТТАС АААСТАТТАС АААСТАТТАС 160 АСАТСАТТТА	ATTATTTGTT ATTATTTGTT ATTATTTGTT ATTATTTGTT ATTATTTGTT ATTATTTAT	TTTT-GAGCC TTTT-GAGCC TTTT-GAGCC TTTT-GAGCC TTTT-GAGCC TTTTIGGCC TTTTIGGCC TTTTIGGCC TTTTIGGCC 14 CCAGAATAAC	TGAATAAGAA TGAATAAGAA TGAATAAGAA TGAATAAGAA TGAATAAGAA TGTATAAGAA TGTATAAGAA TGTATAAGAA TGTATAAGAA TGTATAAGAA 0 GCGTTTTCAG	GTTTTCAGTG GTTTTCAGTG GTTTTCAGTG GTTTTCAGTG GTTTTCAGTG GTTTTCAATC GTTTTCAATC GTTTTCAATC	TGTTTTATAC TGTTTTATAC TGTTTTATAC TGTTTTATAC TGTTTTATAC TGTTTTATAC TGTTTTATAC TGTTTTATAC	AAATTTACTC AAATTTACTC AAATTTACTC AAATTTACTC AAATTTACTC AAGTTTACTC AAGTTTACTC AAGTTTACTC	GTTTCTAAAA GTTTCTAAAA GTTTCTAAAA GTTTCTAAAA GTTTCTAAAA GTTTCTA TGC GTTTCTA TGC	AAGGAATCGT AAGGAATCGT AAGGAATCGT AAGGAATCGT AAGGAATIGT AAGGAATIGT AAGGAATIGT AAGGAATIGT
1. CI8_6 2. CI8_8 3. CI8_4 4. <u>CI8_3</u> <u>5. CI8_1</u> 6. CI8_2 7. CI8_5 8. CI8_7	CCGAATTAGG CCGAATTAGG CCGAATTAGG CCGAATTAGG CCGAATTAGG CCGAATTAGG CCGAAATAAG CCGAAATAAG	CTATTTTTAT CTATTTTTAT CTATTTTTAT CTATTTTTAT CTATTTTTAT CATTTTAT CATTTTAT CATTTTAT	C-AAAGTATA C-AAAGTATA C-AAAGTATA C-AAAGTATA CAAAGTATA CAAAGTATA CAAAGTAGA	ACATCATTTA ACATCATTTA ACATCATTTA ACATCATTTA ACATCATTTA ACATTATTTG ACATTATTTG ACATTATTTG	TTTTTTTGGG TTTTTTTGGG TTTTTTTGGG TTTTTTT	CCAGAATAAG CCAGAATAAG CCAGAATAAG CCAGAATAAG CCAGAATAAG CCAGAATAAG CCAGAATAAG CCAGAATAAG	GCGTTTTCAG GCGTTTTCAG GCGTTTTCAG GCGTTTTCAG GCGTTTTCAG GCGTTTTCAG GCGTTTTCAG GCGTTTTCAG	A A A A				

h) Clones obtained with primers kl9_F and kl9_R

Consensus	1 10 TTCATGTTCG	20 GACAAACACC	30 CCTT <mark>GGGACC</mark>	40 TTAATGAATT	50 TTTAAAGGTT	60 CTTTAAGATT	70 TCCC <mark>GATTTC</mark>	80 GCAAACTTTA	90 TNTTTTTC	100 ACCCTCTTTA	110 TATTCYGCAA	120 TTTTCTTT-A
1. CI9_1 2. CI9_3 3. CI9_4 4. CI9_2	TTCATGTTCG TTCATGTTCG TTCATGTTCG TTCATGTTCG 130	GACAAACACC GACAAACACC GACAAACACC GACAAACACC 140	CCTTGGAACC CCTTGGGACC CTTGAGACC CCTGTGGGACC 150	TTAATGAATT TTAATGAATT TTAATGAATT TT Q ATGAATT 160	TTTAAAGATT TTTAAAGGTT TTTAAAGGTT TTT TTAAT TT 170	CTTTAAGATT CTTTAAGATT CTTTAAGATT TATAAAGTT 180	TCCCGATTTC TCCCGATTTC TCCCAAATTC GCTCTATTTC 190	GCAAACTTTA GCAAACTTT- GCAAACTTTA GCAAACTTTA 200	TT TTTTTC TTTTTC T TTTTTC TTTTTTC TTTTTTTC 210	ACCCACTTTA ACCCCCTTTA ACTCTCTTTA ATCCTTCTTA	TATACIGCGA TATCCOGCAA TATTCITTAI TAATTCGCAA 230	TTTTCTTT-A TTTTCTTT-A TTTTTTTTA TTTTCTTT-A 240
Consensus	TTTTTGCAGG	AGATTAAGCĊ	CTTICGATIAGG	GCCTTCGACT kl9_	GTAAAAAAAAT R	CATGTTCRGA kl9_F	CWAACACCCC	TYRGRACYTT	AAMGAATTTT	TWWARWTTYT	WTAAARTTTY	YCKATTTYGC
1. CI9_1 2. CI9_3 <u>3. CI9_4</u> 4. CI9_2	TTTTTGCAGG TTTTTTGCAGG TTTTTTGCAAG TTTTTTGCAGG 250	AGATTAAGCC AGATTAAGCC AGATTAIGCI AGATTAAGCC 260	CTTCGATAGG CTTCGATAGG CTTGATAGG CTCCAATAGG 270	GCCTTCGACT GCCTTCGACT GCCTTCGACT GCCTTCGACT 280	СТАААААА СТАААААААТ СТСААААААТ АТАААААА 290	CATGTTC A GA CATGTTC <mark>G</mark> GA 300	CTAACACCCC CAAACACCCC 310	TTAGAACOTT TOGGGACOTT 320	AA <mark>A</mark> GAATTTT AACGAATTTT	TAAAGATTOT TTAATTTOT 331	TAAAATTTC ATAAAGTTTT	CC <mark>G</mark> ATTT O GC ICIATTTIIGC
Consensus	AAACTYTTTT	TTTCACCCMM	TKTATATCCY	GCAWITTTC	NTATTWIGY	ARGARATTAA	GCYCWTCGAT	AGGGCCTTCG	ACTGTAAAAA	A		
1. CI9_1 2. CI9_3 3. CI9_4 4. CI9_2	AAACT <mark>B</mark> ITTT AAACTCITTT	TTTCACCCCC TTTCACCCAA	T T TATATCCC T <mark>G</mark> TATATCC T	GCAAITTTCT GCATITTTCT	<mark>G</mark> TATTT <mark>A</mark> IG <mark>T</mark> -TATTTTIGC	A <mark>G</mark> GA A ATTAA A A GA <mark>G</mark> ATTAA	GCCCATCGAT GCCCTTCGAT	AGGGCCTTCG AGGGCCTTCG	АСТСТААААА АСТСТААААА	A		

i) Clones obtained with primers kl10_F and kl10_R

Consensus	1 10 Egacagatiti ggaatee ki10_F	20 30 TTA GACCATTTTA	40 C <mark>G TTAGA TAG</mark>	50 ACATATGCAT	60 <mark>GGCCTATTTT</mark>	70 TTT <mark>GG TTA TT</mark>	80 <mark>G TGAGC TCGA</mark>	90 T <mark>GATTTTTTT</mark>	100 TGTTGGCAGA	110 TAAG TAAA T-	120 - TAAAATTTT
1. Cl10_3 2. CL10_9 3. Cl10_1 4. Cl10_5 5. Cl10_4 6. CL10_8 7. Cl10_2 8. Cl10_6 9. Cl10_7	TGACAGATTT GGAATCC TGACAGATTT GGAATCC TGACAGATTT GGAATCC TGACAGATTT GGAATCC TGACAGATTT GGAATCC TGACAGATTT GGAATCC GACAGATTT GGAATCC TGACAGATTT GGAATCC	TTA GACCATTTA TTA GACCATTTA TTA GACCATTTA TTA GACCATTTA TTA GACCATTTA TTA GACCATTTA TTA GACATTA TTA GACAATTA TTA GACAATATA	CG TTAGA TAG CG TTAGA TAG CG TTAGA TAG CG TTAGA TAG CG TTAGA TAG CG TTAGA TAG CG TTAGA TAG CG TTAGA TAG CG TTAGA TAG	ACA TA TGCA T ACA TA TGCA T ACA TA TGCA T ACA TA TGCA T ACA TA TGCA T ACA TA TGCA T ACA TA TGCA T GC TTA TTTT TCA TA TTTT	GGCC TA TTTT GGCC TA TTTT GGCC TA TTTT GGCC TA TTTT GGCC TA TTTT GGCC TA TTTT AA TG CA AA TT AA C TT TAA TT	TTTGG TTA TT TTTGG TTA TT TTTGG TTA TT TTTGG TTA TT TTTGG TTA TT TTTGG TTA TT TT-GG TTA TT TT -GG TTA TT	G TGAGC TCGA G TGAGC TCGA G TGAGC TCGA G TGAGC TCGA G TGAGC TCGA G TGAGC TCGA A TGA IC T IGG G TGA I T T GA	TGA TTTTTTT TGA TTTTTTT TGA TTTTTTT TGA TTTTTTT TGA TTTTTTT TGA TTTTTTTT TGA TTTTTTTT TGA TTTTTTT GA TTTTTTT	TG TTGGCAGA TG TTGGCAGA TG TTGGCAGA TG TTGGCAGA TG TTGGCAGA TG TTGGCAGA - A CTG C TGG C TA TTGG TAG C	TAAG TAAA T- TAAG TAAA T- TAAG TAAA T- TAAG TAAA T- TAAG TAAA T- TAAG TAAA T- TAAG TAAA T- T NG G TA TTAA TA G G T G A TTAA	- TAAAA TTTT - TAAAA TTTT - TAAAA TTTT - TAAAA TTTT - TAAAA TTTT - TAAAA TTTT - TAAAA TTTT - TAAAA TTTT - TAAAA TTTT - TAAAA TTTT - TAAAA TTTT
Consensus	130 GGCCAAGTTG TCTTATT	140 15 T <mark>GG TTTATTTTGC</mark>	0 160 I <mark>GCAATTTTTA</mark>) 170 TTT <mark>GATTGTT</mark>	180 <u>ATTAAATTTT</u>	GCACAGGAAC) 200 AGATAATT <mark>GG</mark>	210 TTAA T AAAAA) 220 GGGCTAAAAG	230 TCGTTTTA-	240 - CGAG TAGA T
1. CI10_3 2. CL10_9 3. CI10_1 4. CI10_5 5. CI10_4 6. CL10_8 7. CI10_2 8. CI10_6 9. CI10_7	GGCCAAGTTG TCTTATT GGCCAAGTTG TCTTATT GGCCAAGTTG TCTTATT GGCCAAGTTG TCTTATT GGCCAAGTTG TCTTATT GGCCAAGTTG TCTTATT GGCCAAGTTG TCTTATT AAGCALGTTA TUTTATT	TGG TTTATTTTGC TGG TTTATTTTGC TGG TTTATTTTGC TGG TTTATTTTGC TGG TTTATTTTGC TGG TTTATTTTGC TGG TTTATTTTGC CGA ATCATTT-GC CAT ATCATTT-GC	GCAA TTTTTA GCAA TTTTTA GCAA TTTTTA GCAA TTTTTA GCAA TTTTTA GCAA TTTTTA ACAA TTTTGA	TTTGA TTG TT TTTGA TTG TT TTTGA TTG TT TTTGA TTG TT TTTGA TTG TT TTTGA TTG TT TTTGA TTG TT CTCA TG TC TCCA TTG T	A TTAAA TTTT A TTAAA TTTT A TTAAA TTTT A TTAAA TTTT A TTAAA TTTT A TTAAA TTTT A TTAAA TTTT C C A AAA TTTT A C A AAA TTTT	GCACAGGAAC GCACAGGAAC GCACAGGAAC GCACAGGAAC GCACAGGAAC GCACAGGAAC GCACAGGAAC GCICAGAAAI GICGAGAAAI	AGA TAA TTGG AGA TAA TTGG AGA TAA TTGG AGA TAA TTGG AGA TAA TTGG AGA TAA TTGG AGA TAA TTG AGA TAA TTG AGA TAA TTG AGA TAA TAA	ТТАА ТААААА ТТАА ТААААА ТТАА ТААААА ТТАА ТААААА ТТАА ТААААА ТТАА ТААААА ТТАА ТААААА ААСА ДААААА САССТААААА	GGGC TAAAAG GGGC TAAAAG GGGC TAAAAG GGGC TAAAAG GGGC TAAAAG GGGC TAAAAG GGGC TAAAAG GGGC TAAAAG GGGC TAAAAG	TCGTTTTTA - TCGTTTTTA - TCGTTTTTA - TCGTTTTTA - TCGTTTTTA - TCGTTTTTA - TCGTTTTTA - TCGTTTTTA - TCGTTTTTAGA	- CGAG TAGA T - CGAG TAGA T - CGAG TAGA T - CGAG TAGA T - CGAG TAGA T - CGAG TAGA T - CGAG TAGA T - CGAG TAGA T - CGAG TAGA T - CGAG TAGA T
Consensus	CTATTTTTAT GTTTTAA	AAT TTTTGGTAAA	CTGTAAAAAC	TGAAGA TGAC	– – <mark>CG TA TTTT</mark>	GICTAA TA IC	TCCAAAACTA kl10	CGAATCGTAG)_R	A		
1. CI10_3 2. CL10_9 3. CI10_1 4. CI10_5 5. CI10_4 6. CL10_8 7. CI10_2 8. CI10_6 9. CI10_7	CTATTTTTAT GTTTTAA CTATTTTTTAT GTTTTAA CTATTTTTAT GTTTTAA CTATTTTTAT GTTTTAA CTATTTTTAT GTTTTAA CTATTTTTAT GTTTTAA CTATTTTTAT GTTTTAA TTTTTTTTTTTTTTTTTTTTTT	AAT TTTTGG TAAA AAT TTTTGG TAAA AAT TTTTGG TAAA AAT TTTTGG TAAA AAT TTTTGG TAAA AAT TTTTGG TAAA AAT TTTTGG TAAA AAT TTTTGG TAGA GAA TTTTTTTTGA	C TG TA NAAAC C TG TAAAAAC C TG TAAAAAC C TG TAAAAAC C TG TAAAAAC C TG TAAAAAC C TG TAAAAAA T TAAAAAA	TGAAGA TGAC TGAAGA TGAC TGAAGA TGAC TGAAGA TGAC TGAAGA TGAC TGAAGA TGAC TTAAATCGAC TAAATTAAC	C G T A T T T T C G T A T T T T C G T A T T T T C G T A T T T T C G T A T T T T C G T A T T T T T C A T A T T T C C A C A T T T C	$ \begin{array}{c} \mathbf{G} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{A} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{G} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{A} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{G} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{A} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{G} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{A} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{G} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{A} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{G} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{A} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{G} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{A} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{G} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{A} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{G} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{A} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{G} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{G} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{A} \ \mathbf{G} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{G} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{A} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{C} \ \mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}$	ТССААААС ТА ТССААААС ТА ТССААААС ТА ТССААААС ТА ТССААААС ТА ТССААААС ТА ТССААААС ТА ТССААААС ТА	CGAA TCG TAG CGAA TCG TAG	A		

Supplementary Figure 4.2.4. Table with data for 7 clusters (marked uCl) obtained by TRF and array clustering on unassembled reads of *T. castaneum* genome. TRF arameters were the same as for the 10 chromosomes.

	Number of arrays	The average length of monomers (bp)		
uCl1=Cl5	34	309-339		
Cul2=Cl7	27	179-183		
uCl3=Cl1	13	166-167		
uCl4=Cl2	13	169-175		
uCl5	11	222-224		
uCl6=TCAST	9	331-337		
uCl7	9	107-125		

Supplementary Figure 4.2.5. Position of insertion sites of all arrays in Cluster 1 compared to consensus sequence. a) position of first 30 pb of each of the arrays in Cluster 1. b) position of last 30 pb of each of the arrays in Cluster 1.



Supplementary Figure 4.2.6. Position of insertion sites of all arrays in Cluster 2 compared to consensus sequence. a) position of first 30 pb of each of the arrays in Cluster 2. b) position of last 30 pb of each of the arrays in Cluster 2.



Supplementary Figure 4.2.7. Position of insertion sites of all arrays in Cluster 3 compared to consensus sequence. a) position of first 30 pb of each of the arrays in Cluster 3. b) position of last 30 pb of each of the arrays in Cluster 3.



Supplementary Figure 4.2.8. Position of insertion sites of all arrays in Cluster 4 compared to consensus sequence. a) position of first 30 pb of each of the arrays in Cluster 4. b) position of last 30 pb of each of the arrays in Cluster 4.



Supplementary Figure 4.2.9. Position of insertion sites of all arrays in Cluster 5 compared to consensus sequence. a) position of first 30 pb of each of the arrays in Cluster 5. b) position of last 30 pb of each of the arrays in Cluster 5.



Supplementary Figure 4.2.10. Position of insertion sites of all arrays in Cluster 7 compared to consensus sequence. a) position of first 30 pb of each of the arrays in Cluster 7. b) position of last 30 pb of each of the arrays in Cluster 7.



Supplementary Figure 4.2.11. Position of insertion sites of all arrays in Cluster 8 compared to consensus sequence. a) position of first 30 pb of each of the arrays in Cluster 8. b) position of last 30 pb of each of the arrays in Cluster 8.



Supplementary Figure 4.2.12. Position of insertion sites of all arrays in Cluster 9 compared to consensus sequence. a) position of first 30 pb of each of the arrays in Cluster 9. b) position of last 30 pb of each of the arrays in Cluster 9.



Supplementary Figure 4.2.13. Position of insertion sites of all arrays in Cluster 10 compared to consensus sequence. a) position of first 30 pb of each of the arrays in Cluster 10. b) position of last 30 pb of each of the arrays in Cluster 10.



REFERENCES

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